

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:04:52 ; Search time 154.853 Seconds
(without alignments)
8075.738 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccategccaaggagatcgagct 22

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pri.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	48	6	I43071 Sequence 54
2	22	100.0	127	6	CQ816525 Sequence
3	22	100.0	127	6	CQ816526 Sequence
4	22	100.0	139	6	CQ816524 Sequence
5	22	100.0	161	6	CQ816521 Sequence
6	22	100.0	161	6	CQ816522 Sequence
7	22	100.0	231	6	CQ816511 Sequence
8	22	100.0	231	6	CQ816512 Sequence
9	22	100.0	231	6	CQ816513 Sequence
10	22	100.0	270	1	AF445452 Mycobacte
11	22	100.0	270	1	AF445453 Mycobacte
12	22	100.0	270	1	AF445454 Mycobacte
13	22	100.0	271	1	DL6487 Mycobacteri
14	22	100.0	325	6	CQ816510 Sequence
15	22	100.0	381	1	AF271096 Mycobacte
16	22	100.0	381	1	AF271346 Mycobacte
17	22	100.0	386	1	AY943196 Mycobacte
18	22	100.0	397	1	AY341032 Mycobacte

19	22	100.0	397	1	AY341033	Mycobacte
20	22	100.0	409	1	AY943197	Mycobacte
21	22	100.0	417	1	AY856440	Mycobacte
22	22	100.0	418	1	AY911398	Propionib
23	22	100.0	421	1	AY255477	Mycobacte
24	22	100.0	422	1	DQ124111	Mycobacte
25	22	100.0	424	1	AF547802	Mycobacte
26	22	100.0	424	1	AF547803	Mycobacte
27	22	100.0	424	1	AF547804	Mycobacte
28	22	100.0	424	1	AF547805	Mycobacte
29	22	100.0	424	1	AF547806	Mycobacte
30	22	100.0	424	1	AF547807	Mycobacte
31	22	100.0	424	1	AF547808	Mycobacte
32	22	100.0	424	1	AF547809	Mycobacte
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36	22	100.0	424	1	AF547814	Mycobacte
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39	22	100.0	424	1	AF547818	Mycobacte
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41	22	100.0	424	1	AF547820	Mycobacte
42	22	100.0	424	1	AF547821	Mycobacte
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48	22	100.0	424	1	AF547827	Mycobacte
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ALIGNMENTS

RESULT 1

I43071
LOCUS I43071 Sequence 54 from patent US 5631130. 48 bp DNA linear PAT 07-OCT-1997
DEFINITION I43071
ACCESSION I43071
VERSION I43071.1 GI:2468315
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Leckie,G.W., Davis,A.H., Semple-Facey,I.E., Manlove,M.T. and Solomon,N.A.
TITLE Materials and methods for the detection of Mycobacterium tuberculosis
JOURNAL Patent: US 5631130-A 54 20-MAY-1997;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN

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Db 8 CCATGCCCAAGGAGATCGAGCT 29

RESULT 2
LOCUS CQ816525
DEFINITION Sequence 17 from Patent WO2004029296.
ACCESSION CQ816525
VERSION CQ816525.1 GI:48144801
KEYWORDS
SOURCE
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 17 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 17 CCATGCCCAAGGAGATCGAGCT 38

RESULT 3
LOCUS CQ816526
DEFINITION Sequence 18 from Patent WO2004029296.
ACCESSION CQ816526
VERSION CQ816526.1 GI:48144802
KEYWORDS
SOURCE
ORGANISM Mycobacterium simiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 18 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
FEATURES
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QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 17 CCATGCCCAAGGAGATCGAGCT 38

RESULT 4
LOCUS CQ816524
DEFINITION Sequence 16 from Patent WO2004029296.
ACCESSION CQ816524
VERSION CQ816524.1 GI:48144800
KEYWORDS
SOURCE
ORGANISM Mycobacterium chitae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 16 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 17 CCATGCCCAAGGAGATCGAGCT 38

RESULT 5
LOCUS CQ816521
DEFINITION Sequence 13 from Patent WO2004029296.
ACCESSION CQ816521
VERSION CQ816521.1 GI:48144797
KEYWORDS
SOURCE
ORGANISM Mycobacterium xenopi
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 13 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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Db 17 CCATGCCCAAGGAGATCGAGCT 38

RESULT 6
LOCUS CQ816522
DEFINITION Sequence 14 from Patent WO2004029296.
ACCESSION CQ816522
VERSION CQ816522.1 GI:48144798
KEYWORDS
SOURCE
ORGANISM Mycobacterium gallinarum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
```

AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 14 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
 FEATURES
 source
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 Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 7
 CQ816511
 LOCUS 231 bp DNA linear PAT 03-JUN-2004
 DEFINITION Sequence 3 from Patent WO2004029296.
 CQ816511
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium simiae
 Mycobacterium simiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
 AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 3 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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 Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 8
 CQ816512
 LOCUS 231 bp DNA linear PAT 03-JUN-2004
 DEFINITION Sequence 4 from Patent WO2004029296.
 CQ816512
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium smegmatis
 Mycobacterium smegmatis
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
 AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 4 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
 FEATURES
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 Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 9
 CQ816513
 LOCUS 231 bp DNA linear PAT 03-JUN-2004
 DEFINITION Sequence 5 from Patent WO2004029296.
 CQ816513
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium intracellulare
 Mycobacterium intracellulare
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 avium complex (MAC).

REFERENCE
 AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 5 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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 Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 10
 AF445452
 LOCUS 270 bp DNA linear BCT 06-DEC-2001
 DEFINITION Mycobacterium simiae B Hsp65 (hsp65) gene, partial cds.
 AF445452
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium simiae
 Mycobacterium simiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
 AUTHORS El Sahly,H.M., Septimus,E., Soini,H., Septimus,J., Musser,J.M. and
 Graves,E.A.
 TITLE Mycobacterium simiae pseudo-outbreak resulting from contaminated
 hospital water supply in Houston, Texas
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 270)
 AUTHORS El Sahly,H.M., Septimus,E., Soini,H., Septimus,J., Musser,J.M. and
 Graves,E.A.
 TITLE Direct Submission
 JOURNAL Submitted (08-NOV-2001) Pathology, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
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 Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 11
LOCUS AF445453 270 bp DNA linear BCT 06-DEC-2001
DEFINITION Mycobacterium simiae A Hsp65 (hsp65) gene, partial cds.
ACCESSION AF445453
VERSION AF445453.1 GI:17386083
KEYWORDS
SOURCE
ORGANISM Mycobacterium simiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 270)
Graviss, E.A.
Mycobacterium simiae pseudo-outbreak resulting from contaminated
hospital water supply in Houston, Texas
Unpublished
JOURNAL
REFERENCE
AUTHORS El Sahly, H.M., Septimus, E., Soini, H., Septimus, J., Musser, J.M. and
Graviss, E.A.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Pathology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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VLAQALVKEGLRNVAAGANPLGLKRGIEKAVEKVTETLLKSAKQVE"
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Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 13
LOCUS D16487 271 bp DNA linear BCT 20-AUG-1997
DEFINITION Mycobacterium intracellulare DNA for 65kD antigen, partial cds.
ACCESSION D16487 D16488 D16489 D16490
VERSION D16487.1 GI:2339963
KEYWORDS 65kD antigen; PCR.
SOURCE Mycobacterium intracellulare
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
avian complex (MAC).
1 (bases 1 to 271)
Yamazaki, T. and Nakamura, R.M.
Identification of Mycobacterium intracellulare by a polymerase
chain reaction using species-specific primers
Tuber. Lung Dis. 76 (4), 330-335 (1995)
7579315
2 (bases 1 to 271)
Yamazaki, T.
Direct Submission
JOURNAL Submitted (18-JUN-1993) Toshio Yamazaki, National Institute of

```

Health, Dept. Bacteriology; 1-23-1 Toyama, Shinjuku-ku, Tokyo 162,
Japan (Tel:03-5285-1111ex.2277), Fax:03-5285-1163)

FEATURES

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1. .271
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43. .62
66. .70
83. .>271
/function="heat shock protein"
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/product="65kD antigen"
/protein_id="BAA21830.1"
/db_xref="GI:2339964"
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complement(262. .271)

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Query Match 100.0%; Score 22; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 241 CCATGCCCAAGGAGATCGAGCT 262

RESULT 14

LOCUS CQ816510 325 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 2 from Patent WO2004029296.
ACCESSION CQ816510
VERSION CQ816510.1 GI:48144786
KEYWORDS
SOURCE Mycobacterium terrae
ORGANISM Mycobacterium terrae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1
Koeksalan,O.K. and Kocagoez,T.
Molecular size markers for species identification of mycobacteriae
Patent: WO 2004029296-A 2 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)

FEATURES

source
1. .325
/organism="Mycobacterium terrae"
/mol_type="unassigned DNA"
/db_xref="taxon:1788"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

Db 17 CCATGCCCAAGGAGATCGAGCT 38

RESULT 15

LOCUS AF271096 381 bp DNA linear BCT 13-NOV-2000
DEFINITION Mycobacterium ulcerans putative 65 kDa heat shock protein (groEL)
gene, partial cds.

ACCESSION

AF271096

VERSION

AF271096.1 GI:11139537

KEYWORDS

Mycobacterium ulcerans

SOURCE

Mycobacterium ulcerans

ORGANISM

Mycobacterium ulcerans
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 381)
Stinear,T.P., Jenkin,G.A., Johnson,P.D. and Davies,J.K.
Comparative genetic analysis of Mycobacterium ulcerans and
Mycobacterium marinum reveals evidence of recent divergence
J. Bacteriol. 182 (22), 6322-6330 (2000)

JOURNAL

PUBMED 11053375

REFERENCE

2 (bases 1 to 381)

AUTHORS

Stinear,T.P., Jenkin,G.A., Johnson,P.D.R. and Davies,J.K.

TITLE

Direct Submission

JOURNAL

Submitted (16-MAY-2000) Microbiology, Monash University, Wellington
Rd, Clayton, VIC 3168, Australia

FEATURES

source

1. .381
/organism="Mycobacterium ulcerans"
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gene

CDS

Query Match 100.0%; Score 22; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 2 CCATGCCCAAGGAGATCGAGCT 23

RESULT 16

LOCUS AF2711346 381 bp DNA linear BCT 03-NOV-2000
DEFINITION Mycobacterium marinum putative GroEL (groEL) gene, partial cds.
ACCESSION AF2711346
VERSION AF2711346.1 GI:9255843
KEYWORDS
SOURCE Mycobacterium marinum

ORGANISM

Mycobacterium marinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 381)

AUTHORS

Stinear,T.P., Jenkin,G.A., Johnson,P.D. and Davies,J.K.

TITLE

Comparative genetic analysis of Mycobacterium ulcerans and
Mycobacterium marinum reveals evidence of recent divergence

JOURNAL

PUBMED 11053375

REFERENCE

2 (bases 1 to 381)

AUTHORS

Stinear,T.P., Jenkin,G.A., Johnson,P.D.R. and Davies,J.K.

TITLE

Direct Submission

JOURNAL

Submitted (24-MAY-2000) Microbiology, Monash University, Wellington
Rd, Clayton, VIC 3168, Australia

FEATURES

source

1. .381
/organism="Mycobacterium marinum"
/mol_type="genomic DNA"
/strain="NCIC 2275"
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<1..>397
/gene="hsp65"
/codon_start=1
/transl_table=11
/product="Hsp65"
/protein_id="AAQ20897.1"
/db_xref="GI:33519164"
/translation="GVSTAKIELEDPEYKIGAEIVKVEAKTDDVAGDGTATVLA
QALVREGLRNVAAGANPLGKRGIEKAVEATRLSTAKEVTEKEQIAATAGISAGD
QSIGDLIAEALDKVNEGVIIVESNTFGL"

ORIGIN
Query Match 100.0%; Score 22; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
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DB 8 CCATCGCCAAGGAGATCGAGCT 29
|||||

RESULT 20
AY943197
LOCUS
DEFINITION
Mycobacterium canariense strain CIP 107998 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AY943197
VERSION
AY943197.1 GI:61200474
KEYWORDS
Mycobacterium canariense
SOURCE
Mycobacterium canariense
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 409)
AUTHORS
Pichat,C. and Flandrois,J.P.
DIRECT SUBMISSION
Submitted (24-FEB-2005) Dynamique Des Populations Bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
JOURNAL
Location/Qualifiers
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1. .409
/organism="Mycobacterium canariense"
/mol_type="genomic DNA"
/strain="CIP 107998"
/db_xref="CIP 107998"
/db_xref="taxon:228230"
/note="type strain of Mycobacterium canariense"
<1..>409
/gene="hsp65"
<1..>409
/gene="hsp65"
/codon_start=2
/transl_table=11
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/protein_id="AAQ39805.1"
/db_xref="GI:61200475"
/translation="GVSTAKIELEDPEYKIGAEIVKVEAKTDDVAGDGTATVLA
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QSIGDLIAEALDKVNEGVIIVESNTFGL"

ORIGIN
Query Match 100.0%; Score 22; DB 1; Length 409;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCATCGCCAAGGAGATCGAGCT 22

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Db
9 CCATCGCCAAGGAGATCGAGCT 30
|||||

RESULT 21
AY856440/c
LOCUS
DEFINITION
Mycobacterium sp. WJ-3 65 kDa heat shock protein (hsp65) gene,
partial cds.
ACCESSION
AY856440
VERSION
AY856440.1 GI:57235702
KEYWORDS
Mycobacterium sp. WJ-3
SOURCE
Mycobacterium sp. WJ-3
ORGANISM
Mycobacterium sp. WJ-3
Bacteria; Actinobacteridae; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 417)
AUTHORS
Wang,Y., Ogawa,M., Miyamoto,H. and Taniguti,H.
TITLE
Isolate novel Mycobacterium spp. from contaminant soil
JOURNAL
Unpublished
2 (bases 1 to 417)
REFERENCE
Wang,Y., Ogawa,M., Miyamoto,H. and Taniguti,H.
AUTHORS
Direct Submission
TITLE
Submitted (14-DSC-2004) Microbiology, School of Medicine,
University of Occupational and Environmental Health, Japan, 1-1,
Iseigaoka, Yahata-nishi-ku, Kitakyushu, Fukuoka 807-8555, Japan
JOURNAL
Location/Qualifiers
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/db_xref="GI:57235703"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
|||||
DB 413 CCATCGCCAAGGAGATCGAGCT 392
|||||

RESULT 22
AY911398
LOCUS
DEFINITION
Propionibacterium acnes 60kDa heat shock protein (hsp60) gene,
partial cds.
ACCESSION
AY911398
VERSION
AY911398.1 GI:59381105
KEYWORDS
Propionibacterium acnes
SOURCE
Propionibacterium acnes
ORGANISM
Propionibacterium acnes
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium.
REFERENCE
1 (bases 1 to 418)
AUTHORS
Fardel,G.F. and Flandrois,J.P.F.
TITLE
Direct Submission
JOURNAL
Submitted (28-JAN-2005) Dynamique des Populations Bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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    /protein_id="AAW84290.1"
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  /translation="VSIKAEIELDDPYEKIGALVKEVAKTDDVAGDGTATVLAQ
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ORIGIN
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 5 CCATGCCCAAGGAGATCGAGCT 26
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RESULT 23
AY255477 421 bp DNA linear BCT 29-DEC-2004
LOCUS Mycobacterium canariense Hsp65 (hsp65) gene, partial cds.
DEFINITION
ACCESSION AY255477
VERSION AY255477.1 GI:30267690
KEYWORDS
SOURCE Mycobacterium canariense
ORGANISM Mycobacterium canariense
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Jimenez,M.S., Campos-Herrero,M.I., Garcia,D., Luquin,M., Herrera,L.
and Garcia,M.J.
TITLE Mycobacterium canariense sp. nov
PUBMED 15388736
JOURNAL Int. J. Syst. Evol. Microbiol. 54 (Pt 5), 1729-1734 (2004)
REFERENCE
AUTHORS Jimenez,M.S., Campos-Herrero,M.I., Garcia,D., Luquin,M., Herrera,L.
and Garcia,M.J.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2003) Bacteriologia (Mycobacterias), Instituto de
Salud Carlos III (CNM), Carretera Majadahonda-Pozuelo Km 2,
Majadahonda, Madrid 28220, Spain
FEATURES
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gene
CDS

QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 9 CCATGCCCAAGGAGATCGAGCT 30
    |||||

RESULT 25
AF547802 424 bp DNA linear BCT 18-JAN-2005
LOCUS Mycobacterium abscessus strain CIP 104536 65 kDa heat shock protein
DEFINITION
ACCESSION AF547802
VERSION AF547802.1 GI:27502168
KEYWORDS
SOURCE Mycobacterium abscessus
ORGANISM Mycobacterium abscessus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
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Best Local Similarity	100.0%;	Pred. No. 53;	Mismatches	0; Indels
Matches	22;	Conservative	0;	Gaps

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 /protein_id="AA017447.1"
 /db_xref="GI:27502171"
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1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 10 CCATCGCCCAAGGAGATCGAGCT 31

AF547804 424 bp DNA linear BCT 18-JAN-2005
 Mycobacterium aichiense strain DSM 44147 65 kDa heat shock protein
 (hsp65) gene, partial cds.

AF547804
 AF547804.1 GI:27502172
 Mycobacterium aichiense
 Mycobacterium aichiense
 Bacteria: Actinobacteria; Actinobacteridae: Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 1 (bases 1 to 424)
 Devulder, G., de Montclos, M.P. and Flandrois, J.P.
 A multigenic approach to phylogenetic analysis using the genus
 Mycobacterium as a model
 Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
 15653890
 2 (bases 1 to 424)
 Devulder, G., Pichat, C. and Flandrois, J.P.
 Direct Submission
 Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
 Location/Qualifiers
 1. .424
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 /db_xref="GI:27502173"
 /translation="GVSIKAEIELEDPVEKIGAEIVKEVAKTDDVAGDGTATATVLA
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 QTIQDLIAEAMDKVGNEGVITVEESNTFGIQLLETGMR"

1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 10 CCATCGCCCAAGGAGATCGAGCT 31

AF547804
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 gene
 CDS

ORIGIN
 Query Match
 Best Local Similarity
 Matches
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 0; Mismatches
 0; Indels
 0; Gaps
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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ORIGIN
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 0; Mismatches
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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1 CCATCGCCCAAGGAGATCGAGCT 22
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ORIGIN
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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ORIGIN
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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1 CCATCGCCCAAGGAGATCGAGCT 22
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ORIGIN
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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ORIGIN
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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ORIGIN
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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ORIGIN
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1 CCATCGCCCAAGGAGATCGAGCT 22
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AF547804
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ORIGIN
 Query Match
 Best Local Similarity
 Matches
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 0; Mismatches
 0; Indels
 0; Gaps
 0;

1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 10 CCATCGCCCAAGGAGAT

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RESULT 28
AF547805
LOCUS
DEFINITION
Mycobacterium alvei strain CIP 103464 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION
AF547805
VERSION
AF547805.1 GI:27502174
SOURCE
Mycobacterium alvei
ORGANISM
Mycobacterium alvei
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
DEVULDER,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
15653890
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
ORIGIN
Location/Qualifiers
1..424
/organism="Mycobacterium alvei"
/mol_type="genomic DNA"
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QALVKEGLRNVAAGNPLKRGIEKAVEKVTLLKSAKDVETKEQIAATAGISAGD
QSIGDLIAEAMDKVNEGVTVEESNTFGLQLETEGMR"

Query Match 100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCAAGGAGATCGAGCT 22
|||||
Db 10 CCATCGCCAAGGAGATCGAGCT 31

gene
CDS

RESULT 29
AF547806
LOCUS
DEFINITION
Mycobacterium asiaticum strain DSM 44297 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION
AF547806
VERSION
AF547806.1 GI:27502176
SOURCE
Mycobacterium asiaticum
ORGANISM
Mycobacterium asiaticum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
DEVULDER,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
15653890
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
ORIGIN
Location/Qualifiers
1..424
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Query Match 100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCAAGGAGATCGAGCT 22
|||||
Db 10 CCATCGCCAAGGAGATCGAGCT 31

gene
CDS

RESULT 29
AF547806
LOCUS
DEFINITION
Mycobacterium austroafricanum strain CIP 105395 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AF547807
VERSION
AF547807.1 GI:27502178
SOURCE
Mycobacterium austroafricanum
ORGANISM
Mycobacterium austroafricanum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
DEVULDER,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
15653890
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
ORIGIN
Location/Qualifiers
1..424
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QALVKEGLRNVAAGNPLKRGIEKAVEKVTLLKSAKDVETKEQIAATAGISAGD
QSIGDLIAEAMDKVNEGVTVEESNTFGLQLETEGMR"

Query Match 100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCAAGGAGATCGAGCT 22
|||||
Db 10 CCATCGCCAAGGAGATCGAGCT 31

gene
CDS

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PUBMED
15653890
REFERENCE
2 (bases 1 to 424)
DEVULDER,G., Pichat,C. and Flandrois,J.P.
Direct Submission
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES
Location/Qualifiers
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/organism="Mycobacterium asiaticum"
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Db 10 CCATCGCCAAGGAGATCGAGCT 31

RESULT 30
AF547807
LOCUS
DEFINITION
Mycobacterium austroafricanum strain CIP 105395 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AF547807
VERSION
AF547807.1 GI:27502178
KEYWORDS
SOURCE
Mycobacterium austroafricanum
ORGANISM
Mycobacterium austroafricanum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
DEVULDER,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
15653890
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES
Location/Qualifiers
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CDS

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RESULT 31

AF547808
 LOCUS
 DEFINITION
 Mycobacterium avium subsp. avium strain CIP 104244 65 kDa heat
 shock protein (hsp65) gene, partial cds.

AF547808

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Myobacterium avium subsp. avium
 Mycobacterium avium subsp. avium
 Bacteria; Actinobacteria; Actinobacteridae; Mycobacterium; Mycobacterium
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 avium complex (MAC)

REFERENCE

AUTHORS

TITLE

A multi-gene approach to phylogenetic analysis using the genus

Myobacterium as a model

Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

15653890

2 (bases 1 to 424)

Devulder, G., Pichat, C. and Flandrois, J.P.

Direct Submission

Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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RESULT 32

AF547809

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Myobacterium avium subsp. paratuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

avium complex (MAC)

REFERENCE

AUTHORS

TITLE

A multi-gene approach to phylogenetic analysis using the genus

Myobacterium as a model

Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

15653890

2 (bases 1 to 424)

Devulder, G., Pichat, C. and Flandrois, J.P.

Direct Submission

Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

Location/Qualifiers

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RESULT 33

AF547810

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Myobacterium avium subsp. silvaticum

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

avium complex (MAC)

REFERENCE

AUTHORS

TITLE

A multi-gene approach to phylogenetic analysis using the genus

Myobacterium as a model

Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

15653890

2 (bases 1 to 424)

Devulder, G., de Montclos, M.P. and Flandrois, J.P.

A multi-gene approach to phylogenetic analysis using the genus

Myobacterium as a model

AF547809
 Mycobacterium avium subsp. paratuberculosis strain CIP 103963 65
 kDa heat shock protein (hsp65) gene, partial cds.

AF547809
 AF547809.1 GI:27502182

Myobacterium avium subsp. paratuberculosis
 Mycobacterium avium subsp. paratuberculosis
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 avium complex (MAC)

REFERENCE

AUTHORS

TITLE

A multi-gene approach to phylogenetic analysis using the genus

Myobacterium as a model

Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

15653890

2 (bases 1 to 424)

Devulder, G., Pichat, C. and Flandrois, J.P.

Direct Submission

Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

Location/Qualifiers

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JOURNAL      Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED       15653890
REFERENCE    2 (bases 1 to 424)
AUTHORS      Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE        Direct Submission
JOURNAL      Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
              Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
              Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 35
AF547811
LOCUS
DEFINITION      Mycobacterium bohemicum strain CIP 105811 65 kDa heat shock protein
ACCESSION       AF547811
VERSION         AF547811.1 GI:27502186
KEYWORDS
SOURCE          Mycobacterium bohemicum
ORGANISM        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium
                tuberculosis complex.
REFERENCE       1 (bases 1 to 424)
AUTHORS         Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE           A multigene approach to phylogenetic analysis using the genus
                Mycobacterium as a model
JOURNAL         Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED         15653890
AUTHORS         Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE           Direct Submission
JOURNAL         Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
                Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
                Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 34
AF547811
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DEFINITION      Mycobacterium bohemicum strain CIP 105811 65 kDa heat shock protein
ACCESSION       AF547811
VERSION         AF547811.1 GI:27502186
KEYWORDS
SOURCE          Mycobacterium bohemicum
ORGANISM        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE       1 (bases 1 to 424)
AUTHORS         Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE           A multigene approach to phylogenetic analysis using the genus
                Mycobacterium as a model
JOURNAL         Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED         15653890
AUTHORS         Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE           Direct Submission
JOURNAL         Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
                Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
                Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 35
AF547813
LOCUS
DEFINITION      Mycobacterium bovis strain CIP 105234 65 kDa heat shock protein
ACCESSION       AF547813
VERSION         AF547813.1 GI:27502190
KEYWORDS
SOURCE          Mycobacterium bovis
ORGANISM        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                tuberculosis complex.
REFERENCE       1 (bases 1 to 424)
AUTHORS         Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE           A multigene approach to phylogenetic analysis using the genus
                Mycobacterium as a model
JOURNAL         Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED         15653890
AUTHORS         Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE           Direct Submission
JOURNAL         Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
                Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
                Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Query Match      100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 38
AF547817 424 bp DNA linear BCT 18-JAN-2005
LOCUS Mycobacterium celatum strain CIP 106109 65 kDa heat shock protein
DEFINITION (hsp65) gene, partial cds.
ACCESSION AF547817
VERSION AF547817.1 GI:27502198
KEYWORDS
SOURCE Mycobacterium celatum
ORGANISM Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigenic approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATGCCCAAGGATCGAGCT 31

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DEFINITION Mycobacterium chelonae strain CIP 104535 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION  AF547818
VERSION     AF547818.1
KEYWORDS   Mycobacterium chelonae
SOURCE     Mycobacterium chelonae
ORGANISM   Mycobacterium chelonae
REFERENCE  1 (bases 1 to 424)
AUTHORS   Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE     A multigenic approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL   Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBLISHED 15653890
REFERENCE  2 (bases 1 to 424)
AUTHORS   Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE     Direct Submission
JOURNAL   Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGATCGAGCT 22
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Db 10 CCATGCCCAAGGATCGAGCT 31

RESULT 40
AF547819
LOCUS      AF547819.1 GI:27502202
DEFINITION Mycobacterium chitae strain CIP 105383 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION  AF547819
VERSION     AF547819.1
KEYWORDS   Mycobacterium chitae
SOURCE     Mycobacterium chitae
ORGANISM   Mycobacterium chitae
REFERENCE  1 (bases 1 to 424)
AUTHORS   Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE     A multigenic approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL   Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBLISHED 15653890
REFERENCE  2 (bases 1 to 424)
AUTHORS   Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE     Direct Submission
JOURNAL   Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATGCCCAAGGATCGAGCT 31

RESULT 41
AF547820
LOCUS      AF547820.1 GI:27502204
DEFINITION Mycobacterium chlorophenolicum strain CIP 104189 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION  AF547820
VERSION     AF547820.1
KEYWORDS   Mycobacterium chlorophenolicum
SOURCE     Mycobacterium chlorophenolicum
ORGANISM   Mycobacterium chlorophenolicum
REFERENCE  1 (bases 1 to 424)
AUTHORS   Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE     A multigenic approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL   Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBLISHED 15653890
REFERENCE  2 (bases 1 to 424)

```

AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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DB 10 CCATGCCCAAGAGATCGAGCT 31
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RESULT 42
AF547821
LOCUS AF547821 424 bp DNA linear BCT 18-JAN-2005
DEFINITION Mycobacterium chubuense strain CIP 106810 65 kDa heat shock protein (hsp65) gene, partial cds.
ACCESSION AF547821
VERSION AF547821.1 GI:27502206
KEYWORDS Mycobacterium chubuense
SOURCE Mycobacterium chubuense
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE Devulder, G., de Montclos, M.P. and Flandrois, J.P.
AUTHORS A multigene approach to phylogenetic analysis using the genus
TITLE Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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FEATURES

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gene

CDS

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 53;
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DB 10 CCATGCCCAAGAGATCGAGCT 31
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RESULT 43

AF547822

LOCUS AF547822

DEFINITION

AF547822 424 bp DNA linear BCT 18-JAN-2005

Myobacterium confluentis strain CIP 105510 65 kDa heat shock

protein (hsp65) gene, partial cds.

ACCESSION AF547822

VERSION AF547822.1 GI:27502208

KEYWORDS Mycobacterium confluentis

SOURCE Mycobacterium confluentis

ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

Myobacterium as a model

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

PUBMED 15653890

REFERENCE 2 (bases 1 to 424)

AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,

Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

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ORIGIN

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DB 10 CCATGCCCAAGAGATCGAGCT 31
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RESULT 44

AF547823

LOCUS AF547823

DEFINITION

AF547823 424 bp DNA linear BCT 18-JAN-2005

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DEFINITION Mycobacterium conspicuum strain CIP 105165 65 kDa heat shock
ACCESSION AF547823
VERSION AF547823.1 GI:27502210
SOURCE Mycobacterium conspicuum
ORGANISM Mycobacterium conspicuum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 424)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
JOURNAL Mycobacterium as a model
PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 45
AF547824
LOCUS AF547824
DEFINITION Mycobacterium cookii strain CIP 105396 65 kDa heat shock protein
ACCESSION AF547824
VERSION AF547824.1 GI:27502212
KEYWORDS
SOURCE Mycobacterium cookii
ORGANISM Mycobacterium cookii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 424)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
JOURNAL Mycobacterium as a model
PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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QSIGDLIAEMDKVNEGVIIVESNTFGLQLELTGMR"

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 46
AF547825
LOCUS AF547825
DEFINITION Mycobacterium diernhoferi strain CIP 105384 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION AF547825
VERSION AF547825.1 GI:27502214
KEYWORDS
SOURCE Mycobacterium diernhoferi
ORGANISM Mycobacterium diernhoferi
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 424)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
JOURNAL Mycobacterium as a model
PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 47

AF547826
LOCUS
DEFINITION
Mycobacterium doricum strain DSM 44339 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION
AF547826
VERSION
AF547826.1 GI:27502216
KEYWORDS
SOURCE
ORGANISM
Mycobacterium doricum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 424)
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
JOURNAL
PUBMED
15653890
REFERENCE
Devulder, G., Pichat, C. and Flandrois, J.P.
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

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gene

CDS

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Query Match 100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 48

AF547827
LOCUS
DEFINITION
Mycobacterium duvalli strain CIP 104539 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION
AF547827
VERSION
AF547827.1 GI:27502218

KEYWORDS
SOURCE
ORGANISM

Mycobacterium duvalli
Mycobacterium duvalli
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 424)
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
JOURNAL
PUBMED
15653890
REFERENCE
Devulder, G., Pichat, C. and Flandrois, J.P.
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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source
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gene

CDS

ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 49

AF547828
LOCUS
DEFINITION
Mycobacterium elephantis strain CIP 106831 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AF547828
VERSION
AF547828.1 GI:27502220
KEYWORDS
SOURCE
ORGANISM
Mycobacterium elephantis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 424)
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
JOURNAL
PUBMED
15653890
REFERENCE
Devulder, G., Pichat, C. and Flandrois, J.P.
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source
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AL547632.1 GI:27302420
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Mycobacterium fortuitum subsp. acetamidolyticum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigenic approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
Location/Qualifiers
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Db 10 CCATCGCCAAAGGAGATCGAGCT 31

RESULT 53
AF547833
LOCUS
DEFINITION
Mycobacterium fortuitum subsp. fortuitum strain CIP 104534 65 kDa
heat shock protein (hsp65) gene, partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium fortuitum subsp. fortuitum
Mycobacterium fortuitum subsp. fortuitum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigenic approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
Location/Qualifiers
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/mol_type="genomic DNA"

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Db 10 CCATCGCCAGGAGATCGAGCT 31

RESULT 54
AP547834
LOCUS
DEFINITION
Mycobacterium frederiksbergense strain DSM 44346 BCT 18-JAN-2005
protein (hsp65) gene, partial cds.
ACCESSION
AP547834
VERSION
AP547834.1 GI:27502232
KEYWORDS
Mycobacterium frederiksbergense
SOURCE
Mycobacterium frederiksbergense
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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FEATURES
source
gene
CDS

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 Db 10 CCATCGCCAGGAGATCGAGCT 31

RESULT 55
 AF547835

LOCUS
 DEFINITION Mycobacterium gadium strain CIP 105388 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547835
 VERSION AF547835.1 GI:27502234

KEYWORDS
 SOURCE Mycobacterium gadium
 ORGANISM Mycobacterium gadium
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)
 AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
 TITLE A multigenic approach to phylogenetic analysis using the genus Mycobacterium as a model
 JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 2 (bases 1 to 424)
 AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

gene
 CDS

RESULT 56
 AF547837

LOCUS
 DEFINITION Mycobacterium genavense strain DSM 44424 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547837
 VERSION AF547837.1 GI:27502238

KEYWORDS
 SOURCE Mycobacterium genavense
 ORGANISM Mycobacterium genavense
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)
 AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
 TITLE A multigenic approach to phylogenetic analysis using the genus Mycobacterium as a model
 JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 2 (bases 1 to 424)
 AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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 Best Local Similarity 100.0%; Pred. No. 53;
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 Db 10 CCATCGCCAGGAGATCGAGCT 31

RESULT 57
 AF547838

LOCUS
 DEFINITION Mycobacterium gilvum strain DSM 44503 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547838
 VERSION AF547838.1 GI:27502240

KEYWORDS
 SOURCE Mycobacterium gilvum
 ORGANISM Mycobacterium gilvum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)
 AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
 TITLE A multigenic approach to phylogenetic analysis using the genus Mycobacterium as a model
 JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 2 (bases 1 to 424)
 AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 58
AF547839
LOCUS
DEFINITION
Mycobacterium goodii strain CIP 106349 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION
AF547839
VERSION
AF547839.1 GI:27502242
KEYWORDS
SOURCE
Mycobacterium goodii
ORGANISM
Mycobacterium goodii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
JOURNAL
PUBMED
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
Location/Qualifiers
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 60
AF547841
LOCUS
DEFINITION
Mycobacterium haemophilum strain CIP 105049 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AF547841
VERSION
AF547841.1 GI:27502246
KEYWORDS
SOURCE
Mycobacterium haemophilum
ORGANISM
Mycobacterium haemophilum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
JOURNAL
PUBMED
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

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RESULT 59
AF547840
LOCUS
DEFINITION
Mycobacterium gordonae strain CIP 104529 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION
AF547840
VERSION
AF547840.1 GI:27502244
KEYWORDS
SOURCE
Mycobacterium gordonae
ORGANISM
Mycobacterium gordonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
JOURNAL
PUBMED
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Best Local Similarity 100.0%; Pred. No. 53;
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 60
AF547841
LOCUS
DEFINITION
Mycobacterium haemophilum strain CIP 105049 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AF547841
VERSION
AF547841.1 GI:27502246
KEYWORDS
SOURCE
Mycobacterium haemophilum
ORGANISM
Mycobacterium haemophilum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
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PUBMED
2 (bases 1 to 424)
Devulder,G., Pichat,C. and Flandrois,J.P.
Direct Submission
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
Location/Qualifiers
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Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
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PUBMED 15653890
 REFERENCE 2 (bases 1 to 424)
 AUTHORS Devulder,G.; Pichat,C. and Flandrois,J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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ORIGIN

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 Db 10 CCATCGCCCAAGGAGATCGAGCT 31

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 16:58:33 ; Search time 12.7069 Seconds
(without alignments)
3077.569 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	48	2	US-08-242-403A-54
2	22	100.0	48	2	Sequence 54, Appl
3	22	100.0	48	6	PCT-US95-05602-54
4	22	100.0	48	6	Sequence 54, Appl
5	22	100.0	647	2	US-08-997-080-115
6	22	100.0	647	2	Sequence 115, App
7	22	100.0	647	3	US-08-997-362-115
8	22	100.0	647	3	Sequence 115, App
9	22	100.0	647	3	US-09-324-542-115
10	22	100.0	888	3	US-09-205-426-115
11	22	100.0	888	3	Sequence 32, Appl
12	22	100.0	1569	2	US-10-267-311-32
13	22	100.0	1569	2	Sequence 113, App
14	22	100.0	1569	3	US-08-997-362-113
15	22	100.0	1569	3	Sequence 113, App
16	22	100.0	1569	3	US-09-324-542-113
17	22	100.0	1569	3	Sequence 113, App
18	22	100.0	1623	3	US-09-205-426-113
19	22	100.0	1623	3	Sequence 3, Appl
20	22	100.0	1623	3	US-10-267-311-3
21	22	100.0	1626	2	US-09-712-363-23
22	22	100.0	1626	2	Sequence 159, App
23	22	100.0	1626	3	US-08-997-080-159
24	22	100.0	1626	3	Sequence 159, App

25	22	100.0	1920	3	US-09-613-303-16	Sequence 16, Appl
26	22	100.0	1920	3	US-10-267-311-16	Sequence 16, Appl
27	22	100.0	1947	3	US-09-613-303-28	Sequence 28, Appl
28	22	100.0	1947	3	US-10-267-311-28	Sequence 28, Appl
29	22	100.0	2073	3	US-10-068-059-9	Sequence 9, Appl
30	22	100.0	2130	3	US-10-068-059-7	Sequence 7, Appl
31	22	100.0	2175	3	US-10-068-059-11	Sequence 11, Appl
32	22	100.0	2241	3	US-10-068-059-5	Sequence 5, Appl
33	22	100.0	2847	3	US-09-613-303-20	Sequence 20, Appl
34	22	100.0	2847	3	US-10-267-311-20	Sequence 20, Appl
35	22	100.0	4380	3	US-08-955-565A-3	Sequence 3, Appl
36	22	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
37	22	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
38	19.4	88.2	5275	2	US-08-485-588-1	Sequence 1, Appl
39	19.4	88.2	5275	2	US-08-484-565-1	Sequence 1, Appl
40	19.4	88.2	5275	2	US-08-480-751-1	Sequence 1, Appl
41	19.4	88.2	5275	2	US-08-943-986-1	Sequence 1, Appl
42	19.4	88.2	5275	3	US-08-353-784-1	Sequence 1, Appl
43	19.4	88.2	5275	3	US-08-484-719B-1	Sequence 1, Appl
44	19.4	88.2	5275	3	US-08-484-159-1	Sequence 1, Appl
45	19	86.4	1651	3	US-09-902-540-3255	Sequence 3255, Ap
46	19	86.4	4134	3	US-09-162-021B-1	Sequence 1, Appl
47	19	86.4	4134	3	US-09-687-477-17	Sequence 17, Appl
48	19	86.4	4134	3	US-09-687-476-17	Sequence 17, Appl
49	19	86.4	4134	3	US-09-687-372-17	Sequence 17, Appl
50	19	86.4	4134	3	US-09-975-553-17	Sequence 17, Appl
51	19	86.4	4134	3	US-10-270-795-17	Sequence 17, Appl
52	19	86.4	4134	3	US-10-270-876-17	Sequence 17, Appl
53	19	86.4	4134	3	US-10-268-051-7	Sequence 7, Appl
54	19	86.4	4134	3	US-10-411-076-23	Sequence 23, Appl
55	19	86.4	4134	3	US-10-125-772-1	Sequence 1, Appl
56	19	86.4	19954	3	US-09-902-540-1150	Sequence 1150, Ap
57	18.8	85.5	276	3	US-09-252-991A-10595	Sequence 10595, A
C 57	18.8	85.5	606	3	US-09-252-991A-10780	Sequence 10780, A
C 58	18.8	85.5	609	3	US-09-252-991A-7774	Sequence 7774, Ap
C 59	18.8	85.5	720	3	US-09-252-991A-10378	Sequence 10378, A
60	18.8	85.5	720	3	US-09-252-991A-10378	Sequence 10378, A

ALIGNMENTS

RESULT 1
US-08-242-403A-54
; Sequence 54, Application US/08242403A
; Patent No. 5631130
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Semple-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; TITLE OF INVENTION: Mycobacteria tuberculosis
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,403A
; FILING DATE: May 13, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459

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; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium
; US-08-242-403A-54

Query Match 100.0%; Score 22; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 8 CCATGCCCAAGGAGATCGAGCT 29

RESULT 2
US-08-774-128-54
; Sequence 54, Application US/08774128
; Patent No. 5786149
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,128
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/242,403
; FILING DATE: May 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium
; PCT-US95-05602-54

Query Match 100.0%; Score 22; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 8 CCATGCCCAAGGAGATCGAGCT 29

RESULT 4
PCT-US95-05816-54
; Sequence 54, Application PC/TUS9505816
; GENERAL INFORMATION:
; APPLICANT: Solomon, N.
```

APPLICANT: Leckie, G.
APPLICANT: Kratochvil, J.
APPLICANT: O'Donnell, D.
TITLE OF INVENTION: Materials and Methods for the Detection of
TITLE OF INVENTION: Mycobacteria
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05816
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5371.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-4884
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Mycobacterium
PCT-US95-05816-54

Query Match 100.0%; Score 22; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 8 CCATCGCCCAAGGAGATCGAGCT 29

RESULT 5
US-08-997-080-115
Sequence 115, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 647 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
US-08-997-080-115

Query Match 100.0%; Score 22; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3; Length 647;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 6

US-08-997-362-115
Sequence 115, Application US/08997362
Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563

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;
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 647 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic RNA
;
US-08-997-362-115

Query Match      100.0%; Score 22; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
DB      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 7
US-09-855-855-115
; Sequence 115, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
;   APPLICANT: Tan, Paul
;   APPLICANT: Visser, Elizabeth
;   APPLICANT: Skinner, Margot
;   APPLICANT: Prestidge, Ross
;   TITLE OF INVENTION: Compounds and Methods for
;   TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
;   NUMBER OF SEQUENCES: 208
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Law Offices of Ann W. Speckman
;   STREET: 2601 Elliott Avenue, Suite 4185
;   CITY: Seattle
;   STATE: WA
;   COUNTRY: USA
;   ZIP: 98121
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSeq for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/095,855
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/705,347
;   FILING DATE: 29-AUG-1996
;   APPLICATION NUMBER: 08/873,970
;   FILING DATE: 12-JUN-1997
;   APPLICATION NUMBER: 08/997,362
;   FILING DATE: 23-DEC-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Sleath, Janet
;   REGISTRATION NUMBER: 37,007
;   REFERENCE/DOCKET NUMBER: 11000.1002C3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 206-269-0565
;   TELEFAX: 206-269-0563
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 115:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 647 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic RNA
;
US-09-855-855-115

Query Match      100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
DB      161 CCATGCCCAAGGAGATCGAGCT 182

US-09-324-542-115
; Sequence 115, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
;   APPLICANT: Watson, James D.
;   APPLICANT: Tan, Paul L.J.
;   APPLICANT: Prestidge, Ross
;   TITLE OF INVENTION: Methods and Compounds for the Treatment
;   TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
;   FILE REFERENCE: 11000.1007c1
;   CURRENT APPLICATION NUMBER: US/09/324,542
;   CURRENT FILING DATE: 1999-06-02
;   EARLIER APPLICATION NUMBER: US 08/997,080
;   EARLIER FILING DATE: 1997-12-23
;   NUMBER OF SEQ ID NOS: 194
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 115
;   LENGTH: 647
;   TYPE: DNA
;   ORGANISM: Mycobacterium vaccae
;
US-09-324-542-115

Query Match      100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
DB      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 9
US-09-205-426-115
; Sequence 115, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
;   APPLICANT: Watson, James D.
;   APPLICANT: Tan, Paul L. J.
;   TITLE OF INVENTION: Compounds and Methods for Treatment and
;   TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
;   FILE REFERENCE: 11000.1002c4
;   CURRENT APPLICATION NUMBER: US/09/205,426
;   CURRENT FILING DATE: 1998-12-04
;   EARLIER APPLICATION NUMBER: 09/095,855
;   EARLIER FILING DATE: 1998-06-11
;   EARLIER APPLICATION NUMBER: 08/997,362
;   EARLIER FILING DATE: 1997-12-23
;   EARLIER APPLICATION NUMBER: 08/873,970
;   EARLIER FILING DATE: 1997-06-12
;   EARLIER APPLICATION NUMBER: 08/705,347
;   EARLIER FILING DATE: 1996-08-29
;   NUMBER OF SEQ ID NOS: 208
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 115
;   LENGTH: 647
;   TYPE: DNA
;   ORGANISM: Mycobacterium vaccae
;
US-09-205-426-115

Query Match      100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
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Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 10
US-09-613-303-32
; Sequence 32, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-09-613-303-32

Query Match 100.0%; Score 22; DB 3; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 161 CCATGCCCAAGGAGATCGAGCT 182
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RESULT 11
US-10-267-311-32
; Sequence 32, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match 100.0%; Score 22; DB 3; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 12
US-08-997-080-113
; Sequence 113, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-080-113

Query Match 100.0%; Score 22; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 161 CCATGCCCAAGGAGATCGAGCT 182
|||||

RESULT 13
US-08-997-362-113
; Sequence 113, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman

```
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-997-362-113
;
; Query Match 100.0%; Score 22; DB 2; Length 1569;
; Best Local Similarity 100.0%; Pred. No. 1.4;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CCATCGCCCAAGGAGATCGAGCT 22
; Db 161 CCATCGCCCAAGGAGATCGAGCT 182
;
; RESULT 14
; US-09-095-855-113
; Sequence 113, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
;
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-09-095-855-113
;
; Query Match 100.0%; Score 22; DB 3; Length 1569;
; Best Local Similarity 100.0%; Pred. No. 1.4;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CCATCGCCCAAGGAGATCGAGCT 22
; Db 161 CCATCGCCCAAGGAGATCGAGCT 182
;
; RESULT 15
; US-09-324-542-113
; Sequence 113, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-113
;
; Query Match 100.0%; Score 22; DB 3; Length 1569;
; Best Local Similarity 100.0%; Pred. No. 1.4;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CCATCGCCCAAGGAGATCGAGCT 22
; Db 161 CCATCGCCCAAGGAGATCGAGCT 182
;
; RESULT 16
; US-09-205-426-113
; Sequence 113, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
```

;; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
;; FILE REFERENCE: 11000.1002c4
;; CURRENT APPLICATION NUMBER: US/09/205,426
;; CURRENT FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: 09/095,855
;; EARLIER FILING DATE: 1998-06-11
;; EARLIER APPLICATION NUMBER: 08/997,362
;; EARLIER FILING DATE: 1997-12-23
;; EARLIER APPLICATION NUMBER: 08/873,970
;; EARLIER FILING DATE: 1997-06-12
;; EARLIER APPLICATION NUMBER: 08/705,347
;; EARLIER FILING DATE: 1996-08-29
;; NUMBER OF SEQ ID NOS: 208
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 113
;; LENGTH: 1569
;; TYPE: DNA
;; ORGANISM: Mycobacterium vaccae
US-09-205-426-113

Query Match 100.0%; Score 22; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 17
US-09-613-303-3
;; Sequence 3, Application US/09613303
;; Patent No. 6495347
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Marvin
;; APPLICANT: Chu, N. Randall
;; APPLICANT: Mizzen, Lee A.
;; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
;; FILE REFERENCE: 12071/002001
;; CURRENT APPLICATION NUMBER: US/09/613,303
;; CURRENT FILING DATE: 2000-07-10
;; PRIOR APPLICATION NUMBER: US 60/143,757
;; PRIOR FILING DATE: 1999-07-08
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 1623
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: fusion sequence
;; NAME/KEY: CDS
;; LOCATION: (1)....(1620)
US-09-613-303-3

Query Match 100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 18
US-10-267-311-3
;; Sequence 3, Application US/10267311
;; Patent No. 6657055
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Marvin
;; APPLICANT: Chu, N. Randall
;; APPLICANT: Mizzen, Lee A.
;; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

;; FILE REFERENCE: 12071/002001
;; CURRENT APPLICATION NUMBER: US/10/267,311
;; CURRENT FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: US/09/613,303
;; PRIOR FILING DATE: 2000-07-10
;; PRIOR APPLICATION NUMBER: US 60/143,757
;; PRIOR FILING DATE: 1999-07-08
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 1623
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: fusion sequence
;; NAME/KEY: CDS
;; LOCATION: (1)....(1620)
US-10-267-311-3

Query Match 100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 19
US-09-712-363-23
;; Sequence 23, Application US/09712363
;; Patent No. 6892139
;; GENERAL INFORMATION:
;; APPLICANT: Eisenberg, David
;; APPLICANT: Rotstein, Sergio H.
;; APPLICANT: Marcotte, Edward M.
;; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
;; FILE REFERENCE: 07419-032001
;; CURRENT APPLICATION NUMBER: US/09/712,363
;; CURRENT FILING DATE: 2000-11-13
;; PRIOR APPLICATION NUMBER: PCT/US00/02246
;; PRIOR FILING DATE: 2000-01-28
;; PRIOR APPLICATION NUMBER: 60/179,531
;; PRIOR FILING DATE: 2000-02-01
;; PRIOR APPLICATION NUMBER: 60/117,844
;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: 60/118,206,
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: 60/126,593
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: 60/134,093
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/134,092
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/165,124
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/165,086
;; PRIOR FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 292
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 23
;; LENGTH: 1623
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

Db 161 CCATGCCCAAGGAGATCGAGCT 182
|||||

RESULT 20

US-08-997-080-159
; Sequence 159, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-080-159

Query Match 100.0%; Score 22; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

RESULT 21

US-08-997-362-159
; Sequence 159, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-159

Query Match 100.0%; Score 22; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 22

US-09-095-855-159
; Sequence 159, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-095-855-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 23

US-09-324-542-159
Sequence 159, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 159
TYPE: DNA
LENGTH: 1626
ORGANISM: Mycobacterium vaccae
US-09-324-542-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 24

US-09-205-426-159
Sequence 159, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 159
LENGTH: 1626
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-205-426-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 25

US-09-613-303-16
Sequence 16, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1920
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1917)
US-09-613-303-16

Query Match 100.0%; Score 22; DB 3; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 26

US-10-267-311-16
Sequence 16, Application US/10267311
Patent No. 6657055
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311

; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 22; DB 3; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 27
US-09-613-303-28
; Sequence 28, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-09-613-303-28

Query Match 100.0%; Score 22; DB 3; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-267-311-28
; Sequence 28, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311

; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-267-311-28

Query Match 100.0%; Score 22; DB 3; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 29
US-10-068-059-9
; Sequence 9, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match 100.0%; Score 22; DB 3; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 30
US-10-068-059-7
; Sequence 7, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059

; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-7

Query Match 100.0%; Score 22; DB 3; Length 2130;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 668 CCATGCCCAAGGAGATCGAGCT 689
|||||

RESULT 31

US-10-068-059-11

; Sequence 11, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:

; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11

; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 22; DB 3; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 713 CCATGCCCAAGGAGATCGAGCT 734
|||||

RESULT 32

US-10-068-059-5

; Sequence 5, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:

; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05

Query Match 100.0%; Score 22; DB 3; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 713 CCATGCCCAAGGAGATCGAGCT 734
|||||

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 22; DB 3; Length 2241;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 779 CCATGCCCAAGGAGATCGAGCT 800
|||||

RESULT 33

US-09-613-303-20

; Sequence 20, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:

; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20

; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match 100.0%; Score 22; DB 3; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 221 CCATGCCCAAGGAGATCGAGCT 242
|||||

RESULT 34

US-10-267-311-20

; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:

; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55

Query Match 100.0%; Score 22; DB 3; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 221 CCATGCCCAAGGAGATCGAGCT 242
|||||

```
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
```

;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below: 9
;; APPLICATION NUMBER: 08/353,784
;; FILING DATE: 9 December, 1994
;; APPLICATION NUMBER: PCT/US/94/12117
;; FILING DATE: 21 October, 1994
;; APPLICATION NUMBER: U.S. 08/292,827
;; FILING DATE: 23 August, 1994
;; APPLICATION NUMBER: U.S. 08/009,389
;; FILING DATE: 23 February, 1993
;; APPLICATION NUMBER: U.S. 08/017,127
;; FILING DATE: 12 February, 1993
;; APPLICATION NUMBER: U.S. 07/934,161
;; FILING DATE: 21 August, 1992
;; APPLICATION NUMBER: U.S. 07/834,044
;; FILING DATE: 11 February, 1992
;; APPLICATION NUMBER: U.S. 07/749,451
;; FILING DATE: 23 August, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Heber, Sheldon O.
;; REGISTRATION NUMBER: 38,179
;; REFERENCE/DOCKET NUMBER: 213/005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5275 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 515..3769
;; OTHER INFORMATION:
US-08-485-588-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 39
US-08-484-565-1
; Sequence 1, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: FASTSEQ
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,565
;; FILING DATE: 7 June, 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below: 9
;; APPLICATION NUMBER: 08/353,784
;; FILING DATE: 9 December, 1994
;; APPLICATION NUMBER: PCT/US/94/12117
;; FILING DATE: 21 October, 1994
;; APPLICATION NUMBER: U.S. 08/292,827
;; FILING DATE: 23 August, 1994
;; APPLICATION NUMBER: U.S. 08/141,248
;; FILING DATE: 22 October, 1993
;; APPLICATION NUMBER: U.S. 08/009,389
;; FILING DATE: 23 February, 1993
;; APPLICATION NUMBER: U.S. 08/017,127
;; FILING DATE: 12 February, 1993
;; APPLICATION NUMBER: U.S. 07/934,161
;; FILING DATE: 21 August, 1992
;; APPLICATION NUMBER: U.S. 07/834,044
;; FILING DATE: 11 February, 1992
;; APPLICATION NUMBER: U.S. 07/749,451
;; FILING DATE: 23 August, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Heber, Sheldon O.
;; REGISTRATION NUMBER: 38,179
;; REFERENCE/DOCKET NUMBER: 213/006
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5275 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 515..3769
;; OTHER INFORMATION:
US-08-484-565-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 40
US-08-480-751-1
; Sequence 1, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward P. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-480-751-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 41

US-08-943-986-1
Sequence 1, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-943-986-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 42
US-08-353-784-1
; Sequence 1, Application US/08353784
; Patent No. 6011068
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen, Manuel
; APPLICANT: F. Balandrin, Forrest H. Fuller,
; APPLICANT: Eric G. Delmar, and Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,784
; FILING DATE: 9 December, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 8
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hebert, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 209/069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-353-784-1

Query Match 88.2%; Score 19.4; DB 3; Length 5275;

Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CATGCCCAAGGAGATCGAGCT 22
DB 2311 CATGCCCAAGGAGATCGAGTT 2331
RESULT 43
US-08-484-719B-1
; Sequence 1, Application US/08484719B
; Patent No. 6031003
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen,
; APPLICANT: Manuel P. Balandrin,
; APPLICANT: Forrest H. Fuller, Eric G.
; APPLICANT: Delmar, Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Word
; SOFTWARE: FASTSEQ for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,719B
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Douglas C. Murdock
; REGISTRATION NUMBER: 37,549
; REFERENCE/DOCKET NUMBER: 213/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; US-08-484-719B-1

Query Match      88.2%; Score 19.4; DB 3; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
Db      2311 CATGCCAAGGAGATCGAGTT 2331

RESULT 44
US-08-484-159-1
; Sequence 1, Application US/08484159
; Patent No. 6313146
; GENERAL INFORMATION:
; APPLICANT: Bradford C. Van Wagenen
; APPLICANT: Manuel F. Balandrin
; APPLICANT: Eric G. Del Mar
; APPLICANT: Edward F. Nemeth
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,159
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 214/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
; US-08-484-159-1

Query Match      88.2%; Score 19.4; DB 3; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
Db      2311 CATGCCAAGGAGATCGAGTT 2331

RESULT 45
US-09-902-540-3255
; Sequence 3255, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3255
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-3255

Query Match      86.4%; Score 19; DB 3; Length 1651;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TCGCCAAGGAGATCGAGCT 22
Db      164 TCGCCAAGGAGATCGAGCT 182

RESULT 46
US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; CURRENT FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
```

SEQ ID NO 1
LENGTH: 4134
TYPE: DNA
ORGANISM: squalas acanthias
FEATURE:
NAME/KEY: CDS
LOCATION: (439)...(3522)
US-09-162-021B-1

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 47

US-09-687-477-17
Sequence 17, Application US/09687477
Patent No. 6463883
GENERAL INFORMATION:
APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.1004-000
CURRENT APPLICATION NUMBER: US/09/687,477
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-687-477-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 48

US-09-687-476-17
Sequence 17, Application US/09687476
Patent No. 6475792
GENERAL INFORMATION:
APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.2001-000
CURRENT APPLICATION NUMBER: US/09/687,476
CURRENT FILING DATE: 2000-10-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-687-476-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 49

US-09-687-372-17
Sequence 17, Application US/09687372
Patent No. 6481379
GENERAL INFORMATION:
APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.2002-000
CURRENT APPLICATION NUMBER: US/09/687,372
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-687-372-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 50

US-09-975-553-17
Sequence 17, Application US/09975553
Patent No. 6564747
GENERAL INFORMATION:
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.1004-001
CURRENT APPLICATION NUMBER: US/09/975,553
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/687,477
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 09/687,476
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 09/687,372
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-975-553-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 51
US-10-270-795-17
; Sequence 17, Application US/10270795
; Patent No. 663771
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/10/270,795
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,372
; PRIOR FILING DATE: 2000-10-12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 52
US-10-270-876-17
; Sequence 17, Application US/10270876
; Patent No. 6655318
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 53
US-10-268-051-7
; Sequence 7, Application US/10268051
; Patent No. 6748900
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-268-051-7

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 54
US-10-411-076-23
; Sequence 23, Application US/10411076
; Patent No. 6854422
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Growing Marine Fish in Freshwater
; FILE REFERENCE: 2213.1003007
; CURRENT APPLICATION NUMBER: US/10/411,076
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US01/31625
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,373
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Mustelus canis
US-10-411-076-23

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 55
US-10-125-772-1
; Sequence 1, Application US/10125772
; Patent No. 6951739

GENERAL INFORMATION:

APPLICANT: Marical
APPLICANT: Harris, H. William
APPLICANT: Nearing, Jacqueline A.
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
FILE REFERENCE: 2213.1006-006
CURRENT APPLICATION NUMBER: US/10/125,772
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 10/121,441
PRIOR FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US01/31704
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/240,392
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/240,003
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 4134
TYPE: DNA
ORGANISM: Squalus acanthias
US-10-125-772-1

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
DB 2256 CATGCCAAGGAGATCGAG 2274

RESULT 56

US-09-902-540-1150
Sequence 1150, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1150
LENGTH: 19954
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1150

Query Match 86.4%; Score 19; DB 3; Length 19954;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGCCAAGGAGATCGAGCT 22
DB 7764 TCGCCAAGGAGATCGAGCT 7782

RESULT 57

US-09-252-991A-10595/c
Sequence 10595, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10595
LENGTH: 276
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10595

Query Match 85.5%; Score 18.8; DB 3; Length 276;
Best Local Similarity 90.9%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22
DB 225 CCATGCCAAGGAGATCGAGCT 204

RESULT 58

US-09-252-991A-10780/c
Sequence 10780, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10780
LENGTH: 606
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10780

Query Match 85.5%; Score 18.8; DB 3; Length 606;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22
DB 109 CCATGCCAAGGAGATCGAGCT 88

RESULT 59

US-09-252-991A-7774/c
Sequence 7774, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7774
LENGTH: 609
TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7774

Query Match 85.5%; Score 18.8; DB 3; Length 609;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCAAGGAGATCGAGCT 22
Db 430 CCGTCGCCAAGGAATCGAGCT 409

RESULT 60

US-09-252-991A-10378
; Sequence 10378, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 10378

; LENGTH: 720

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-10378

Query Match 85.5%; Score 18.8; DB 3; Length 720;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCAAGGAGATCGAGCT 22
Db 240 CCATCGACAAGGACATCGAGCT 261

Search completed: April 1, 2006, 17:06:14
Job time : 25.7069 secs

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 21:55:10 ; Search time 44.7112 Seconds
(without alignments)
3279.340 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccacgcgaagagatcgagct 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

N Geneseq 21:.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	22	100.0	22 14 ADV99121	Adv99121 groEL2 ge
2	22	100.0	45 4 AAH46029	Aah46029 BCG deriv
3	22	100.0	647 2 AAV34609	Aav34609 M. vaccae
4	22	100.0	647 2 AAZ11344	Aaz11344 Nucleotid
5	22	100.0	647 6 ABL36250	Ab136250 M vaccae
6	22	100.0	647 8 ACA42532	Acc42532 Mycobacte
7	22	100.0	888 5 AAF25022	Aaf25022 Nucleotid
8	22	100.0	1496 13 ADW23618	Adw23618 HSP65 DNA
9	22	100.0	1569 2 AAV34608	Aav34608 M. vaccae
10	22	100.0	1569 2 AAZ11343	Aaz11343 Nucleotid
11	22	100.0	1569 6 ABL36249	Ab136249 M vaccae
12	22	100.0	1620 8 ACA38272	Acc38272 Prokaryot
13	22	100.0	1620 13 ADL12623	Adl12623 Gene vacc
14	22	100.0	1623 4 AAH51969	Aah51969 Mycobacte
15	22	100.0	1623 5 AAF25002	Aaf25002 Nucleotid
16	22	100.0	1623 8 ACA40326	Acc40326 Prokaryot
17	22	100.0	1623 8 ACA37725	Acc37725 Prokaryot
18	22	100.0	1623 12 ADN11336	Adn11336 Chaperonin
19	22	100.0	1626 2 AAZ11371	Aaz11371 Nucleotid

20	22	100.0	1626 6 ABL36277	Ab136277 M vaccae
21	22	100.0	1626 8 ACC42531	Acc42531 Mycobacte
22	22	100.0	1626 8 ACA39632	Acc39632 Prokaryot
23	22	100.0	1626 9 ACC70275	Acc70275 Nucleotid
24	22	100.0	1632 13 ADT46122	Adt46122 Bacterial
25	22	100.0	1701 9 AAD57198	Aad57198 Mycobacte
26	22	100.0	1752 8 ACC49833	Acc49833 Human rec
27	22	100.0	1761 14 ADX05272	Adx05272 HSP65-MUC
28	22	100.0	1800 10 ADK68629	Adk68629 HSP65-MUC
29	22	100.0	1914 8 ACC49834	Acc49834 Human rec
30	22	100.0	1920 5 AAF25012	Aaf25012 Nucleotid
31	22	100.0	1947 5 AAF25019	Aaf25019 Nucleotid
32	22	100.0	1965 13 ADW23606	Adw23606 Hepatitis
33	22	100.0	1980 12 ADN00588	Adn00588 BCG vacci
34	22	100.0	2016 12 ADK72374	Adk72374 BCG-HER-2
35	22	100.0	2073 6 ABS54448	Abs54448 BCG Hsp65
36	22	100.0	2130 6 ABS54447	Abs54447 BCG Hsp65
37	22	100.0	2175 6 ABS54449	Abs54449 BCG Hsp65
38	22	100.0	2241 6 ABS54446	Abs54446 His tagge
39	22	100.0	2585 13 ADR30583	Adr30583 Arthrobac
40	22	100.0	2847 5 AAF25014	Aaf25014 Nucleotid
41	22	100.0	3613 1 AAN80339	Aan80339 Clone Y31
42	22	100.0	4260 1 AAN81768	Aan81768 Sequence
43	22	100.0	4380 1 AAN80222	Aan80222 Sequence
44	22	100.0	4380 2 AAV05708	Aav05708 Mycobacte
45	22	100.0	4380 6 ABA99141	Abas99141 hsp65 enc
46	22	100.0	4380 4 AAS59637	Aas59637 Propionib
47	22	100.0	4380 8 ACF64566	Acc64566 Propionib
48	22	100.0	86114 6 ABX09143	Abx09143 Mycobacte
49	22	100.0	110000 4 AAI99682_05	Continuation (6 of
50	22	100.0	110000 4 AAI99682_05	Continuation (6 of
51	21	95.5	48 2 AAT06825	Aat06825 65 KD hea
52	21	95.5	48 2 AAT06550	Aat06550 65 KD hea
53	20.4	92.7	1728 13 ADS56335	Ads56335 Bacterial
54	20.4	92.7	99090 12 ADM72250	Adm72250 O. minuta
55	20	90.9	20 9 ACF04316	Acc04316 Mycobacte
56	19.4	88.2	5275 2 AAV28962	Aav28962 Bovine pa
57	19.4	88.2	5275 2 AAT95857	Aat95857 Bovine pa
58	19.4	88.2	5275 2 AAZ25053	Aaz25053 Bovine pa
59	19.4	88.2	5275 2 AAV82483	Aav82483 Bovine pa
60	19.4	88.2	5275 3 AAZ89296	Aaz89296 Bovine Ca

ALIGNMENTS

RESULT 1
ADV99121
ID ADV99121 standard; DNA; 22 BP.
XX
AC ADV99121;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene forward primer, STGROF1, SEQ ID 1.
XX
KW Microorganism identification; microorganism detection; groEL2;
XX
KW potato scab; PCR; primer; ss.
XX
OS Streptomyces sp.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces

PT species, useful in identifying the genus Streptomyces, and for isolating

PT or purifying natural products using such microorganisms.

XX Claim 1; SEQ ID NO 1; 34pp; English.

XX The present invention relates to novel primers STGR0F1 (ADV99121) and

CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of

CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment

CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces

CC species. Primers ADV99121 and ADV99122 are useful in a method for

CC identifying Streptomyces species, comprising amplifying groEL2 gene

CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC gene fragment amplified, and comparing the nucleotide sequence obtained

CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 22 BP; 6 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22

Db 1 CCATCGCCCAAGGAGATCGAGCT 22

RESULT 2

AAH46029

ID AAH46029 standard; DNA; 45 BP.

XX AC AAH46029;

DT 12-SEP-2001 (first entry)

XX BCG derived synthetic oligonucleotide 3.

XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;

KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;

KW lymphoma; ss; BCG.

XX Mycobacterium bovis.

OS Synthetic.

OS WO200144465-A2.

PN 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA001467.

XX 13-DEC-1999; 99US-0170325P.

PR 29-AUG-2000; 2000US-0228925P.

XX (BION-) BIONICHE LIFE SCI INC.

PA Phillips NC, Fillion MC;

XX WPI; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise multiple

PT repeats of dinucleotides such as GT, TG useful for treating cancer by

PT inducing cell cycle arrest, inhibiting proliferation, activating

PT caspases.

XX Example 20; Page 33; 77pp; English.

XX The present sequence is that of a synthetic BCG (Bacillus Calmette-

CC Guerin) derived oligonucleotide useful to the invention. The invention

CC relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH

CC synthetic oligonucleotide which comprises multiple repeats of

CC dinucleotides such as GT, TG, etc., according to specific formula and

CC having cytostatic activity. The oligonucleotide compositions are useful

CC for inducing cell cycle arrest, inhibition of proliferation, activation

CC of caspases and induction of apoptosis or production of cytokines such as

CC interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor

CC (TNF)-alpha by immune system cells, in an animal having cancer such as

CC primary carcinoma, secondary carcinoma, primary sarcoma and secondary

CC sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal,

CC ovarian or bone cancer. The compositions induce apoptosis independent of

CC Fas, p53/p21, p21/waf-1/CIP, p15(ink4), p16(ink4), drug resistance,

CC caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone

CC dependence

XX Sequence 45 BP; 13 A; 11 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 45;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22

Db 2 CCATCGCCCAAGGAGATCGAGCT 23

RESULT 3

AAV34609

ID AAV34609 standard; RNA; 647 BP.

XX AC AAV34609;

DT 25-AUG-1998 (first entry)

XX M. vaccae antigen GV-27A encoding DNA.

DE Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;

KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;

KW mycobacteria infection; vaccine; cancer; ss.

XX Mycobacterium vaccae.

OS Key Location/Qualifiers

FT 1..645

FT CDS /tag= a

FT /product= "GV-27A antigen"

FT /note= "the stop codon is not indicated"

XX WO9808542-A2.

XX 05-MAR-1998.

XX 28-AUG-1997; 97WO-NZ000105.

XX 29-AUG-1996; 96US-00705347.

PR 12-JUN-1997; 97US-00873970.

XX (GENE-) GENESIS RES & DEV CORP.

XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;

PI WPI; 1998-216926/19.

DR P-PSDB; AAW60145.

XX Mycobacterium vaccae polypeptides - used to develop products for use in

PT detection, therapy and prevention of mycobacteria infections or as immune

PT response enhancers.

XX Example 6; Page 116; 153pp; English.

XX This RNA encodes a Mycobacterium vaccae antigen GV-27A. The invention

CC provides M. vaccae polypeptides that comprise an immunogenic portion of a

CC soluble M. vaccae antigen, or a variant, where the antigen induces an

CC immune response in patients previously exposed to a mycobacterium. Such
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific
 CC immune response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by mycobacteria
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B
 CC cells, or macrophages. They can be used for enhancing immune responses
 CC for use in vaccines or immunotherapy of infectious diseases and cancers

SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 647;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 4

AAZ11344

ID AAZ11344 standard; DNA; 647 BP.

XX

AC AAZ11344;

XX

XX

DT 25-OCT-1999 (first entry)

XX

DE Nucleotide sequence of M. vaccae antigen GV-27A.

XX

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KW squamous cell carcinoma; melanoma; sb.

OS Mycobacterium vaccae.

XX

XX

PN WO9932634-A2.

XX

XX 01-JUL-1999.

PD

PF 23-DEC-1998; 98WO-NZ000189.

XX

PR 23-DEC-1997; 97US-00996624.

XX

PR 23-DEC-1997; 97US-00997080.

XX

PR 23-DEC-1997; 97US-00997362.

XX

PR 11-JUN-1998; 98US-00095855.

XX

PR 17-SEP-1998; 98US-00156181.

XX

PR 04-DEC-1998; 98US-00205426.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;

XX

XX WPI; 1999-430163/36.

XX

DR P-PSDB; RAY14892.

XX

XX Enhancing immune response to an antigen.

XX

XX Example 14; Page 190-191; 243pp; English.

XX

XX The invention provides heat-killed Mycobacterium vaccae, or recombinant

CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T

CC cells and natural killer cells, to stimulate the production of cytokines,

CC to enhance the expression of co-stimulatory molecules on dendritic cells

CC and monocytes, and to enhance dendritic cell maturation and function. The

CC proteins can be expressed by standard recombinant methodology.

CC Pharmaceutical compositions comprising the proteins or nucleic acid

CC prevention, encoding the proteins can be used for the treatment,

CC prevention, and detection of disorders including infectious diseases,

CC

CC immune disorders and cancer. In particular, the compounds and methods are
 CC used for treatment of diseases of the respiratory system, such as
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
 CC sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma

SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 647;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 5

ABL36250

ID ABL36250 standard; DNA; 647 BP.

XX

AC ABL36250;

XX

XX

DT 08-APR-2002 (first entry)

XX

DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 115.

XX

KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipruritic; dermatological; antiinflammatory; antiallergic;
 KW Th2 immune response; immunomodulatory; gene; ds.

OS Mycobacterium vaccae.

XX

PN US6328978-B1.

XX

XX 11-DEC-2001.

XX

XX 02-JUN-1999; 99US-00324542.

XX

XX 23-DEC-1997; 97US-00997080.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Watson JD, Tan PLJ, Prestidge R;

XX

XX WPI; 2002-138361/18.

XX

XX P-PSDB; ABB73498.

XX

PT Inhibiting skin inflammation associated with skin disorder e.g.

PT psoriasis, by administering composition comprising delipidated and

PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae

PT culture filtrate.

XX

PS Example 4; Col 125-126; 116pp; English.

XX

CC The present invention relates to a method of inhibiting skin inflammation
 CC associated with a skin disorder selected from psoriasis, atopic
 CC dermatitis and allergic contact dermatitis, which involves administering
 CC a composition containing delipidated and deglycolipidated Mycobacterium
 CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 CC treated may also include alopecia areata, and skin cancers such as basal
 CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
 CC acts by inhibiting the Th2 immune response. The present sequence is a
 CC coding sequence described in the exemplification of the invention

SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 647;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 6
ACC42532
ID ACC42532 standard; DNA; 647 BP.
XX
AC ACC42532;
XX
DT 26-AUG-2003 (first entry)
XX
DE Mycobacterium vaccae antigen GV-27A coding sequence, SEQ ID 15.
XX
KW Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
KW antidiabetic; antipsoriatic; dermatological; anti-inflammatory;
KW immune response; Notch signalling pathway; autoimmune disorder;
KW Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
KW apoptotic cell death; cell proliferation; gene; ds.
XX
OS Mycobacterium vaccae.
XX
FH Key Location/Qualifiers
FT CDS 1..645
FT /tag= a
FT /partial
FT /product= "Antigen GV-27A"
FT /note= "No stop codon given"
XX
PN WO2003013595-A1.
XX
PD 20-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-NZ000135.
XX
PR 26-JUL-2001; 2001US-0308446P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Abernethy N;
XX
DR WPI; 2003-239567/23.
DR P-PSDB; ABP70892.
XX
PT Methods for modulating immune responses by modulating the Notch signaling
PT and Toll-like receptor signaling pathways, and treating e.g. autoimmune
PT disorders.
XX
PS Claim 7; Page 109; 136pp; English.
XX
CC The present invention relates to methods for modulating immune responses
CC by modulating the Notch signalling and Toll-like receptor signalling
CC pathways using compositions comprising mycobacteria antigens (ACC42518-
CC ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
CC immune responses and treating e.g. autoimmune disorders (such as multiple
CC sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
CC systemic lupus erythematosus, scleroderma), allergic disease and graft
CC rejection and also disorders characterised by undesired apoptotic cell
CC death or undesired cell proliferation
XX
SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 8; Length 647;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 7
AAF25022
ID AAF25022 standard; DNA; 888 BP.
XX
AC AAF25022;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of Hsp65-E7 fusion protein.
XX
KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW E7 protein; ss.
XX
OS Synthetic.
OS Mycobacterium bovis.
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT CDS 1..888
FT /tag= a
FT /product= "Hsp65-E7 fusion protein"
XX
PN WO200104344-A2.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018828.
XX
PR 08-JUL-1999; 99US-0143757P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mizzen LA;
XX
DR WPI; 2001-138361/14.
DR P-PSDB; AAB31615.
XX
PT Screening for compounds that stimulate Th1-like responses in CD4+ T
PT lymphocyte cells.
XX
PS Example 12; Fig 11; 88pp; English.
XX
CC The present sequence encodes a fusion protein comprising a Mycobacterium
CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a Hpv16 E7
CC protein. The fusion protein is used in the method of the invention. The
CC specification describes a method of determining whether a compound
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
CC lymphocyte cells. The method comprises contacting naive lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
XX
SQ Sequence 888 BP; 224 A; 235 C; 272 G; 157 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 5; Length 888;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 8
ADW23618
ID ADW23618 standard; DNA; 1496 BP.
XX
AC ADW23618;
XX

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DT 10-MAR-2005 (first entry)
DE HSP65 DNA.
KW recombinant protein; vaccine; fusion protein; HSP65; ds.
OS Unidentified.
XX CN1462636-A.
XX 24-DEC-2003.
XX 30-MAY-2002; 2002CN-00122116.
XX 30-MAY-2002; 2002CN-00122116.
XX (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX Wang L, Sun M, Yu Y;
XX WPI; 2004-239553/23.
XX Vaccine of recombinant albumen for preventing and treating infection of
XX human hepatitis C virus.
XX Example 1; Page 14; 54pp; Chinese.
XX The invention relates to a recombinant protein vaccine which is a fusion
XX protein of BCG vaccine's heat shock protein 65 and the core antigen of
XX multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
XX and nucleotide sequence for coding it, the expression carrier containing
XX nucleotide sequence, the host cell containing expression carrier, the
XX preparing process of recombinant protein vaccine, the vaccine containing
XX recombinant protein for preventing and treating hepatitis C and a method
XX for detecting the activity of specifically killing T-lymphocytes by the
XX hepatitis C induced by vaccine and its cell model are disclosed. The
XX present sequence represents a HSP65 DNA.
XX Sequence 1496 BP; 300 A; 456 C; 523 G; 217 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 13; Length 1496;
XX Best Local Similarity 100.0%; Pred. No. 3.2;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 163 CCATCGCCCAAGGAGATCGAGCT 184

RESULT 9
AAV34608
ID AAV34608 standard; DNA; 1569 BP.
XX AC AAV34608;
XX
DT 25-AUG-1998 (first entry)
DE M. vaccae antigen GV-27 encoding DNA.
XX Mycobacterium vaccae; antigen; prevention; cytokine production;
XX M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
XX mycobacteria infection; vaccine; cancer; ss.
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
XX CDS 1..1569
XX /*tag= a
XX /product= "GV-27 antigen"
XX /note= "the stop codon is not indicated"
XX
XX WO9808542-A2.

```

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PD 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX P-PSDB; AAW60144.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
XX detection, therapy and prevention of mycobacteria infections or as immune
XX response enhancers.
XX
XX Example 6; Page 114; 153pp; English.
XX
XX This DNA encodes a Mycobacterium vaccae antigen GV-27. The invention
XX provides M. vaccae polypeptides that comprise an immunogenic portion of a
XX soluble M. vaccae antigen, or a variant, where the antigen induces an
XX immune response in patients previously exposed to a mycobacterium. Such
XX M. vaccae polypeptides can be used in methods for enhancing non-specific
XX immune response. The methods and products can be used for the detection,
XX treatment and prevention of infectious diseases caused by mycobacteria
XX such as M. vaccae, M. avium or M. tuberculosis. The products also have
XX the ability to induce cell proliferation and cytokine production (e.g.,
XX interferon-gamma and interleukin-12 production) in T cells, NK cells, B
XX cells, or macrophages. They can be used for enhancing immune responses
XX for use in vaccines or immunotherapy of infectious diseases and cancers
XX
XX Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 2; Length 1569;
XX Best Local Similarity 100.0%; Pred. No. 3.2;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 10
AAZ11343
ID AAZ11343 standard; DNA; 1569 BP.
XX AC AAZ11343;
XX
XX 25-OCT-1999 (first entry)
XX
XX Nucleotide sequence of M. vaccae antigen GV-27.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
XX dendritic cell maturation; infectious disease; immune disorder; cancer;
XX respiratory system; mycobacterial infection; allergy; tuberculosis;
XX leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
XX dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
XX squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
XX
XX WO993634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 23-DEC-1997; 97US-00997362.
XX 11-JUN-1998; 98US-00095855.

```


CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1620;
 Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAGGAGATCGAGCT 22
 DB 161 CCATCGCCAGGAGATCGAGCT 182

RESULT 13

ADRI12623

ID ADRI12623 standard; DNA; 1620 BP.

XX AC

XX ADRI12623;

DT 04-NOV-2004 (first entry)

XX DE Gene vaccine nucleic acid #41.

KW ds; gene; antimalarial; antitubercular; tuberculostatic; anti-HIV;
 KW antibacterial; haemostatic; protozoacide; antiinflammatory;
 KW neuroprotective; virucide; gene vaccine; ubiquitin; antigen;
 KW intracellular parasite; protozoan parasite infection; malaria;
 KW tuberculosis; toxoplasmosis; trypanosomiasis; AIDS;
 KW cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis;
 KW Ebola hemorrhagic fever; Trypanosoma; Chagas disease;
 KW Japanese encephalitis; influenza; rubeola; dengue virus; poliomyelitis;
 KW Herpes virus; severe acute respiratory syndrome.

XX OS Unidentified.

XX PN WO2004067040-A1.

XX PD 12-AUG-2004.

XX PF 30-JAN-2004; 2004WO-JP000975.

XX PR 31-JAN-2003; 2003JP-00023507.

XX PA (KYUS-) KYUSHU TLO CO LTD.

XX PI Himeno K, Ishii K;

XX

DR WPI; 2004-594036/57.

DR P-PSDB; ADR12624.

XX Gene vaccine having nucleic acids encoding ubiquitin and antigen protein
 PT of intracellular parasite, useful for treating parasite infections such
 PT as malaria, tuberculosis, toxoplasmosis.

XX Disclosure; SEQ ID NO 90; 266pp; Japanese.

XX A gene vaccine (1) comprises nucleic acid sequence encoding ubiquitin,
 CC and a nucleic acid sequence encoding the antigen protein of an
 CC intracellular parasite containing T-cell target sequence. (1) is useful
 CC for preventing or treating the disease resulting from intracellular
 CC protozoan parasite infection such as malaria, tuberculosis,
 CC toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection,
 CC achlamydia disease, infections caused by Rickettsia, leishmaniasis,
 CC Ebola hemorrhagic fever, Trypanosoma infections, Chagas disease, Japanese
 CC encephalitis, influenza, rubeola and dengue viral infections,
 CC poliomyelitis, Herpes virus (alpha) infections, or severe acute
 CC respiratory syndrome. This sequence represent a nucleic acid used in the
 CC method of the invention.

SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 1620;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAGGAGATCGAGCT 22

DB 161 CCATCGCCAGGAGATCGAGCT 182

RESULT 14

AAH51969

ID AAH51969 standard; DNA; 1623 BP.

XX AC AAH51969;

DT 04-SEP-2001 (first entry)

XX Mycobacterium tuberculosis potential drug target gene SEQ ID 23.

XX Drug target; growth; organism viability; characterisation; ds.

XX Mycobacterium tuberculosis.

XX WO200135317-A1.

XX 17-MAY-2001.

XX 13-NOV-2000; 2000WO-US031152.

XX 12-NOV-1999; 99US-0165086P.

XX 12-NOV-1999; 99US-0165124P.

XX 01-FEB-2000; 2000US-0179531P.

XX (REGC) UNIV CALIFORNIA.

XX Eisenberg D, Rotstein SH, Marcotte EM;

XX WPI; 2001-329193/34.

XX P-PSDB; AAG81118.

XX Identifying nucleotide or polypeptide sequence for use as drug target,

XX involves providing algorithm that analyzes a functional relationship
 PT between nucleotide or polypeptide sequences, and comparing the sequences.

XX Disclosure; Page 63-64; 207pp; English.

XX This invention relates to a method for identifying a nucleotide or
 CC polypeptide sequence that may be a drug target, or essential for growth

or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241. Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism

Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 1623;

Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCATGCCCAAGGAGATCGAGCT 22
161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 15

AAAF25002
ID AAF25002 standard; DNA; 1623 BP.

XX AAF25002;

30-APR-2001 (first entry)

Nucleotide sequence of M. bovis BCG heat shock protein 65 (Hsp65).

Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; ss.

Mycobacterium bovis.

Key Location/Qualifiers
CDS 1..1623
/*tag= a
/product= "Hsp65"

WO200104344-A2.

18-JAN-2001.

10-JUL-2000; 2000WO-US018828.

08-JUL-1999; 99US-0143757P.

(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

Siegel M, Chu NR, Mizzen LA;

WPI; 2001-138361/14.

P-PSDB; AAB31606.

Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.

Example 2; Fig 1A-B; 88pp; English.

The present sequence encodes the Mycobacterium bovis BCG heat shock protein (Hsp) 65. Hsp65 is used in the course of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial

CC pathogens

XX Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 1623;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCATGCCCAAGGAGATCGAGCT 22
161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 16

ACA40326
ID ACA40326 standard; DNA; 1623 BP.

XX ACA40326;

19-JUN-2003 (first entry)

Prokaryotic essential gene #21983.

Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

Mycobacterium tuberculosis.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-0072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

P-PSDB; ABU36456.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 28196; 1765pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies on a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent

SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

identifying proteins or screening for homologous nucleic acids for cellular proliferation to isolate candidate molecules for

drug discovery programs, or for screening ho-

required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

K. pneumoniae or P. aeruginosa. In prokaryotic essential genes Note:

not form part of the printed or electronic format directly from

XX US 50

Query Match	100.0%	Score 22:	DB 8:	Length 1623
sequence 1623	257	304	A; 343	C; 366
				G; 208
				1; 0
				0; 0
				0
				Other

BEST LOCAL SIMILARITY 100.0%; Pred. No. 3.3;
Matches 22: Conservative 0: Mismatched

1 CCATCGGCCAAGGAGATCGAGCT 22

161 CCATCGCCAAGGAGATCGAGCT 18

KW Antisense; ds; prokaryotic essential gene; cell proliferation;

[illegible]

OS *Mycobacterium avium*.

PN WO200277183-A2.

PD 03-OCT-2002.

XX
PF
21-MAR-2002: 2002WO-US009107

XX
PR 21-MAR-2001: 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P

PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (ELIT-) ELITRA PHARM INC

XX	Wang L.	Zamudio C.	Malone C.	Hasselbeck P.	Ohlson K.T.	Zysk
PT						

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu H

DR WPI; 2003-029926/02.
DR D. DEBB. ADU23055

32 XX

PT for homologous nucleic acids required for cellular proliferation

PT isolate candidate molecules for rational drug discovery program

PS Claim 14; SEQ ID NO 25595; 1766pp; English.

The invention relates to an isolated nucleic acid comprising at least one of the 6213 antisense sequences given in the specification where the nucleic acid inhibits proliferation of a cell. Also included in the invention are:

- (1) a vector comprising a promoter operably linked to the nucleic acid;
- (2) a host cell containing the vector;
- (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid;
- (4) an antibody capable of specifically binding to the polypeptide or its fragment.

Handwriting practice lines with dashed midlines and arrows indicating stroke direction.

PS Claim 6; Fig 2; 39pp; English.

XX The present invention relates to heat shock proteins (I) and their coding
CC sequences (II), which are useful in the manufacture of a medicament for
CC use in pain relief. (I) is a chaperonin derived from Mycobacterium
CC tuberculosis (ADN1335, ADN1337 or ADN1339). (I) and (II) are useful in
CC the manufacture of a medicament used as a pain relief, where the pain is
CC at least one chosen from backache, headache, toothache, earache,
CC arthritis, Gout, soft tissue trauma, ligament/tendon traumatic damage,
CC broken bones, cancer, post operative pain, menstrual pain, obstetric
CC pain, renal tract pain, visceral pain, burns, abscesses and other
CC infections. The present sequence is a coding sequence for one such
CC chaperonin.

XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 1623;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 19

AAZ11371
ID AAZ11371 standard; DNA; 1626 BP.

AC AAZ11371;
XX

DT 25-OCT-1999 (first entry)
XX

DE Nucleotide sequence of M. vaccae antigen GV-27.

XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.

XX Mycobacterium vaccae.

XX WO932634-A2.

PN 01-JUL-1999.

PD 23-DEC-1998; 98WO-NZ000189.

PP 23-DEC-1997; 97US-00996624.

PR 23-DEC-1997; 97US-00997080.

PR 11-JUN-1998; 98US-00095855.

PR 17-SEP-1998; 98US-00156181.

PR 04-DEC-1998; 98US-00205426.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;

DR WPI; 1999-430163/36.

XX P-PSDB; AAY14909.

XX Enhancing immune response to an antigen.

XX Claim 3; Page 212-213; 243pp; English.

XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The

CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment,
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma

XX SQ Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 20

ABL36277
ID ABL36277 standard; DNA; 1626 BP.

XX ABL36277;
AC

DT 08-APR-2002 (first entry)
XX

DE M vaccae GroEL homologue GV-27 coding sequence SEQ ID NO: 159.

XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; gene; ds.

XX Mycobacterium vaccae.

XX US6328978-B1.

XX 11-DEC-2001.

XX 02-JUN-1999; 99US-00324542.

XX 23-DEC-1997; 97US-00997080.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Tan PLJ, Prestidge R;

XX WPI; 2002-138361/18.

XX P-PSDB; ABB73515.

XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.

XX Example 4; Col 167-170; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC coding sequence described in the exemplification of the invention

XX SQ Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 21
ACC42531
ID ACC42531 standard; DNA; 1626 BP.
XX AC ACC42531;
XX DT 26-AUG-2003 (first entry)
XX DE Mycobacterium vaccae antigen GV-27 coding sequence, SEQ ID 14.
XX KW Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
KW antidiabetic; antipsoriatic; dermatological; anti-inflammatory;
KW immune response; Notch signalling pathway; autoimmune disorder;
KW Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
KW apoptotic cell death; cell proliferation; gene; ds.
XX OS Mycobacterium vaccae.
XX FH Key Location/Qualifiers
FT CDS 1..1626
FT /tag=a
FT /product="Antigen GV-27"
XX PN WO2003013595-A1.
XX PD 20-FEB-2003.
XX PF 26-JUL-2002; 2002WO-NZ000135.
XX PR 26-JUL-2001; 2001US-0308446P.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Watson JD, Tan PLJ, Abernethy N;
XX DR WPI; 2003-239567/23.
XX P-PSDB; ABP70891.
XX PT Methods for modulating immune responses by modulating the Notch signaling
PT and Toll-like receptor signalling pathways, and treating e.g. autoimmune
PT disorders.
XX PS Claim 7; Page 108-109; 136pp; English.
XX CC The present invention relates to methods for modulating immune responses
CC by modulating the Notch signalling and Toll-like receptor signalling
CC pathways using compositions comprising mycobacteria antigens (ACC42518-
CC ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
CC immune responses and treating e.g. autoimmune disorders (such as multiple
CC sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
CC systemic lupus erythematosus, scleroderma), allergic disease and graft
CC rejection and also disorders characterised by undesired apoptotic cell
CC death or undesired cell proliferation
XX SQ Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 22
ACA39632
ID ACA39632 standard; DNA; 1626 BP.
XX AC ACA39632;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #21289.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX OS Mycobacterium leprae.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX P-PSDB; ABU35762.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 27502; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1626 BP; 352 A; 450 C; 540 G; 284 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 23
ACCT0275
ID ACC70275 standard; DNA; 1626 BP.
XX
AC ACC70275;
XX
DT 11-AUG-2003 (first entry)
XX
DE Nucleotide sequence of the Rhodococcus equi GroEL2 protein.
XX
KW GroEL protein; protein aggregation; protein folding; immune response;
KW antigen; pathogenic infection; gene; ss.
XX
OS Rhodococcus equi.
XX
FH Key Location/Qualifiers
FT CDS 1
FT /*tag= a
FT /product= "GroEL2"
XX
PN WO2003035676-A1.
XX
PD 01-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-AU001460.
XX
PR 26-OCT-2001; 2001AU-00008523.
XX
PA (UYSA-) UNIV SOUTH AUSTRALIA.
PA (MEDV-) MEDVET SCI PTY LTD.
PA (RURA-) RURAL IND RES & DEV CORP.
XX
PI Vamiasinkam T, Barton M, Heuzenroeder MW;
XX
WPI; 2003-482030/45.
DR P-PSDB; ABR55530.
XX
PT New GroEL protein, useful for preparing a composition for preventing or
PT treating pathogenic infections.
XX
PS Disclosure; Fig 1; 77pp; English.
XX
CC The present sequence encodes a GroEL protein. The groEL2 gene is highly
CC conserved between species, and the protein facilitates the correct
CC folding of various bacterial proteins as well as prevent the aggregation
CC of denatured proteins by an ATP-dependent mechanism. The specification
CC describes a chimeric protein, consisting of a GroEL protein which has a
CC modification or analogue comprising a surface exposed exogenous amino
CC acid sequence inserted to it. The exogenous amino acid sequence is
CC configured to elicit an immune response specifically reactive to the
CC antigenic determinant. The chimeric protein is useful for preparing a
CC composition for preventing or treating pathogenic infections
XX
SQ Sequence 1626 BP; 300 A; 544 C; 549 G; 233 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 9; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 24
ADT46122
ID ADT46122 standard; cDNA; 1632 BP.
XX
AC ADT46122;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #20873.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOX/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 44560; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX

```
SQ Sequence 1632 BP; 356 A; 514 C; 507 G; 255 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 13; Length 1632;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 25
AADS7198
ID AADS7198 standard; DNA; 1701 BP.
XX
AC AADS7198;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mycobacterium avium subspecies paratuberculosis protein gene #11.
XX
KW Immunogenic fragment; vaccine; Map infection; wild-type infection;
KW antibacterial; gene; ds.
XX
OS Mycobacterium avium.
XX
FH Key Location/Qualifiers
CDS 76..1701
FT /*tag= a
FT /product= "Protein"
XX
PN WO2003058248-A2.
XX
PD 17-JUL-2003.
XX
PF 13-JAN-2003; 2003WO-NL000020.
XX
PR 11-JAN-2002; 2002EP-00075089.
XX
PA (IDLE-) ID-LELYSTAD INST DIERHOUDRIJ EN DIERGEZ.
XX
PI Willemsen PTJ, Westerveen SP, Bakker D, Van Zijderveld FG;
PI Thole JER;
XX
DR WPI; 2003-598398/56.
DR P-PSDB; AAE37881.
XX
PT Novel Mycobacterium avium subspecies paratuberculosis protein, useful as
PT vaccine for combating the bacterial infection, and for diagnosing the
PT infection.
XX
PS Disclosure; Page 84-86; 88pp; English.
XX
SS The invention relates to Mycobacterium avium subspecies paratuberculosis
CC protein or an immunogenic fragment of the protein. The invention is
CC useful in the manufacture of a vaccine for combating Map infection. The
CC nucleic acids, the proteins and antibodies are also useful in
CC diagnostics. The vaccines are also suitable as marker vaccines, in that
CC it allows discrimination of vaccinated and field-infected mammals on the
CC basis of characteristic antibody panel induced by wild-type infection.
CC The present sequence is Mycobacterium avium subspecies paratuberculosis
CC protein gene
XX
SQ Sequence 1701 BP; 318 A; 569 C; 591 G; 223 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 236 CCATCGCCCAAGGAGATCGAGCT 257

RESULT 26
ACC49833
ID ACC49833 standard; DNA; 1752 BP.
XX
AC ACC49833;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human recombinant protein vaccine gene.
XX
KW Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
KW antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
CDS 1..1752
FT /*tag= a
FT
XX
PN CN1362263-A.
XX
PD 07-AUG-2002.
XX
PF 15-NOV-2001; 2001CN-00134935.
XX
PR 04-JAN-2001; 2001CN-00100380.
XX
PA (BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
XX
PI Wang L, Li D, Yu Y;
XX
DR WPI; 2003-230415/23.
DR P-PSDB; ABR40246.
XX
PT Recombinant protein vaccine for preventing and treating human prostate
PT cancer.
XX
PS Claim 7; Page 15-19; 35pp; Chinese.
XX
SS The invention relates to a novel recombinant protein vaccine, a fusion
CC protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of
CC human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The
CC vaccine of the invention is useful for treating and preventing carcinoma
CC of prostate. The invention also discloses the genes encoding the
CC recombinant protein vaccines. The present sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 1752 BP; 356 A; 535 C; 595 G; 266 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 8; Length 1752;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 27
ADX05272
ID ADX05272 standard; DNA; 1761 BP.
XX
AC ADX05272;
XX
DT 21-APR-2005 (first entry)
XX
DE HSP65-MUC1-ME fusion protein coding sequence, SEQ ID 1.
XX
KW Fusion protein; Cytostatic; Gene Therapy; heat shock protein 65; HSP65;
KW mucin; MUC1; carcinoma; gene; ds.
XX
```

OS	Mycobacterium bovis BCG.
OS	Homo sapiens.
OS	Synthetic.
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1761
FT	/tag= a
FT	/product= "HSP65-MUC1-ME fusion protein"
XX	
XX	US2005031649-A1.
XX	
XX	PN PN
XX	PD PD
XX	10-FEB-2005.
XX	XX XX
XX	06-AUG-2003; 2003US-00635211.
XX	PF PF
XX	06-AUG-2003; 2003US-00635211.
XX	PR PR
XX	(YUYU/) YU Y.
PA	(LIHH/) LI H.
PA	(WANG/) WANG L.
PI	
PI	Yu Y, Li H, Wang L;
XX	
XX	WPI; 2005-131970/14.
DR	P-PSDB; ADX05273.
DR	DR DR
XX	
XX	New recombinant fusion protein comprises Bacillus Calmette Guerin (BCG)
PT	heat shock protein 65 and 1-5 copies of an epitope of MUC1, useful for
PT	treating or preventing human MUC1 expressing carcinomas.
XX	
XX	Claim 31; SEQ ID NO 1; 19pp; English.
PS	
PS	The present invention relates to a novel recombinant fusion protein
CC	(HSP65-MUC1-ME, ADX05273) which comprises Bacillus Calmette Guerin (BCG)
CC	heat shock protein 65 (HSP65) and an epitope of mucin protein MUC1 (MUC1-
CC	ME). The BCG HSP65 is located at the amino terminal portion of the fusion
CC	protein and the epitope of MUC1 is located at the carboxy terminal
CC	portion of the fusion protein. The MUC1 epitope can generate MUC1
CC	specific cytotoxic T lymphocytes. The recombinant fusion protein is
CC	useful for treating or preventing human carcinomas, preferably MUC1
CC	expressing carcinomas. The present sequence is the coding sequence for
CC	the fusion protein of the invention.
XX	
XX	Sequence 1761 BP; 338 A; 543 C; 608 G; 272 T; 0 U; 0 Other;
SQ	
Query Match	100.0%; Score 22; DB 14; Length 1761;
Best Local Similarity	100.0%; Pred. No. 3.3;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCATGCCCAAGGAGATCGAGCT 22
Db	161 CCATGCCCAAGGAGATCGAGCT 182
RESULT 28	
ADK68629	
ID	ADK68629 standard; cDNA; 1800 BP.
XX	
AC	ADK68629;
XX	
DT	06-MAY-2004 (first entry)
DE	HSP65-MUC1 antigen CTL epitope related cDNA #1.
XX	
KW	Human breast cancer; Mycobacterium bovis; heat shock protein 65; BCG;
KW	HSP65; cytotoxic T lymphocyte; CTL; MUC1; HSP65-MUC1 antigen CTL epitope;
KW	gene; ss.
OS	Unidentified.
XX	
PN	CN1368384-A.
XX	
PD	11-SEP-2002.
PT	
PT	Recombinant protein vaccine for preventing and treating human prostate
PT	cancer.
PT	
XX	
XX	Sequence 1800 BP; 347 A; 561 C; 616 G; 276 T; 0 U; 0 Other;
SQ	
Query Match	100.0%; Score 22; DB 10; Length 1800;
Best Local Similarity	100.0%; Pred. No. 3.3;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCATGCCCAAGGAGATCGAGCT 22
Db	161 CCATGCCCAAGGAGATCGAGCT 182
RESULT 29	
ACC49834	
ID	ACC49834 standard; DNA; 1914 BP.
XX	
AC	ACC49834;
XX	
DT	27-JUN-2003 (first entry)
XX	
DE	Human recombinant protein vaccine gene.
XX	
KW	Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
KW	antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	1..1914
FT	/tag= a
XX	
XX	CN1362263-A.
XX	
XX	07-AUG-2002.
XX	
XX	15-NOV-2001; 2001CN-00134935.
XX	
XX	04-JAN-2001; 2001CN-00100380.
XX	
XX	(BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
PA	
PI	Wang L, Li D, Yu Y;
XX	
XX	WPI; 2003-230415/23.
DR	P-PSDB; ABR40247.
DR	
XX	
XX	Recombinant protein vaccine for preventing and treating human prostate
PT	cancer.
PT	
XX	
XX	Sequence 1800 BP; 347 A; 561 C; 616 G; 276 T; 0 U; 0 Other;
SQ	
Query Match	100.0%; Score 22; DB 10; Length 1800;
Best Local Similarity	100.0%; Pred. No. 3.3;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCATGCCCAAGGAGATCGAGCT 22
Db	161 CCATGCCCAAGGAGATCGAGCT 182
RESULT 29	
ACC49834	
ID	ACC49834 standard; DNA; 1914 BP.
XX	
AC	ACC49834;
XX	
DT	27-JUN-2003 (first entry)
XX	
DE	Human recombinant protein vaccine gene.
XX	
KW	Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
KW	antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	1..1914
FT	/tag= a
XX	
XX	CN1362263-A.
XX	
XX	07-AUG-2002.
XX	
XX	15-NOV-2001; 2001CN-00134935.
XX	
XX	04-JAN-2001; 2001CN-00100380.
XX	
XX	(BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
PA	
PI	Wang L, Li D, Yu Y;
XX	
XX	WPI; 2003-230415/23.
DR	P-PSDB; ABR40247.
DR	
XX	
XX	Recombinant protein vaccine for preventing and treating human prostate
PT	

XX Claim 7; Page 23-26; 35pp; Chinese.

XX The invention relates to a novel recombinant protein vaccine, a fusion

XX protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of

XX human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The

XX vaccine of the invention is useful for treating and preventing carcinoma

XX of prostate. The invention also discloses the genes encoding the

XX recombinant protein vaccines. The present sequence is used in the

XX exemplification of the invention

XX Sequence 1914 BP; 397 A; 576 C; 633 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1914;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 30

AAF25012

ID AAF25012 standard; DNA; 1920 BP.

XX AC AAF25012;

XX 30-APR-2001 (first entry)

XX DE Nucleotide sequence of Hsp65-E7 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

XX lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

XX E7 protein; ss.

XX Synthetic.

XX Mycobacterium bovis.

XX Human papillomavirus.

XX Key Location/Qualifiers

XX CDS 1..1920

XX /*tag= a

XX /product= "Hsp65-E7 fusion protein"

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mizzen LA;

XX WPI; 2001-138361/14.

XX P-PSDB; AAB31609.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T

XX lymphocyte cells.

XX Example 5; Fig 4A-B; 88pp; English.

XX The present sequence encodes a fusion protein comprising a Mycobacterium

XX bovis heat shock protein (Hsp) 65 fused at its C terminal to a Hpv16 E7

XX protein. The fusion protein is used in the method of the invention. The

XX specification describes a method of determining whether a compound

XX stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

XX lymphocyte cells. The method comprises contacting naive lymphocytes in

XX vitro with a fusion protein comprising at least a fragment of Hsp, and

XX then detecting the Th1-like response exhibited by the cell sample. The

CC proteins which may be used in the method of the invention are Hsp65,

CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify

CC compounds that stimulate Th1-like responses in response to microbial

CC pathogens

XX Sequence 1920 BP; 415 A; 551 C; 638 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 1920;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 31

AAF25019

ID AAF25019 standard; DNA; 1947 BP.

XX AC AAF25019;

XX 30-APR-2001 (first entry)

XX DE Nucleotide sequence of Hsp65-E7 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

XX lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

XX E7 protein; ss.

XX Synthetic.

XX Mycobacterium bovis.

XX Human papillomavirus.

XX Key Location/Qualifiers

XX CDS 1..1947

XX /*tag= a

XX /product= "Hsp65-E7 fusion protein"

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mizzen LA;

XX WPI; 2001-138361/14.

XX P-PSDB; AAB31614.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T

XX lymphocyte cells.

XX Example 11; Fig 10A-B; 88pp; English.

XX The present sequence encodes a fusion protein comprising a Mycobacterium

XX bovis heat shock protein (Hsp) 65 fused at its C terminal to a Hpv16 E7

XX protein. The fusion protein is used in the method of the invention. The

XX specification describes a method of determining whether a compound

XX stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

XX lymphocyte cells. The method comprises contacting naive lymphocytes in

XX vitro with a fusion protein comprising at least a fragment of Hsp, and

XX then detecting the Th1-like response exhibited by the cell sample. The

XX proteins which may be used in the method of the invention are Hsp65,

XX Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify

XX compounds that stimulate Th1-like responses in response to microbial

XX pathogens

XX Sequence 1947 BP; 417 A; 557 C; 653 G; 320 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 1947;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 32
ADW23606
ID ADW23606 standard; DNA; 1965 BP.
XX
AC ADW23606;
XX
DT 10-MAR-2005 (first entry)
XX
DE Hepatitis C virus related DNA SEQ ID NO 6.
XX
KW recombinant protein; vaccine; fusion protein; hepatitis C; ds; gene.
XX
OS Synthetic.
XX
PN CN1462636-A.
XX
PD 24-DEC-2003.
XX
PF 30-MAY-2002; 2002CN-00122116.
XX
PR 30-MAY-2002; 2002CN-00122116.
XX
PA (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX
PI Wang L, Sun M, Yu Y;
XX
DR WPI; 2004-239553/23.
DR P-PSDB; ADW23607.
XX
PT Vaccine of recombinant albumen for preventing and treating infection of
PT human hepatitis C virus.
XX
PS Claim 9; SEQ ID NO 6; 54pp; Chinese.
XX
CC The invention relates to a recombinant protein vaccine which is a fusion
CC protein of BCG vaccine's heat shock protein 65 and the core antigen of
CC multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
CC and nucleotide sequence for coding it, the expression carrier containing
CC nucleotide sequence, the host cell containing expression carrier, the
CC preparing process of recombinant protein vaccine, the vaccine containing
CC recombinant protein for preventing and treating hepatitis C and a method
CC for detecting the activity of specifically killing T-lymphocytes by the
CC hepatitis C induced by vaccine and its cell model are disclosed. The
CC present sequence represents a hepatitis C virus related DNA.
XX
SQ Sequence 1965 BP; 405 A; 593 C; 658 G; 309 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 1965;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 33
ADN00588
ID ADN00588 standard; DNA; 1980 BP.
XX
AC ADN00588;
XX
DT 17-JUN-2004 (first entry)

XX BCG vaccine HSP65-MOMP fusion protein coding sequence, SEQ ID 3.
DE
XX Antibacterial; gynaecological; protein vaccine;
KW BCG vaccine heat shock protein 65; major outer membrane protein; MOMP;
KW Chlamydia infection; urogenital infection; gene; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1980
FT /*tag= a
FT /product= "BCG vaccine HSP65-MOMP fusion protein"
XX
XX W02004020471-A1.
PN
XX 11-MAR-2004.
PD
XX 03-JUN-2003; 2003WO-CN000430.
PF
XX 29-AUG-2002; 2002CN-00141977.
PR
XX (BEIJ-) BEIJING HYDVAX BIOTECHNOLOGY CO LTD.
PA
XX Wang L, Yang S, Yu Y;
PI
XX WPI; 2004-248232/23.
DR P-PSDB; ADN00589.
DR
XX Heat shock protein-based recombinant protein for vaccines against human
PT Chlamydia trachomatis, applicable in preventing or/and treating human
PT Chlamydia infections.
XX
PS Claim 7; SEQ ID NO 3; 49pp; Chinese.
XX
CC The present invention relates to a recombinant protein vaccine
CC (ADN00589), which is a fusion protein of BCG vaccine heat shock protein
CC (HSP) 65 with the major outer membrane protein (MOMP) of Chlamydia
CC trachomatis (ADN00587). The fusion protein comprises the BCG vaccine HSP
CC 65 at the amino-end, with the MOMP protein at the carboxy-end. The
CC vaccine is capable of activating cytotoxic T-lymphocytes and can be used
CC for preventing or/and treating human Chlamydia infections, particularly
CC urogenital infections. The present sequence is the coding sequence for
CC the fusion protein, used to illustrate the invention.
XX
SQ Sequence 1980 BP; 407 A; 595 C; 653 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 1980;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 34
ADK72374
ID ADK72374 standard; DNA; 2016 BP.
XX
AC ADK72374;
XX
DT 06-MAY-2004 (first entry)
XX
DE BCG-HER-2 fusion gene construct for breast cancer vaccine treatment.
XX
KW vaccine; fusion protein; BCG; heat-shock protein 65; HSP65; HER-2;
KW antigen; breast cancer; gene; ds.
XX
OS Homo sapiens.
OS Bacillus sp.
OS Chimeric.
XX


```

FT CDS 1..2130
FT /*tag= a
FT /product= "HisHepCorT(149/87S97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2001; 2001US-0266733P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizzen L, Liu H, Siegel M;
XX
XX WPI; 2002-706903/76.
XX
XX P-PSDB; ABG70776.
XX
XX Novel isolated fusion protein useful for treating hepatitis B virus
XX infection in a subject, comprises a stress protein or its portion, and a
XX hepatitis B virus core antigen.
XX
XX Example 1; Fig 7; 58pp; English.
XX
XX The invention discloses an isolated fusion protein, and the
XX polynucleotide encoding it, that comprises a stress protein (e.g.
XX Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
XX hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
XX when administered to an individual, induces or enhances an immune
XX response against the HBV core antigen. HBV is a non-cytopathic DNA virus
XX against which a vaccine has been developed. However, due to the morbidity
XX and mortality arising from chronic HBV infection occurring over a period
XX of decades, the impact of vaccinations will not be apparent for some time
XX yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
XX therapy and as a pharmaceutical composition for inducing or enhancing an
XX immune response against an HBV core antigen in a subject for treating an
XX HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
XX The sequence presented is the DNA encoding the truncated hepatitis B
XX virus core antigen fused to the N-terminus of the M. bovis variant
XX Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65,
XX hisHepCorT(149/87S97F)Hsp65. The core antigen the DNA encodes has been
XX truncated to include residues 1 to 149, had an N-terminal histidine tag
XX added, had two amino acids changed from the wild-type sequence and there
XX has been an additional residue added between the HBV core protein and the
XX Hsp65 protein. (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 2130 BP; 444 A; 616 C; 681 G; 389 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 6; Length 2130;
XX Best Local Similarity 100.0%; Pred. NO. 3.3;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCATCGCCCAAGGAGATCGAGCT 22
XX 668 CCATCGCCCAAGGAGATCGAGCT 689
XX
XX Db
XX
XX RESULT 37
XX ABS54449
XX ID ABS54449 standard; DNA; 2175 BP.
XX
XX AC ABS54449;
XX
XX 07-AUG-2003 (revised)
XX 09-DEC-2002 (first entry)
XX
XX BCG Hsp65/mutant HBV core antigen, HepCor(97F)Hsp65, DNA.
XX
XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
XX Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity;
XX mortality; infection; gene therapy; hepatitis; cirrhosis;
XX hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
XX
XX antiinflammatory; BCG; chimera; mutant.
XX
XX Hepatitis B virus.
XX Mycobacterium bovis.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..2175
XX /*tag= a
XX /product= "HepCor(97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2001; 2001US-0266733P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizzen L, Liu H, Siegel M;
XX
XX WPI; 2002-706903/76.
XX
XX P-PSDB; ABG70778.
XX
XX Novel isolated fusion protein useful for treating hepatitis B virus
XX infection in a subject, comprises a stress protein or its portion, and a
XX hepatitis B virus core antigen.
XX
XX Example 1; Fig 11; 58pp; English.
XX
XX The invention discloses an isolated fusion protein, and the
XX polynucleotide encoding it, that comprises a stress protein (e.g.
XX Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
XX hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
XX when administered to an individual, induces or enhances an immune
XX response against the HBV core antigen. HBV is a non-cytopathic DNA virus
XX against which a vaccine has been developed. However, due to the morbidity
XX and mortality arising from chronic HBV infection occurring over a period
XX of decades, the impact of vaccinations will not be apparent for some time
XX yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
XX therapy and as a pharmaceutical composition for inducing or enhancing an
XX immune response against an HBV core antigen in a subject for treating an
XX HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
XX The sequence presented is the DNA encoding the hepatitis B virus core
XX antigen fused to the N-terminus of the M. bovis variant Bacille-Calmette-
XX Guerin (BCG) heat shock protein (Hsp) 65, HepCor(97F)Hsp65. The core
XX antigen the DNA encodes has had an amino acid changed from the wild-type
XX sequence. (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 2175 BP; 459 A; 628 C; 691 G; 397 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 6; Length 2175;
XX Best Local Similarity 100.0%; Pred. NO. 3.3;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCATCGCCCAAGGAGATCGAGCT 22
XX 713 CCATCGCCCAAGGAGATCGAGCT 734
XX
XX Db
XX
XX RESULT 38
XX ABS54446
XX ID ABS54446 standard; DNA; 2241 BP.
XX
XX AC ABS54446;
XX
XX 07-AUG-2003 (revised)
XX 09-DEC-2002 (first entry)
XX
XX His tagged BCG Hsp65/mutant HBV core antigen, hisHepCor(97F)Hsp65, DNA.
```

XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein; Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity; morbidity; infection; gene therapy; hepatitis; cirrhosis; hepatocellular carcinoma; virucide; immunostimulant; hepatotropic; antiinflammatory; BCG; chimera; mutant.

XX Hepatitis B virus.

OS Mycobacterium bovis.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 1..2241

FT /*tag= a

FT /product= "HisHepCor(97F)Hsp65"

XX WO200262959-A2.

XX 15-AUG-2002.

XX 05-FEB-2002; 2002WO-US003460.

XX 05-FEB-2001; 2001US-0266733P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Mizzen L, Liu H, Siegel M;

XX WPI: 2002-706903/76.

XX P-PSDB; ABG70775.

XX Novel isolated fusion protein useful for treating hepatitis B virus infection in a subject, comprises a stress protein or its portion, and a hepatitis B virus core antigen.

XX Example 1; Fig 5; 58pp; English.

XX The invention discloses an isolated fusion protein, and the polynucleotide encoding it, that comprises a stress protein (e.g. Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a hepatitis B virus (HBV) core antigen (HBe), where the fusion protein, when administered to an individual, induces or enhances an immune response against the HBV core antigen. HBV is a non-cytopathic DNA virus against which a vaccine has been developed. However, due to the morbidity and mortality arising from chronic HBV infection occurring over a period of decades, the impact of vaccinations will not be apparent for some time yet. The polynucleotide and polypeptide can be used as a vaccine, in gene therapy and as a pharmaceutical composition for inducing or enhancing an immune response against an HBV core antigen in a subject for treating an HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma. The sequence presented is the DNA encoding the full length hepatitis B virus core antigen fused to the N-terminus of the M. bovis variant Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65, had an N-hisHepCor(97F)Hsp65. The core antigen the DNA encodes has had an N-terminal histidine tag added and had an amino acid changed from the wild-type sequence. Two additional residues have also been added between the HBV core protein and the Hsp65 protein. (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 2241 BP; 474 A; 650 C; 709 G; 408 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 2241;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCAAGAGATCGAGCT 22

Db 779 CCATGCCAAGAGATCGAGCT 800

RESULT 39

ADR30583

ID ADR30583 standard; DNA; 2585 BP.

XX AC ADR30583;

XX DT 18-NOV-2004 (first entry)

XX DE Arthrobacter heat shock protein 60 (hsp60) encoding DNA SEQ ID NO:1.

XX KW Arthrobacter; heat shock protein 60; hsp60; antibacterial; virucide; vaccine; bacterial kidney disease; salmonid rickettsial septicemia; infectious salmonia anaemia virus; infectious pancreatic necrosis virus; infectious disease; environmental stress; gene; ds.

XX OS Arthrobacter sp.

XX Key Location/Qualifiers

FT CDS 953..2578

FT /*tag= a

FT /product= "heat shock protein 60 (hsp60)"

XX WO2004071387-A2.

XX 26-AUG-2004.

XX 13-FEB-2004; 2004WO-EP001368.

XX 14-FEB-2003; 2003GB-00003507.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS PHARMA GMBH.

XX Griffiths SG, Ritchie RJ, Simard NC;

XX WPI: 2004-625750/60.

XX P-PSDB; ADR30584.

XX New Arthrobacter hsp60 gene, useful in preparing a vaccine for treating or preventing Bacterial Kidney Disease, Salmonid Rickettsial Septicemia, Infectious Salmonia Anemia Virus or Infectious Pancreatic Necrosis Virus.

XX Claim 3; SEQ ID NO 1; 33pp; English.

XX The present sequence encodes Arthrobacter heat shock protein 60 (hsp60) (I). The present invention describes: (1) a chimeric nucleic acid sequence comprising (I) fused in-frame to a heterologous coding sequence encoding an antigen from an animal pathogen; (2) a DNA expression vector (II) comprising (I) operably linked to a transcriptional regulatory sequence; (3) a host cell transformed with (II); (4) an isolated Arthrobacter hsp60 amino acid sequence (III) or its fragment, derivative or homologue; (5) an antibody raised against (III); (6) a vaccine composition comprising (I)-(III) or an Arthrobacter cell extract enriched in hsp60 and a carrier; (7) a kit comprising the vaccine composition and a heterologous antigen or a nucleic acid sequence encoding the antigen for separate, sequential or simultaneous administration; (8) a method of inducing or enhancing an immune response to an immunogen or a hapten in an animal; (9) a method of treating or preventing infectious disease in fish; and (10) a method of preparing a vaccine composition. Hsp60 has antibacterial and virucide activities, and can be used in vaccines. The Arthrobacter hsp60 amino acid or nucleic acid sequence can be used as a non-specific vaccine adjuvant. The Arthrobacter hsp60 amino acid or nucleic acid sequence, DNA expression vector or an Arthrobacter cell extract enriched in hsp60 is useful in the manufacture of a vaccine for treating or preventing bacterial kidney disease, salmonid rickettsial septicemia, infectious salmonia anaemia virus or infectious pancreatic necrosis virus or for diagnosing infectious diseases or environmental stresses. The promoter sequence of Arthrobacter hsp60 gene is useful in expressing a heterologous gene. The antibody is useful in the manufacture of a medicament for the treatment or diagnosis of infectious disease.

XX Sequence 2585 BP; 515 A; 781 C; 824 G; 465 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 2585;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 1113 CCATGCCCAAGGAGATCGAGCT 1134

RESULT 40
AAP25014
ID AAF25014 standard; DNA; 2847 BP.
XX AC AAF25014;
XX 30-APR-2001 (first entry)
XX Nucleotide sequence of Hsp65-ovalbumin fusion protein.
XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW ovalbumin; ss.
XX Synthetic.
OS Mycobacterium bovis.
OS Gallus sp.
XX Location/Qualifiers
FH Key 1..2847
FT CDS /*tag= a
FT /product= "Hsp65-ovalbumin fusion protein"
XX WO200104344-A2.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000MO-US018828.
XX 08-JUL-1999; 99US-0143757P.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX Siegel M, Chu NR, Mizzen LA;
XX WPI; 2001-138361/14.
DR P-PSDB; AAB31611.
XX Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
XX Example 8; Fig 7A-B; 88pp; English.
XX The present sequence encodes a fusion protein comprising a Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to an ovalbumin protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 221 CCATGCCCAAGGAGATCGAGCT 242

RESULT 41
AAN80339
ID AAN80339 standard; DNA; 3613 BP.
XX AC AAN80339;
XX 25-MAR-2003 (revised)
DT 10-OCT-1990 (first entry)
XX Clone Y3178 insert contg. M. leprae 65kD antigen gene.
XX Leprosy; antigen; vaccine; armadillo; ss.
XX Mycobacterium leprae.
XX Location/Qualifiers
FH Key 56..1832
FT CDS /*tag= a
FT /product= "61,856 dalton protein"
FT misc_RNA 207..1832
FT /*tag= b
FT /product= "56,686 dalton protein"
XX WO8800974-A.
XX 11-FEB-1988.
XX 28-JUL-1987; 87WO-US001825.
XX 31-JUL-1986; 86US-00892095.
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX Young RA;
XX WPI; 1988-049978/07.
DR P-PSDB; AAP80364.
XX DNA encoding antigens of mycobacterium leprae - used for producing immuno-determinant protein antigen for prevention diagnosis and treatment of leprosy.
XX Claim 7; Fig 1; 46pp; English.
XX The gene was isolated by probing a lambda gt11 library of M. leprae DNA with MAb directed against M. leprae specific antigens. The sequences were determined with a rapid primer extension method. The antigen appears as a doublet on SDS PAGE with mol. wt. 55-65 kD so translation may initiate at the start of either CDS in the feature table, producing two polypeptides. The sequence can be used in the development of highly specific serological tests for screening populations for individuals producing Abs to M. leprae, in the development of vaccines and in the assessment of efficacy of treatment. (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 3613 BP; 724 A; 960 C; 1183 G; 746 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 22; DB 1; Length 3613;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 367 CCATGCCCAAGGAGATCGAGCT 368

RESULT 42
AAN81768
ID AAN81768 standard; DNA; 4260 BP.
XX AC AAN81768;

```

XX 25-MAR-2003 (revised)
DT 29-DEC-1990 (first entry)
XX
DE Sequence encoding Mycobacterium tuberculosis 540 and 517 AA residue
DE proteins.
XX
KW Diagnosis; assay; M.bovis; vaccine; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT CDS 252..1874
FT /tag= a
FT /label= 540 AA protein
FT /note= "AAP81351"
FT CDS complement(3948..2395)
FT /tag= b
FT /label= 517 AA protein
FT /note= "AAP81868"
XX
PN WO8806591-A.
XX
XX
XX 07-SEP-1988.
XX
XX 25-FEB-1988; 88WO-US000598.
XX
XX 26-FEB-1987; 87US-00019529.
XX 24-FEB-1988; 88US-00159667.
XX
XX (SCHI ) SCRIPPS CLINIC & RE.
XX
XX Shinnick T, Houghten R;
XX
XX WPI; 1988-271136/38.
XX P-PSDB; AAP81351, AAP81868.
XX
XX Recombinant mycobacterial peptide(s) - used in assays for diagnosis of
XX infection, for producing vaccines and for producing antibodies.
XX
XX Disclosure; Fig 2a-2d; 117pp; English.
XX
XX An isolated DNA molecule that consists essentially of the nucleotide
XX sequence that corresponds to the sequence represented by position 3950 to
XX about 2390 and from position 3948 through position 2398 of AAP81768 is
XX claimed. Also claimed is a peptide sequence that consists of a 5-40 AA
XX residue sequence that corresponds to a sequence of the 540 AA residue
XX protein (AAP81351) or the 517 AA residue protein (AAP81868) coded for by
XX the DNA sequence. The proteins can be used for determining previous
XX immunological exposure of a mammal to M.tuberculosis or M.bovis and for
XX producing a vaccine. (Updated on 25-MAR-2003 to correct PR field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 4260 BP; 733 A; 1332 C; 1481 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 1; Length 4260;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db |||||
412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 43
AAN80222
ID AAN80222 standard; DNA; 4380 BP.
XX
XX AAN80222;
XX AC
XX DT 25-MAR-2003 (revised)
XX 19-MAR-1991 (first entry)
XX

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```

DE Sequence of Mycobacterium tuberculosis DNA contg. gene encoding 65
DE protein.
XX
XX Antigen; vaccine; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT CDS 192..1874
FT /tag= a
FT CDS complement(2398..4101)
FT /tag= b
XX
XX WO8805823-A.
XX
XX 11-AUG-1988.
XX
XX 01-FEB-1988; 88WO-US000281.
XX
XX 02-FEB-1987; 87US-00010007.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Husson RN, Young RA, Nick TM;
XX
XX WPI; 1988-235175/33.
XX P-PSDB; AAP80215, AAP80216.
XX
XX Genes encoding Mycobacterium tuberculosis protein antigens - useful for
XX developing reagents for diagnosis, prevention and treatment of
XX tuberculosis.
XX
XX Claim 12; Fig 8; 82pp; English.
XX
XX The gene was isolated by probing a lambda gt11 expression library of
XX M.tuberculosis DNA with monoclonal antibodies directed against
XX M.tuberculosis-specific antigens. The 19kD, 71kD and the 65kD proteins
XX and genes are claimed, and so is a vaccine comprising DNA encoding
XX M.tuberculosis protein in a recombinant vaccine vector. AAP80216 is
XX encoded on the complementary strand. (Updated on 25-MAR-2003 to correct
XX PA field.)
XX
SQ Sequence 4380 BP; 757 A; 1373 C; 1512 G; 738 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 1; Length 4380;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db |||||
412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 44
AAV05708
ID AAV05708 standard; DNA; 4380 BP.
XX
XX AC
XX AAV05708;
XX
XX 22-JUN-1998 (first entry)
XX
XX Mycobacterium tuberculosis 65 kDa heat shock protein gene.
XX
XX Heat shock protein; Mt Hsp65; autoimmune disease; immunotherapy;
XX gene therapy; rheumatoid arthritis; multiple sclerosis; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
XX 252..1874
XX /tag= a
XX /product= "65 kDa heat shock protein"
XX

```

```
PN WO9746253-A2.
XX
XX
PD 11-DEC-1997.
XX
XX PF 03-JUN-1997; 97WO-US009427.
XX
XX PR 03-JUN-1996; 96US-0019100P.
XX PR 03-JUN-1997; 97US-00019100.
XX
XX PA (AURA-) AURAGEN INC.
XX
XX PI Haynes JR, Prayaga SK, Ramshaw IA;
XX
XX DR WPI; 1998-041892/04.
XX
XX DR P-PSDB; AAW44702.
XX
XX
PT Treatment of auto-immune diseases - by administering auto-antigen-coated
PT particles or auto-antigen-encoding nucleic acid construct.
XX
XX PS Example 2; Page 55-59; 72pp; English.
XX
XX CC This DNA sequence encodes the 65 kDa heat shock protein (see AAW44702),
XX designated Mt Hsp65, of Mycobacterium tuberculosis. This protein cross-
XX reacts with a component of articular cartilage, human Hsp60, that is up-
XX regulated in the joints of arthritic patients. A claimed method for
XX treating or preventing an autoimmune disease in a mammal comprises: (a)
XX providing a particle coated with an antigen against which an immune
XX response is mounted in the autoimmune disease; (b) delivering the
XX particle into the recipient cell of the mammal; and (c) repeating step
XX (b) until either a reduction in a cytotoxic immune response or a
XX desensitizing immune response is induced in the mammal. Alternatively,
XX step (a) comprises providing a nucleic acid construct comprising a coding
XX sequence for the antigen, operably linked to control elements such that
XX the coding sequence can be transcribed and translated in a recipient
XX cell, and delivering the construct to the recipient cell using a gene
XX gun. The antigen of step (a) is selected from collagen, Mt Hsp65, myelin
XX basic protein, myelin oligodendrocyte glycoprotein, proteolipid protein,
XX and epitopes thereof. These antigens mitigate cytotoxic responses and
XX elicit antigen desensitization. The method is used especially for
XX treating rheumatoid arthritis or multiple sclerosis. It represents a
XX novel use for the known Mt Hsp65 gene
XX
XX SQ Sequence 4380 BP; 757 A; 1371 C; 1514 G; 738 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 2; Length 4380;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 45
ABA99141
XX ABA99141 standard; DNA; 4380 BP.
XX
XX AC ABA99141;
XX
XX DT 23-MAY-2002 (first entry)
XX
XX DE hsp65 encoding sequence.
XX
XX KW hsp65; heat shock protein; cytosolic; antibacterial; antiparasitic;
XX MHC class I; ds.
XX
XX OS Mycobacterium tuberculosis.
XX
XX PN US6331388-B1.
XX
XX PD 18-DEC-2001.
XX
XX PR 17-OCT-1997; 97US-00955565.
XX
XX PF
```

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XX
XX 17-OCT-1997; 97US-00955565.
XX
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX PI Malkovsky M, Wells AD;
XX
XX DR WPI; 2002-138381/18.
XX
XX
PT Increasing expression of an MHC class I molecule in a cell, useful in
PT increasing antigen presentation and enhancing immune recognition of cells
PT infected with pathogens, by expressing a heat shock protein introduced by
PT a vector.
XX
XX PS Example 5; Fig 9; 89pp; English.
XX
XX CC This invention relates to increasing expression of an MHC class I
XX molecule in a target cell, infected with a pathogen that is processed by
XX the MHC class I endogenous pathway. The method of expressing a HSP is
XX achieved by the introduction of an expression vector encoding HSP to
XX produce a transfected cell with increased expression of at least one MHC
XX class I molecule. The method is cytostatic, antibacterial and
XX antiparasitic. The method can be used to increase expression of an MHC
XX class I molecule in a target cell and to increase presentation of an
XX antigen on a cell surface by an MHC class I molecule. The method can
XX enhance the immunogenicity of the endogenous antigen in vivo, by
XX enhancing the generation of antibodies to an otherwise poorly immunogenic
XX antigen or cell. The method can be used in the immunotherapy of cancer
XX and pathogen infections, and for enhancing or reducing radiation
XX resistance of cells. The expression of the heat shock protein in a cell
XX enhances the presentation of endogenous antigens by MHC class I molecules
XX onto the cell surface in vitro, and can enhance the immunogenicity of the
XX endogenous antigen in vivo, by enhancing the generation of antibodies to
XX an otherwise poorly immunogenic antigen or cell. This sequence represents
XX hsp65 encoding sequence
XX
XX SQ Sequence 4380 BP; 757 A; 1372 C; 1513 G; 738 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 6; Length 4380;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 46
AAS59637
XX AAS59637 standard; DNA; 13380 BP.
XX
XX AC AAS59637;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE Propionibacterium acnes immunogenic protein encoding DNA #132.
XX
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant; ds.
XX
XX OS Propionibacterium acnes.
XX
XX PN WO200181581-A2.
XX
XX PD 01-NOV-2001.
XX
XX PF 20-APR-2001; 2001WO-US012865.
XX
XX PR 21-APR-2000; 2000US-0199047P.
XX PR 02-JUN-2000; 2000US-0208841P.
XX PR 07-JUL-2000; 2000US-0216747P.
```

XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI; 2001-616774/71.
 XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 XX PT vaccinating against and diagnosing infections, especially useful for
 XX PT treating acne vulgaris.
 XX PS Claim 1; SEQ ID NO 132; 1069pp; English.
 XX CC Sequences AAS59506-AAS59804 represent DNA molecules encoding
 XX CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
 XX CC associated DNA sequences are used in the treatment, prevention and
 XX CC diagnosis of medical conditions caused by P. acnes. The disorders include
 XX CC SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and
 XX CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
 XX CC infections of bone, joints and the central nervous system, however it is
 XX CC particularly involved in the inflammatory lesions associated with acne
 XX CC vulgaris. A method for detecting the presence or absence of P. acnes in a
 XX CC patient comprises contacting a sample with a binding agent that binds to
 XX CC the proteins of the invention and determining the amount of bound protein
 XX CC in the sample. The polypeptides may be used as antigens in the production
 XX CC of antibodies specific for P. acnes proteins. These antibodies can be
 XX CC used to downregulate expression and activity of P. acnes polypeptides and
 XX CC therefore treat P. acnes infections. The antibodies may also be used as
 XX CC diagnostic agents for determining P. acnes presence, for example, by
 XX CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
 XX CC polypeptides shown in AAU63885-AAU64031 and AAU67712. Note: The sequence
 XX CC data for this patent did not form part of the printed specification, but
 XX CC was obtained in electronic format directly from WIPO at
 XX CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13380 BP; 2486 A; 3689 C; 4274 G; 2930 T; 0 U; 1 Other;
 Query Match 100.0%; Score 22; DB 4; Length 13380;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCAGGAGATCGAGCT 22
 |||||
 Db 4674 CCATCGCCAGGAGATCGAGCT 4695
 RESULT 47
 ACF64566
 ID ACF64566 standard; DNA; 13380 BP.
 AC ACF64566;
 XX AC
 XX AC
 XX DT 17-OCT-2003 (first entry)
 XX DE
 XX DE Propionibacterium acnes DNA contig sequence #132.
 XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX KW immunostimulant; immune response; vaccine; ds.
 XX XX Propionibacterium acnes.
 XX OS
 XX OS WO2003033515-A1.
 XX PN
 XX PN 24-APR-2003.
 XX PD
 XX PF 11-OCT-2002; 2002WO-US032727.
 XX PF
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PR
 XX PA (CORI-) CORIXA CORP.
 XX PA Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 XX PI

PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallie-Douglass J;
 XX WPI; 2003-381789/36.
 XX DR
 XX DR
 XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 XX PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 XX PT or for stimulating an immune response specific for a P. acnes protein.
 XX PS Claim 1; SEQ ID NO 132; 1481pp; English.
 XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 XX CC encoding a Propionibacterium acnes protein. The invention also relates to
 XX CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 XX CC immunogenic fragments of P. acnes polypeptides. The invention
 XX CC additionally encompasses expression vectors and host cells comprising a
 XX CC polynucleotide of the invention; antibodies against polypeptides of the
 XX CC invention; fusion proteins comprising a polypeptide of the invention; a
 XX CC method for stimulating an immune response specific for a P. acnes
 XX CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 XX CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 XX CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 XX CC antigen-presenting cells that express the polypeptide); a method and kit
 XX CC for detecting or determining the presence or absence of P. acnes in a
 XX CC patient; and a method for inhibiting the development of P. acnes in a
 XX CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 XX CC proteins, T cell populations or antigen-presenting cells that express the
 XX CC polypeptides are useful for diagnosing, preventing or treating acne
 XX CC vulgaris, or for stimulating an immune response specific for a P. acnes
 XX CC protein. The polynucleotides can also be used as probes or primers for
 XX CC nucleic acid hybridisation. The vaccine composition is useful for the
 XX CC stimulation of an immune response against P. acnes, or for treating acne,
 XX CC and the kit is useful for performing a diagnostic assay. The present
 XX CC sequence represents a P. acnes DNA contig which is specifically claimed
 XX CC in the invention. Note: The sequence data for this patent did not form
 XX CC part of the printed specification, but was obtained in electronic format
 XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13380 BP; 2486 A; 3689 C; 4274 G; 2930 T; 0 U; 1 Other;
 Query Match 100.0%; Score 22; DB 8; Length 13380;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCAGGAGATCGAGCT 22
 |||||
 Db 4674 CCATCGCCAGGAGATCGAGCT 4695
 RESULT 48
 ABX09143
 ID ABX09143 standard; DNA; 86114 BP.
 AC ABX09143;
 XX AC
 XX AC
 XX DT 08-APR-2003 (first entry)
 XX DE
 XX DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv265.
 XX KW Mycobacteriosis; survival; virulence; protective antigen; vaccine;
 XX KW mycobacterial disease; tuberculosis; leprosy; ds; cosmid.
 XX OS
 XX OS Mycobacterium tuberculosis.
 XX PN
 XX PN WO200274903-A2.
 XX PD
 XX PD 26-SEP-2002.
 XX PF
 XX PF 22-FEB-2002; 2002WO-IB001973.
 XX PF
 XX PR 22-FEB-2001; 2001US-0270123P.
 XX PR
 XX PR (INSP) INST PASTEUR.
 XX PA

XX Cole S;
PI WPI; 2002-759885/82.
XX
PT Identifying and selecting genes for survival or virulence of mycobacteria
PT by a comparative genomic analysis of the sequences of Mycobacterium
PT tuberculosis and M. leprae.
XX
PS Disclosure; Fig 7; 874pp; English.
XX
CC This invention relates to a novel method for identifying essential genes
CC for survival or virulence of mycobacteria species. The method comprises
CC aligning the genomic sequence of a first mycobacterium species on a
CC genomic sequence of a second mycobacterium species and selecting a
CC polynucleotide sequence that is highly conserved in both genomes with no
CC counterparts in other bacterial genomic sequences and that corresponds to
CC an essential gene for the survival or virulence of mycobacterium species.
CC The method of the invention is useful for detecting M. tuberculosis or M.
CC leprae infection. The method reduces the number of potential new targets
CC and protective antigens for new drugs and vaccine compositions to treat
CC and prevent mycobacterial diseases, particularly tuberculosis and
CC leprosy. The present sequence represents a Mycobacterium cosmid DNA
CC sequence used in the method of the invention
XX

SQ Sequence 86114 BP; 14693 A; 27103 C; 28984 G; 15334 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 86114;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAGGAGATCGAGCT 22
Db 15365 CCATCGCCAGGAGATCGAGCT 15386
|||||

RESULT 49

AAI99682_05
Continuation (6 of 45) of AAI99682 from base 500001 (Mycobacterium tuberculosis strain H
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682

WP	Fragment Name	Begin	End
WP	AAI99682_01	100001	110000
WP	AAI99682_02	200001	210000
WP	AAI99682_03	300001	410000
WP	AAI99682_04	400001	510000
WP	AAI99682_05	500001	610000
WP	AAI99682_06	600001	710000
WP	AAI99682_07	700001	810000
WP	AAI99682_08	800001	910000
WP	AAI99682_09	900001	1010000
WP	AAI99682_10	1000001	1110000
WP	AAI99682_11	1100001	1210000
WP	AAI99682_12	1200001	1310000
WP	AAI99682_13	1300001	1410000
WP	AAI99682_14	1400001	1510000
WP	AAI99682_15	1500001	1610000
WP	AAI99682_16	1600001	1710000
WP	AAI99682_17	1700001	1810000
WP	AAI99682_18	1800001	1910000
WP	AAI99682_19	1900001	2010000
WP	AAI99682_20	2000001	2110000
WP	AAI99682_21	2100001	2210000
WP	AAI99682_22	2200001	2310000
WP	AAI99682_23	2300001	2410000
WP	AAI99682_24	2400001	2510000
WP	AAI99682_25	2500001	2610000
WP	AAI99682_26	2600001	2710000
WP	AAI99682_27	2700001	2810000
WP	AAI99682_28	2800001	2910000
WP	AAI99682_29	2900001	3010000
WP	AAI99682_30	3000001	3110000
WP	AAI99682_31	3100001	3210000

WP	AAI99682_32	3200001	3310000
WP	AAI99682_33	3300001	3410000
WP	AAI99682_34	3400001	3510000
WP	AAI99682_35	3500001	3610000
WP	AAI99682_36	3600001	3710000
WP	AAI99682_37	3700001	3810000
WP	AAI99682_38	3800001	3910000
WP	AAI99682_39	3900001	4010000
WP	AAI99682_40	4000001	4110000
WP	AAI99682_41	4100001	4210000
WP	AAI99682_42	4200001	4310000
WP	AAI99682_43	4300001	4410000
WP	AAI99682_44	4400001	4411529

Query Match 100.0%; Score 22; DB 4; Length 110000;

Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAGGAGATCGAGCT 22
Db 28765 CCATCGCCAGGAGATCGAGCT 28787
|||||

RESULT 50

AAI99683_05
Continuation (6 of 44) of AAI99683 from base 500001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession AAI99683

WP	Fragment Name	Begin	End
WP	AAI99683_01	100001	110000
WP	AAI99683_02	200001	210000
WP	AAI99683_03	300001	410000
WP	AAI99683_04	400001	510000
WP	AAI99683_05	500001	610000
WP	AAI99683_06	600001	710000
WP	AAI99683_07	700001	810000
WP	AAI99683_08	800001	910000
WP	AAI99683_09	900001	1010000
WP	AAI99683_10	1000001	1110000
WP	AAI99683_11	1100001	1210000
WP	AAI99683_12	1200001	1310000
WP	AAI99683_13	1300001	1410000
WP	AAI99683_14	1400001	1510000
WP	AAI99683_15	1500001	1610000
WP	AAI99683_16	1600001	1710000
WP	AAI99683_17	1700001	1810000
WP	AAI99683_18	1800001	1910000
WP	AAI99683_19	1900001	2010000
WP	AAI99683_20	2000001	2110000
WP	AAI99683_21	2100001	2210000
WP	AAI99683_22	2200001	2310000
WP	AAI99683_23	2300001	2410000
WP	AAI99683_24	2400001	2510000
WP	AAI99683_25	2500001	2610000
WP	AAI99683_26	2600001	2710000
WP	AAI99683_27	2700001	2810000
WP	AAI99683_28	2800001	2910000
WP	AAI99683_29	2900001	3010000
WP	AAI99683_30	3000001	3110000
WP	AAI99683_31	3100001	3210000
WP	AAI99683_32	3200001	3310000
WP	AAI99683_33	3300001	3410000
WP	AAI99683_34	3400001	3510000
WP	AAI99683_35	3500001	3610000
WP	AAI99683_36	3600001	3710000
WP	AAI99683_37	3700001	3810000
WP	AAI99683_38	3800001	3910000
WP	AAI99683_39	3900001	4010000
WP	AAI99683_40	4000001	4110000
WP	AAI99683_41	4100001	4210000
WP	AAI99683_42	4200001	4310000
WP	AAI99683_43	4300001	4403765

```
Query Match      100.0%; Score 22; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
DB 30208 CCATGCCCAAGGAGATCGAGCT 30229

RESULT 51
AAT06825
ID AAT06825 standard; DNA; 48 BP.
AC AAT06825;
XX
XX 03-JUL-1996 (first entry)
DE 65 kD heat shock gene nucleotides 405-452, target sequence.
XX
XX probe; modified ligase chain reaction; Mycobacterium tuberculosis;
KW M. avium; M. intracellulare; M. kansasii; detection; diagnosis; ss.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9531571-A2;
XX 23-NOV-1995.
XX
XX 04-MAY-1995; 95WO-US005816.
XX
XX 13-MAY-1994; 94US-00223330.
XX
XX (ABBO ) ABBOTT LAB.
XX Kratochvil JD, Leckie GW, Odonnell DL, Solomon NA;
XX WPI; 1996-010956/01.
XX
XX New probes for detection of Mycobacterium species - derived from the 16S
PT ribosomal RNA gene, the protein antigen b gene and the 65 kD and 10 kD
PT heat shock protein genes of M. tuberculosis.
XX
XX Claim 1; Page 43; 60pp; English.
XX
XX The present sequence is a target DNA sequence of the 65 kD heat shock
CC protein gene (nucleotides 405-452) of M. tuberculosis. Probe set 12
CC (AAT06826-829) were utilised to detect bacteria of the genus
CC Mycobacteria. The probes were labelled with biotin and fluorescein. A
CC modified ligase chain reaction was utilised which uses two pairs of
CC probes designated A, B (primary probes) and A', B' (secondary probes).
CC Probe pairs were directed to the same target strand and ultimately
CC ligated to one another after annealing to the target strand. At least one
CC of the probes of a pair had a modified end with respect to the point of
CC ligation. The modified end had bases omitted to create a gap between one
CC probe terminus and the next probe terminus when the pair was annealed to
CC the target sequence. Other modified ends include a base mismatched with
CC the target sequence. The presence of modified ends reduced the falsely
CC positive signal created by blunt-end ligation of the complementary probe
CC duplexes to one another in the absence of target. "Correction" of the
CC modification, in a target dependent manner, was subsequently carried out
CC to render the probes ligatable. Once ligated, the fused (reorganised)
CC probe was dissociated (e.g. melted) from the target and, as with
CC conventional LCR, the process was repeated for several cycles
XX
XX Sequence 48 BP; 12 A; 10 C; 18 G; 8 T; 0 U; 0 Other;

Query Match      95.5%; Score 21; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   |||||
DB 8 CATGCCCAAGGAGATCGAGCT 28

RESULT 53
ADS56335
ID ADS56335 standard; cDNA; 1728 BP.
```

```
RESULT 52
AAT06550
ID AAT06550 standard; DNA; 48 BP.
XX
XX AC AAT06550;
XX
XX 25-MAR-2003 (revised)
DT 03-JUL-1996 (first entry)
XX
XX 65 kD heat shock gene nucleotides 405-452, target sequence.
XX
XX probe; modified ligase chain reaction; Mycobacterium tuberculosis;
KW M. avium; M. intracellulare; M. kansasii; detection; diagnosis; ss.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9531570-A1.
XX
XX 23-NOV-1995.
XX
XX 04-MAY-1995; 95WO-US005602.
XX
XX 13-MAY-1994; 94US-00242403.
XX
XX (ABBO ) ABBOTT LAB.
XX Leckie GW, Davis AH, Semplefacey IE, Manlove MT, Solomon NA;
XX WPI; 1996-010955/01.
XX
XX New probes for detection of M. tuberculosis - derived from e.g. the gene
PT coding for protein antigen b and from the insertion-like element IS6110
PT of M. tuberculosis.
XX
XX Example 10; Page 43; 60pp; English.
XX
XX The present sequence is a target DNA sequence of the 65 kD heat shock
CC protein gene (nucleotides 405-452) of M. tuberculosis. Probe set 12
CC (AAT06551-554) were utilised to detect bacteria of the genus
CC Mycobacteria. The probes were labelled with biotin and fluorescein. A
CC modified ligase chain reaction was utilised which uses two pairs of
CC probes designated A, B (primary probes) and A', B' (secondary probes).
CC Probe pairs were directed to the same target strand and ultimately
CC ligated to one another after annealing to the target strand. At least one
CC of the probes of a pair had a modified end with respect to the point of
CC ligation. The modified end had bases omitted to create a gap between one
CC probe terminus and the next probe terminus when the pair was annealed to
CC the target sequence. Other modified ends include a base mismatched with
CC the target sequence. The presence of modified ends reduced the falsely
CC positive signal created by blunt-end ligation of the complementary probe
CC duplexes to one another in the absence of target. "Correction" of the
CC modification, in a target dependent manner, was subsequently carried out
CC to render the probes ligatable. Once ligated, the fused (reorganised)
CC probe was dissociated (e.g. melted) from the target and, as with
CC conventional LCR, the process was repeated for several cycles. (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 48 BP; 12 A; 10 C; 18 G; 8 T; 0 U; 0 Other;

Query Match      95.5%; Score 21; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   |||||
DB 8 CATGCCCAAGGAGATCGAGCT 28

RESULT 53
ADS56335
ID ADS56335 standard; cDNA; 1728 BP.
```

XX AC AD556335;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polynucleotide #8322.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polynucleotide; gene; ss.
XX OS Bacteria.
XX US2003233675-A1.
XX PN 18-DEC-2003.
XX PD 20-FEB-2003; 2003US-00369493.
XX PF 21-FEB-2002; 2002US-0360039P.
XX PR (CAOY/) CNO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 32009; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 1728 BP; 335 A; 570 C; 579 G; 244 T; 0 U; 0 Other;
SQ Query Match 92.7%; Score 20.4; DB 13; Length 1728;
Best Local Similarity 95.5%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22

Db 269 CCATCGCTAAGGAGATCGAGCT 290
||||| |||||||
RESULT 54
ID ADM72250/c
AD 72250 standard; DNA; 99090 BP.
XX ADM72250;
AC ADM72250;
XX 03-JUN-2004 (first entry)
DT O. minuta Pi2 region contiguous sequence.
DE O. minuta Pi2 region contiguous sequence.
XX Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance;
KW gene; ds.
XX Oryza minuta.
OS WO2004022715-A2.
PN 18-MAR-2004.
XX 08-SEP-2003; 2003WO-US027913.
XX 09-SEP-2002; 2002US-0409216P.
PR 18-MAR-2003; 2003US-0455713P.
PR 05-SEP-2003; 2003US-00656394.
XX (OHIS) UNIV OHIO STATE.
PA Wang G;
PI WPI; 2004-257576/24.
XX New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX Example 3; SEQ ID NO 13; 120pp; English.
XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a Pi2
CC region contiguous sequence
XX Sequence 99090 BP; 28990 A; 20403 C; 21246 G; 28450 T; 0 U; 1 Other;
SQ Query Match 92.7%; Score 20.4; DB 12; Length 99090;
Best Local Similarity 95.5%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
Db 38860 CCATCGCCCAAGGAGATCGAGCT 38839
RESULT 55
ID ACF04316
AD ACF04316 standard; DNA; 20 BP.
XX ACF04316;
AC ACF04316;
XX 06-NOV-2003 (first entry)
DT Mycobacterium hsp65 gene PCR primer #1.
XX Mycobacterium; hsp65; heat shock protein 65; identification;
KW tuberculosis; PCR; primer; ss.
XX Mycobacterium sp.
XX

PR 19-AUG-1994; 94US-00292827.
 PR 21-OCT-1994; 94WO-US012117.
 PR 08-DEC-1994; 94US-00353784.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSP-) NPS PHARM INC.
 XX
 PI Garrett JE, Fuller FH, Brown EM, Hebert SC;
 XX
 DR WPI; 1998-008040/01.
 DR P-PSDB; AAW38272.
 XX
 PT DNA encoding calcium receptor polypeptide(s) - useful for therapeutic
 PT purposes, e.g. hyperparathyroidism and osteoporosis.
 XX
 PS Claim 1; Col 107-116; 174pp; English.
 XX
 CC The present sequence encodes bovine parathyroid cell calcium receptor 1
 CC (BoPCar 1). The specification includes details of molecules that can
 CC modulate one or more inorganic ion receptor activities, and antibodies
 CC and antibody fragments targeted to inorganic ion receptor proteins. The
 CC proteins, nucleic acids and antibodies may be used to treat disorders by
 CC modulating one or more inorganic ion receptor activities, preferably
 CC disorders of calcium homeostasis, e.g. hyperparathyroidism and
 CC osteoporosis
 XX
 SQ Sequence 5275 BP; 1277 A; 1476 C; 1315 G; 1207 T; 0 U; 0 Other;
 Query Match 88.2%; Score 19.4; DB 2; Length 5275;
 Best Local Similarity 95.2%; Pred. No. 56;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CATGCCCAAGGAGATCGAGCT 22
 Db 2311 CATGCCCAAGGAGATCGAGTT 2331
 RESULT 58
 AA225053
 ID AA225053 standard; cDNA to mRNA; 5275 BP.
 XX
 AC AA225053;
 XX
 DT 08-DEC-1999 (first entry)
 XX
 DE Bovine parathyroid calcium receptor 1 nucleotide sequence.
 XX
 KW Parathyroid; calcium receptor; inorganic ion receptor; modulator;
 KW receptor expression; detection; ss.
 XX
 OS Bos taurus.
 XX
 FH Key Location/Qualifiers
 FT CDS 515..3772
 FT /*tag= a
 FT /product= "BoPCar 1"
 FT /note= "parathyroid calcium receptor"
 XX
 XX US5962314-A.
 XX
 XX 05-OCT-1999.
 XX
 XX 03-OCT-1997; 97US-00943986.
 XX
 XX 23-FEB-1993; 93US-00009389.
 PR 22-OCT-1993; 93US-00141248.
 PR 19-AUG-1994; 94US-00292827.
 PR 21-OCT-1994; 94WO-US012117.
 PR 08-DEC-1994; 94US-00353784.
 PR 07-JUN-1995; 95US-00484565.
 XX
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Brown EM, Hebert SC, Garrett JE;
 XX WPI; 1999-571274/48.
 DR P-PSDB; AAY41778.
 XX
 PT Nucleic acids encoding protein calcium receptors useful for identifying
 PT modulators of receptor expression and activity and for the production of
 PT antigens specific for calcium receptors.
 XX
 PS Claim 5; Fig 47; 174pp; English.
 XX
 CC The present sequence encodes bovine parathyroid calcium receptor 1
 CC (BoPCar 1). Calcium receptor polynucleotides may be used: (i) for
 CC producing receptor proteins (or fragments) useful for determining
 CC structure and activity relationships, for assaying molecular activity on
 CC the receptor (i.e. identifying modulators of receptor function) and for
 CC producing antibodies specific for the receptor; (ii) for sequencing the
 CC normal form of the nucleic acids (the derived sequence may be compared
 CC with other receptors to identify conserved sequences, mutations and
 CC variations that may influence calcium receptor activity and to determine
 CC target sites for antisense molecules, ribozymes, hybridization probes and
 CC polymerase chain reaction (PCR) amplification primers; (iii) as
 CC hybridization probes to detect the presence of similar sequences in
 CC samples; and (iv) as PCR primers to generate particular nucleic acid
 CC sequence regions; (e.g. to generate regions to be probes by hybridization
 CC detection probes)
 XX
 SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T; 0 U; 0 Other;
 Query Match 88.2%; Score 19.4; DB 2; Length 5275;
 Best Local Similarity 95.2%; Pred. No. 56;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CATGCCCAAGGAGATCGAGCT 22
 Db 2311 CATGCCCAAGGAGATCGAGTT 2331
 RESULT 59
 AAV82483
 ID AAV82483 standard; cDNA to mRNA; 5275 BP.
 XX
 AC AAV82483;
 XX
 DT 19-MAR-1999 (first entry)
 XX
 DE Bovine parathyroid calcium receptor BoPCar 1 encoding cDNA.
 XX
 KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
 KW depression; anxiety; ss.
 XX
 OS Bos sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 515..3772
 FT /*tag= a
 XX
 XX US5858684-A.
 XX
 XX 12-JAN-1999.
 XX
 XX 07-JUN-1995; 95US-00480751.
 XX
 XX 23-AUG-1991; 91US-00749451.
 PR 11-FEB-1992; 92US-00834044.
 PR 21-AUG-1992; 92US-00934161.
 PR 12-FEB-1993; 93US-00017127.
 PR 23-FEB-1993; 93US-00009389.

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PR 22-OCT-1993; 93US-00141248.
PR 19-AUG-1994; 94US-00292827.
PR 21-OCT-1994; 94WO-US012117.
PR 08-DEC-1994; 94US-00353784.
XX
XX (NPSF-) NPS PHARM INC.
XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
XX Del Mar EG, Balandrin MF, Van Wagenen BC, Nemeth EF, Brown EM;
XX Garrett JE, Hebert SC;
XX
XX WPI; 1999-119871/10.
XX DR P-PSDB; AAW89563.
XX
XX Screening for calcium receptor-active compounds - by recombinant
XX expression of nucleic acid encoding calcium receptor and determining the
XX effect of compounds on calcium receptor activity.
XX
XX Claim 1; Fig 47; 176pp; English.
XX
XX A method has been developed of screening for a compound able to affect
XX one or more activities of a calcium receptor (CR) comprises: (A)
XX contacting a recombinant cell with a test compound, where the recombinant
XX cell comprises a recombinant nucleic acid expressing the CR, provided
XX that the cell does not have functional CR expression from endogenous
XX nucleic acid; (B) determining the ability of the test compound to affect
XX one or more activities of the calcium receptor; and (C) comparing the
XX ability with the ability of the test compound to affect the one or more
XX CR activities in a cell not comprising the recombinant nucleic acid. The
XX present sequence encodes bovine parathyroid CR, designated a BoPCar 1.
XX The nucleic acid sequence of BoPCar 1 can be used as part of the
XX recombinant nucleic acid in the method described above. The compounds
XX identified can be used to treat diseases or disorders characterized by
XX abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and
XX other bone and mineral-related disorders. They can also be used for the
XX treatment of diseases and disorders associated with disrupted Ca2+
XX responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced
XX nerve cell damage such as in cardiac arrest or neonatal distress,
XX epilepsy, neurodegenerative diseases such as Alzheimer's disease,
XX Huntington's disease and Parkinson's disease, dementia, muscle tension,
XX depression, and anxiety
XX
XX Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T; 0 U; 0 Other;
XX
XX Query Match 88.2%; Score 19.4; DB 2; Length 5275;
XX Best Local Similarity 95.2%; Pred. No. 56;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 CATGCCCAAGGATCGAGCT 22
XX DB 2311 CATGCCCAAGGATCGAGTT 2331
XX
XX RESULT 60
XX ID AA289296 standard; cDNA to mRNA; 5275 BP.
XX AC AA289296;
XX
XX 09-JUN-2000 (first entry)
XX
XX DE Bovine calcium receptor BoPCar1 cDNA.
XX
XX Calcium receptor; treatment; calcimimetic; calcilytic; osteopathic;
XX cerebroprotective; cytostatic; neuroprotective; dermatological;
XX tranquilizer; vulnary; antiulcer; immunosuppressive; hypotensive;
XX cardiac; parathyroid hormone; osteoporosis; calcitonin secretion;
XX hyperparathyroidism; Paget's disease; bovine; ss.
XX
XX Bos taurus.
XX
XX Key Location/Qualifiers
XX CDS 515..3772
XX
XX FT

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/*tag= a
/product= "calcium receptor"

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US6031003-A.

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29-FEB-2000.

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07-JUN-1995; 95US-00484719.

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23-AUG-1991; 91US-00749451.

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11-FEB-1992; 92US-00834044.

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21-AUG-1992; 92US-00934161.

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12-FEB-1993; 93US-00017127.

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23-FEB-1993; 93US-00009389.

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22-OCT-1993; 93US-00141248.

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19-AUG-1994; 94US-00292827.

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21-OCT-1994; 94WO-US012117.

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08-DEC-1994; 94US-00353784.

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(NPSF-) NPS PHARM INC.

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(BGHM) BRIGHAM & WOMENS HOSPITAL.

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Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;

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WPI; 2000-301969/26.

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P-PSDB; AAY51825.

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Treating disorders or diseases in a patient by modulating inorganic ion
receptor activities especially calcium receptor for hyperparathyroidism,
by administering a calcimimetic or calcilytic compound.

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Example 25; Col 107-116; 194pp; English.

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This invention describes a novel method of treating disorders by modulating calcium receptor activity in vitro by administering a calcimimetic, or a calcilytic compound. The products of the invention have osteoprotective, cerebroprotective, cytostatic, neuroprotective, dermatological, tranquilizer, vulnary, antiulcer, immunosuppressive, hypotensive and cardiac activity. The method is suitable for reducing parathyroid hormone level in a patient to that of a normal individual, treating a patient having osteoporosis, to inhibit bone resorption, and to stimulate calcitonin secretion in vitro or in vivo. The level of parathyroid hormone is reduced to cause a decrease in plasma Ca²⁺. The method is useful in treating disorders in humans such as hyperparathyroidism, Paget's disease and osteoporosis. Also for treatment or prevention, based on the affected cells, of other disorders and conditions like seizures, stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, Alzheimer's disease, Huntington's disease, Parkinson's disease, dementia, muscle tension, depression, anxiety, panic disorder, OCD (not defined), post-traumatic stress disorder, schizophrenia, neuroleptic malignant syndrome and Tourette's syndrome, diseases involving excess water reabsorption by the kidney such as syndrome of inappropriate ADH secretion (SIADH), cirrhosis, congestive heart failure and nephrosis, hypertension, preventing and/or decreasing renal toxicity from cationic antibiotics (e.g. aminoglycoside antibiotics), gut motility disorders such as diarrhoea and spastic colon, GI (gastrointestinal) ulcer diseases, GI diseases with excessive calcium absorption such as sarcoidosis and autoimmune diseases and organ transplant rejection. This sequence encodes the bovine calcium receptor BoPCar1 which is described in the method of the invention

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Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T; 0 U; 0 Other;

```

```

Query Match 88.2%; Score 19.4; DB 3; Length 5275;

```

```

Best Local Similarity 95.2%; Pred. No. 56;

```

```

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 CATGCCCAAGGATCGAGCT 22

```

```

DB 2311 CATGCCCAAGGATCGAGTT 2331

```

Search completed: April 1, 2006, 22:21:34
Job time : 50.7112 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:06:31 ; Search time 303.022 Seconds
(without alignments)
3396.840 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccacgcgaagagatcgagct 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_ges1:*
10: gb_ges2:*
11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	100.0	828	10	CL693779 PRI0162C
2	21	95.5	539	7	CR928307
3	21	95.5	1319	8	DN666868 CFW34-F12
4	21	95.5	1370	8	DN665225 CFW34-H08
5	20.4	92.7	916	10	AG859232
6	19.4	88.2	340	1	AW281326 fj53e02.Y
7	19.4	88.2	588	2	BG729640 f081h07.Y
8	19.4	88.2	649	7	C0503864
9	19.4	88.2	658	9	BZ566239 pac82-164
10	19.4	88.2	815	8	DR424057
11	19.4	88.2	840	9	CC475958 CH240_301
12	19.4	88.2	1402	8	DN737348 CNB92-C09
13	19.4	88.2	1480	8	DN721479 CNB139-F0
14	18.8	85.5	123	8	CV849414 ID0AEE8BA
15	18.8	85.5	180	7	CN758177 ID0AAA21C
16	18.8	85.5	308	7	CN764299 ID0AAA9CB
17	18.8	85.5	308	10	CW773364 OG_BBA009
18	18.8	85.5	312	8	CV836743 ID0ACC3AG
19	18.8	85.5	312	8	CV837906 ID0ACC6BH
20	18.8	85.5	316	7	CN764328 ID0AAA9CD
21	18.8	85.5	317	7	CN754372 ID0AAA12D
22	18.8	85.5	318	8	CV834150 ID0ACC24D

23	18.8	85.5	319	7	CN755308
24	18.8	85.5	319	7	CN755404
25	18.8	85.5	323	10	CZ112870 OM_Ba015
26	18.8	85.5	332	8	CV828800 ID0ACC10D
27	18.8	85.5	332	8	CV829374
28	18.8	85.5	332	8	CV830911
29	18.8	85.5	332	8	CV831091
30	18.8	85.5	332	8	CV832760 ID0ACC20D
31	18.8	85.5	332	8	CV838428 ID0ACC7DG
32	18.8	85.5	340	7	CN764316 ID0AAA9CC
33	18.8	85.5	407	7	CN750782 ApDT-XXVI
34	18.8	85.5	414	6	CN999580 S34P-G03
35	18.8	85.5	424	6	CN583674 USDA-FP_1
36	18.8	85.5	436	5	C25159 C25159 Rice
37	18.8	85.5	471	3	BM087289 500025 MA
38	18.8	85.5	483	7	CN750359 ApDT-XII
39	18.8	85.5	484	7	CN749153
40	18.8	85.5	492	6	CD451510
41	18.8	85.5	523	3	BJ645375 BJ645375
42	18.8	85.5	534	10	CW768437
43	18.8	85.5	551	6	CF292206 14ROOT--0
44	18.8	85.5	569	7	CN583982 USDA-FP_1
45	18.8	85.5	570	6	CF292207 14ROOT--0
46	18.8	85.5	572	7	CN585977 USDA-FP_1
47	18.8	85.5	581	6	CB087986
48	18.8	85.5	599	6	CD450119
49	18.8	85.5	612	7	CN584119
50	18.8	85.5	629	10	CL612592
51	18.8	85.5	640	6	CB690026
52	18.8	85.5	646	6	CF587912
53	18.8	85.5	656	9	AQ257000
54	18.8	85.5	665	6	CB000900
55	18.8	85.5	671	7	CN755289 ID0AAA15B
56	18.8	85.5	671	9	AQ576753 nbx00898
57	18.8	85.5	672	10	CN775708
58	18.8	85.5	673	10	CW506965
59	18.8	85.5	684	9	AQ287315
60	18.8	85.5	696	6	CF588105 USDA-FP_1

ALIGNMENTS

RESULT 1
CL693779/c 828 bp DNA linear GSS 10-JUL-2004

LOCUS PRI0162C_A12.2 - PRI0162C.BR (828) Mixed stage fosmid library of P. pacificus var. California *Pristionchus pacificus* genomic, genomic survey sequence.

DEFINITION CL693779 GI:50215687

ACCESSION CL693779

VERSION GSS.

KEYWORDS *Pristionchus pacificus*

SOURCE *Pristionchus pacificus*

ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; *Pristionchus*.

REFERENCE 1 (bases 1 to 828)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. ApadB: an Acedb database for the nematode satellite organism *Pristionchus pacificus*

AUTHORS Nucleic Acids Res. 32 (1), D421-D422 (2004)

TITLE 14681447

JOURNAL Contact: Sommer RJ

PUBMED Evolutionary Biology

COMMENT Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

```

FEATURES
  source
    Location/Qualifiers
      1..828
        /organism="Pristionchus pacificus"
        /mol_type="genomic DNA"
        /strain="California"
        /db_xref="taxon:54126"
        /clone_lib="Mixed stage fosmid library of P. pacificus
        var. California"
        /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
  Query Match 100.0%; Score 22; DB 10; Length 828;
  Best Local Similarity 100.0%; Pred. No. 31;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
   |||||
Db 224 CCATCGCCCAAGGAGATCGAGCT 203

RESULT 2
CR928307 539 bp mRNA linear EST 13-DEC-2004
LOCUS CR928307 PUR-Z1+Z2 Danio rerio cDNA clone 226-B07-2, mRNA sequence.
DEFINITION CR928307
ACCESSION CR928307
VERSION CR928307.1 GI:56557540
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 539)
  AUTHORS Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W.,
  Wang,W., Wen,Z. and Peng,J.
  TITLE 15000 unique zebrafish EST clusters and their future use in
  microarray for profiling gene expression patterns during
  embryogenesis
  JOURNAL Genome Res. 13 (3), 455-466 (2003)
  PUBMED 12618376
  COMMENT Contact: Peng J
  Lab of Functional Genomics
  Institute of Molecular and Cell Biology
  30 Medical Drive, Singapore, 117609, Singapore
  Email: pengj@imcb.a-star.edu.sg
  Clone requests: pengj@imcb.a-star.edu.sg
  Institute of Molecular and Cell Biology,
  61 Biopolis Drive (Proteos) Singapore 138673.

FEATURES
  source
    Location/Qualifiers
      1..539
        /organism="Danio rerio"
        /mol_type="mRNA"
        /strain="local wildtype"
        /db_xref="taxon:7955"
        /clone="226-B07-2"
        /tissue_type="whole embryo or fish"
        /dev_stage="mixed stages"
        /clone_lib="FJR-Z1+Z2"

ORIGIN
  Query Match 95.5%; Score 21; DB 7; Length 539;
  Best Local Similarity 100.0%; Pred. No. 86;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21
   |||||
Db 314 CCATCGCCCAAGGAGATCGAGC 334

RESULT 3
DN666868 1319 bp mRNA linear EST 29-MAR-2005
LOCUS DN666868
DEFINITION CFW34-F12.y1d-s SHGC-CFW Gasterosteus aculeatus cDNA clone
  CFW34-F12 5', mRNA sequence.

FEATURES
  source
    Location/Qualifiers
      1..1319
        /organism="Gasterosteus aculeatus"
        /mol_type="mRNA"
        /strain="Conner Creek sticklebacks, WA USA"
        /db_xref="taxon:69293"
        /clone="CFW34-F12"
        /sex="mixed male and female"
        /tissue_type="gills"
        /dev_stage="adult"
        /lab_host="DH10B (T1 phage resistant)"
        /clone_lib="SHGC-CFW"
        /note="Vector: Express 1; Total and poly A+ RNA was
        isolated from the indicated stickleback tissue, and a cDNA
        library was constructed in the Express 1 plasmid vector by
        Open Biosystems. First strand cDNA synthesis was primed
        with an 54 bp linker primer containing an oligodT sequence
        preceded by a synthetic NotI site (first strand primer:
        5'-GACTAGTTCTAGATCGCGCGCCG(T)25-3'). Following
        second strand synthesis, cDNAs were made blunt at the end
        corresponding to the original 5 prime end of mRNA, and
        cloned directionally into the NotI and EcoRV sites of
        Express 1. Note that the EcoRV site is typically destroyed
        in the blunt end cloning, leaving a junction of the form
        'xxxATC' (where ATC is the second half of the EcoRV
        site, and xxx is derived from the cDNA sequence). A map of
        the Express 1 vector is available at:
        http://www.openbiosystems.com/cdna_library_construction_fa
        q.php#8 The primary library was transformed and amplified
        in DH10B (T1 phage resistant) bacteria. Clones available
        from Open Biosystems:
        http://www.openbiosystems.com/stickleback"

ORIGIN
  Query Match 95.5%; Score 21; DB 8; Length 1319;
  Best Local Similarity 100.0%; Pred. No. 92;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21
   |||||
Db 123 CCATCGCCCAAGGAGATCGAGC 143

RESULT 4
DN665225 1370 bp mRNA linear EST 29-MAR-2005
LOCUS DN665225
DEFINITION CFW24-H08.y1d-s SHGC-CFW Gasterosteus aculeatus cDNA clone
  CFW24-H08 5', mRNA sequence.
  DN665225
  ACCESSION DN665225

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VERSION      DN655225.1  GI:61985281
KEYWORDS     EST.
SOURCE       Gasterosteus aculeatus (three spined stickleback)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
              Gasterosteidae; Gasterosteus.
REFERENCE    1 (bases 1 to 1370)
AUTHORS      Kingsley, D.M., Feichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,
              Schmutz, J., and Myers, R.M.
TITLE        Expressed sequence tags from Gasterosteus aculeatus
JOURNAL      Unpublished (2003)
COMMENT      Contact: Grimwood, Jane
              Stanford Human Genome Center
              Stanford University School of Medicine
              975 S California Ave, Palo Alto, CA 94304, USA
              Tel: 650 320 5917
              Fax: 650 320 5801
              Email: jane@shgc.stanford.edu
              Plate: 24
              High quality sequence start: 30
              High quality sequence stop: 872.

FEATURES     source
              1..1370
                /organism="Gasterosteus aculeatus"
                /mol_type="mRNA"
                /strain="Conner Creek sticklebacks, WA USA"
                /db_xref="taxon:69293"
                /clone="CFW24-H08"
                /sex="mixed male and female"
                /tissue_type="gills"
                /dev_stage="adult"
                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="SHGC-CFW"
                /note="Vector: Express 1; Total and poly A+ RNA was
              isolated from the indicated stickleback tissue, and a cDNA
              library was constructed in the Express 1 plasmid vector by
              Open Biosystems. First strand cDNA synthesis was primed
              with an 54 bp linker primer containing an oligodT sequence
              preceded by a synthetic NotI site (first strand primer:
              5'-GACTAGTTCAGTCGCGAGCGGCC(T)25-3'). Following
              second strand synthesis, cDNAs were made blunt at the end
              corresponding to the original 5 prime end of mRNA, and
              cloned directionally into the NotI and EcoRV sites of
              Express 1. Note that the EcoRV site is typically destroyed
              in the blunt end cloning, leaving a junction of the form
              'xxxATC' (where is ATC is the second half of the EcoRV
              site, and xxx is derived from the cDNA sequence). A map of
              the Express 1 vector is available at:
              http://www.openbiosystems.com/cdna library construction fa
              q.php#8 The primary library was transformed and amplified
              in DH10B (T1 phage resistant) bacteria. Clones available
              from Open Biosystems:
              http://www.openbiosystems.com/stickleback"

ORIGIN
Query Match      95.5%; Score 21; DB 8; Length 1370;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCAAGGAGATCGAGC 21
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Db 186 CCATCGCAAGGAGATCGAGC 206

RESULT 5
AG859232
LOCUS
DEFINITION
Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,
BAC clone:K0172D09_F, genomic survey sequence.
ACCESSION
AG859232
VERSION
AG859232.1  GI:55325467

KEYWORDS     GSS.
SOURCE       Oryza sativa (indica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 Katagiri, S., Wu, J., Ito, Y., Karasawa, W., Shibata, M., Kanamori, H.,
              Katayose, Y., Nami, N., Matsumoto, T. and Sasaki, T.
              End Sequencing and Chromosomal in silico Mapping of BAC Clones
              Derived from an indica Rice Cultivar, Kasalath
              Breeding Science 54, 273-279 (2004)
JOURNAL
REFERENCE    2 (bases 1 to 916)
AUTHORS      Sasaki, T., Matsumoto, T. and Wu, J.
TITLE        Direct Submission
JOURNAL
COMMENT      Submitted (29-OCT-2004) Takuji Sasaki, National Institute of
              Agrobiological Sciences, Rice Genome Research Program; Kannondai
              2-1-2 Tsukuba, Ibaraki 305-8602, Japan
              (E-mail: tsasakion@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
              Tel: 81-298-38-7441, Fax: 81-298-38-7468)
              The orientation of the sequence is from T7 side of the BAC clone.

FEATURES     source
              1..916
                /organism="Oryza sativa (indica cultivar-group)"
                /mol_type="genomic DNA"
                /cultivar="Kasalath"
                /db_xref="taxon:39946"
                /clone="K0172D09_F"

ORIGIN
Query Match      92.7%; Score 20.4; DB 10; Length 916;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCGCCAAAGGAGATCGAGCT 22
|||||
Db 387 CCATCGCCAAAGGAGATCGAGCT 408

RESULT 6
AW281326
LOCUS
DEFINITION
fj53e02.y1 zebrafish adult brain Danio rerio cDNA 5' similar to
TT:Q16732 Q16732 NA+/K+ ATPASE ALPHA SUBUNIT ;, mRNA sequence.
ACCESSION
AW281326
VERSION
AW281326.1  GI:6669875
KEYWORDS     EST.
SOURCE       Danio rerio (zebrafish)
ORGANISM     Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.
REFERENCE    1 (bases 1 to 340)
AUTHORS      Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
              Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
              Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
              Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
              Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
              Waterston, R. and Wilson, R.
              WashU Zebrafish EST Project 1998
              Unpublished (1998)
              Contact: Stephen L. Johnson
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: zbratfish@watson.wustl.edu
              cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
              Matthew Clark. DNA Sequencing by: Washington University Genome
              Sequencing Center Clone distribution: Genome Systems, St. Louis,
              Missouri (web address: www.genomesystems.com) (email contact:
              info@genomesystems.com) and Research Genetics, Huntsville, Alabama
              (web address: www.resgen.com) (email contact: info@resgen.com) and


```

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Trace considered overall poor quality

Seq primer: T7

High quality sequence stop: 1.

FEATURES

source

1. .340
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZiPlox; Site 1: NotI; Site 2: SalI;
Original library was constructed in lambdaZiPlox. Mass
excision of the cDNA library was performed to yield
pZiPlox plasmids. Insert check was done in original
library."

ORIGIN

Query Match 88.2%; Score 19.4; DB 1; Length 340;
Best Local Similarity 95.2%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGC 21

Db 66 CCATGCCCAAGGAAATCGAGC 86

RESULT 7

BG729640

LOCUS

DEFINITION

BG729640 588 bp mRNA linear EST 09-MAY-2001
f081h07.y1 zebrafish gridded kidney Danio rerio cDNA clone
IMAGE:4726525 5' similar to SW:ATN3 RAT P06687
SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-3 CHAIN ;, mRNA
sequence.

ACCESSION BG729640 1 GI:114014715

VERSION BG729640

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 588)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Bady, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swallet, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: f081h07.x1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address:
www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Seq primer: T3 ET from Amersham

High quality sequence stop: 462.

Location/Qualifiers

FEATURES

source

1. .588
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4726525"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XL0LR"
/clone_lib="zebrafish gridded kidney"
/note="Organ: kidney; Vector: pBK-CMV; Site 1: EcoRI;
Site 2: XhoI; Oligo dr cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."

ORIGIN

Query Match 88.2%; Score 19.4; DB 2; Length 588;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGC 21

Db 290 CCATGCCCAAGAGATCGAGC 310

RESULT 8

CO503864

LOCUS

DEFINITION

CO503864 649 bp mRNA linear EST 13-JUL-2004
GGEZCB1010E10.g chicken breast muscle - CBI Gallus gallus CDNA
clone GGEZCB1010E10, mRNA sequence.

ACCESSION CO503864

VERSION CO503864.1 GI:50274050

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 649)

Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,
Patricio, M., Ledur, M.C. and Coutinho, L.L.
Discovery of new genes expressed in the chicken breast muscle
Unpublished (2004)

TITLE

JOURNAL

COMMENT

Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llicoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

FEATURES

source

1. .849
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="GGEZCB1010E10"
/tissue_type="breast muscle"
/dev_stage="1 and 21 days old"
/lab_host="DH5 alpha"
/clone_lib="chicken breast muscle - CBI"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This
cDNA library was constructed with the SuperScript Plasmid
System with Gateway Technology kit (Invitrogen), following a
manufacturer's protocols. Plasmid DNA was purified using a
modified alkaline lysis method. Sequencing reactions were
conducted using the DYEnamic Cycle Sequencing Kit for
MegabACE (Amersham Biosciences) according to the
manufacturer's recommendations. Clones were sequenced by
the 5' end with T7 primer. Sequencing reactions were
analyzed on MegabACE1000 DNA Sequencer (Amersham
Biosciences). The quality and clustering of the ESTs were
analyzed using the softwares Phred/cap3. Only EST

sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."

ORIGIN

Query Match 88.2%; Score 19.4; DB 7; Length 649;
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCATCGCCCAAGGAGATCGAGC 21
 |||||
 Db 182 CCATCGCCCAAGGAGATCGAGC 202

RESULT 9

BZ566239 658 bp DNA linear GSS 17-DEC-2002
 LOCUS pac2-164_5975.y2 pac2-164_pseudomonas aeruginosa genomic clone
 DEFINITION pac2-164_5975, genomic survey sequence.

ACCESSION

BZ566239

VERSION

BZ566239.1 GI:27195398

KEYWORDS

GSS.

SOURCE

Pseudomonas aeruginosa

ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

REFERENCE

1 (bases 1 to 658)

AUTHORS

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,

TITLE

Burns, J.L., Kaul, R. and Olsen, M.V.

JOURNAL

Whole-Genome-Sequence variation among multiple isolates of

COMMENT

Pseudomonas aeruginosa library

J. Bacteriol. (2002) In press

Contact: Chris K. Raymond

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

1. 658

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

/db_xref="taxon:287"

/clone="pac2-164_5975"

/clone_lib="pac2-164"

/note="clinical isolate 2-164 Whole genomic shotgun

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REFERENCE

1 (bases 1 to 815)

AUTHORS

Wislow, G., Peterson, K. and McMurtry, J.

TITLE

NEIBank analysis of 15day post-hatched chicken eye

JOURNAL

Unpublished (2005)

COMMENT

Contact: Wislow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 02 row: f column: 12

Seq primer: Universal M13 Reverse.

Location/Qualifiers

1. 815

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="naw02f12"

/tissue type="Whole eye"

/dev stage="15d post-hatched"

/lab_host="EMDH108"

/clone_lib="Chicken eye (hatched). Unnormalized (naw)"

/note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted

from pooled 15day post-hatched chicken eye. A

directionally cloned cDNA library in the pCMVSPORT6 vector

(Invitrogen) was constructed at Bioserve Biotechnology

(Laurel MD) essentially following the protocols of the

SuperScript Plasmid System, full details of which are

contained in the manufacturer's instruction manual

(http://www.lifetech.com/). First strand synthesis was

carried out using a Not I primer-adaptor

[5'-pGACTAGTCTAGATCGAGCGGCCG(T)15-3']. cDNA was

cloned in Not I/Sal I sites. EST analysis was performed at

the NIH Intramural Sequencing Center (NISC). Analyzed data

available through http://neibank.nei.nih.gov."

available through http://neibank.nei.nih.gov."

available through http://neibank.nei.nih.gov."

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available through http://neibank.nei.nih.gov."

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available through http://neibank.nei.nih.gov."

ORIGIN

Query Match 88.2%; Score 19.4; DB 8; Length 815;
 Best Local Similarity 95.2%; Pred. No. 4.7e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21

|||||

Db 508 CCATCGCCCAAGGAGATCGAGC 528

RESULT 11

CC475958 840 bp DNA linear GSS 16-JUN-2003
 LOCUS CH240_301N21.T7 CHORI-240 Bos taurus genomic clone CH240_301N21,
 DEFINITION genomic survey sequence.

ACCESSION

CC475958

VERSION

CC475958.1 GI:31753167

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 840)

Holt, R., Stott, J., Yang, G., Barber, S., Small, D., Prabhu, A.-L.,

Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,

Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,

Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,

Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Unpublished (2003)

Other_GSSs: CH240_301N21.TARBAC13P2

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

The British Columbia Cancer Agency Genome Science Centre

The British Columbia Cancer Agency Genome Science Centre

RESULT 10

DR424057 815 bp mRNA linear EST 29-JUN-2005
 LOCUS naw02f12.y1 Chicken eye (hatched). Unnormalized (naw) Gallus gallus
 DEFINITION cDNA clone naw02f12 5', mRNA sequence.

ACCESSION

DR424057

VERSION

DR424057.1 GI:69326073

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240
 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/ordering/information.htm>). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.

Plate: 301 row: N column: 21
 Seq primer: T7

Class: BAC ends.

FEATURES source

Location/Qualifiers
 1. .840
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_30IN21"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull LI Domino 9375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 840;
 Best Local Similarity 95.2%; Pred. No. 4.7e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCGCCCAAGGAGATCGAGCT 22

Db 751 CATCGCCCAAGGAGATCGAGTT 771

RESULT 12

DN737348

LOCUS

DEFINITION CNB92-C09.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone

Accession DN737348

Version DN737348.1 GI:62113709

Keywords EST.

Source Gasterosteus aculeatus (three spined stickleback)

Organism Gasterosteus aculeatus

Reference 1 (bases 1 to 1402)

Authors Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,

Schmutz,J. and Myers,R.M.

Title Expressed sequence tags from Gasterosteus aculeatus

Journal Unpublished (2003)

Comment Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@shgc.stanford.edu

Plate: 92

High quality sequence stop: 804.

Location/Qualifiers

1. .1402

/organism="Gasterosteus aculeatus"

/mol_type="mRNA"

/strain="Conner Creek sticklebacks, WA USA"

/db_xref="taxon:69293"

/db_xref="taxon:69293"

FEATURES source

Location/Qualifiers
 1. .1402
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"

/clone="CNB92-C09"
 /sex="mixed male and female"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CNB"

/notes="Vector: Express 1; Total and poly A+ RNA was
 isolated from the indicated stickleback tissue, and a cDNA
 library was constructed in the Express 1 plasmid vector by
 Open Biosystems. First strand cDNA synthesis was primed
 with an 54 bp linker primer containing an oligodT sequence
 preceded by a synthetic NotI site (first strand primer:
 5'-GACTAGTCTAGATCGGAGCGCGCC(T)25-3'). Following
 second strand synthesis, cDNAs were made blunt at the end
 corresponding to the original 5 prime end of mRNA, and
 cloned directionally into the NotI and EcoRV sites of
 Express 1. Note that the EcoRV site is typically destroyed
 in the blunt end cloning, leaving a junction of the form
 'xxxATC' (where is ATC is the second half of the EcoRV
 site, and xxx is derived from the cDNA sequence). A map of
 the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa
 q.php#8 The primary library was transformed and amplified
 in DH10B (T1 phage resistant) bacteria. Clones available
 from Open Biosystems:
<http://www.openbiosystems.com/stickleback>

ORIGIN

Query Match 88.2%; Score 19.4; DB 8; Length 1402;
 Best Local Similarity 95.2%; Pred. No. 4.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGC 21

Db 828 CCATCGCCCAAGGAGATCGAGC 848

RESULT 13

DN721479

LOCUS

DEFINITION CNB139-F07.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone

Accession DN721479

Version DN721479.1 GI:62097715

Keywords EST.

Source Gasterosteus aculeatus (three spined stickleback)

Organism Gasterosteus aculeatus

Reference 1 (bases 1 to 1480)

Authors Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,

Schmutz,J. and Myers,R.M.

Title Expressed sequence tags from Gasterosteus aculeatus

Journal Unpublished (2003)

Comment Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@shgc.stanford.edu

Plate: 139

High quality sequence stop: 757.

Location/Qualifiers

1. .1480

/organism="Gasterosteus aculeatus"

/mol_type="mRNA"

/strain="Conner Creek sticklebacks, WA USA"

/db_xref="taxon:69293"

/clone="CNB139-F07"

/sex="mixed male and female"

/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CNB"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGAGCGCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5' prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8. The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: <http://www.openbiosystems.com/stickleback>"

ORIGIN

Query Match 88.2%; Score 19.4; DB 8; Length 1480;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21
||||| |||||||
Db 414 CCATCGCCCAAGGAGATCGAGC 434

RESULT 14

CV849414
LOCUS ID0AEE8BA06RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AEE8BA06
DEFINITION 5', mRNA sequence.
ACCESSION CV849414
VERSION CV849414.1 GI:55815097
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 123)
Sabater-Munoz, B., Legeai, F., Bonhomme, J., Dang, P., Dossat, C.,
Duclert, A., Gauthier, J.P., Hunter, W., Martinez-Torres, D., Moya, A.,
Nakabachi, A., Prunier-Leterme, N., Rahbe, Y., Shigenobu, S.,
Simon, J.C., Stern, D., Wincker, P. and Tagu, D.

Annotated ESTs of the pea aphid

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAAACAGCTATGACC

Plate: 8B row: A column: 6.

Location/Qualifiers

1..123

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="yr2"

/db_xref="taxon:7029"

/clone="ID0AEE8BA06"

/tissue_type="antennae"

/dev_stage="L3"

/lab_host="XL1-Blue"

FEATURES

source

/clone_lib="ID0AEE"
/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AEE ; Plant growth place: INRA Rennes, UMR
Bio3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 15/04/2004 ; Harvesting
date: 15/04/2004 ; Description: Aphids inoculated on
one-week old Vicia faba under non-sterile conditions. A.
pisum YR2 is holocyclic, i.e. able to change its
reproductive mode under short photoperiods (sexual) versus
long photoperiods (clonal). experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 123;
Best Local Similarity 90.9%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
||||| |||||||
Db 23 CCAAGGCCAAGGAGATCGAGCT 44

RESULT 15

CN758177
LOCUS ID0AAA21CA12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA21CA12
DEFINITION 5', mRNA sequence.
ACCESSION CN758177
VERSION CN758177.1 GI:47532100
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

1 (bases 1 to 180)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchner) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAAACAGCTATGACC

Plate: 21 row: A column: 12.

Location/Qualifiers

1..180

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA21CA12"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XL1-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;

Soil conditions: Soil ; Sowing date: 01/06/1999 ;

Harvesting date: 01/06/1999 ; Stress date: no stress ;

Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 180;
Best Local Similarity 90.9%; Pred. No. 7.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22
Db 80 CCAAGCCCAAGGATCGAGCT 101

RESULT 16

CN764299 308 bp mRNA linear EST 20-MAY-2004
LOCUS ID0AAA9CB05RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA9CB05 5',
DEFINITION mRNA sequence.

ACCESSION CN764299.1 GI:47538222

VERSION EST.
KEYWORDS Acyrthosiphon pisum (pea aphid)

SOURCE Acyrthosiphon pisum

ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 308)

AUTHORS Hunter, W., Martinez-Torres, D., Rabhe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

JOURNAL Unpublished (2004)

COMMENT Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACACAGCTATGACC

Plate: 9 row: 8 column: 5.

Location/Qualifiers

1. .308

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA9CB05"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA; Plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University;

Soil conditions: Soil; Sowing date: 01/06/1999;

Harvesting date: 01/06/1999; Stress date: no stress;

Description: Aphids inoculated on one-week old Vicia faba

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 308;
Best Local Similarity 90.9%; Pred. No. 8.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22
Db 208 CCAAGCCCAAGGATCGAGCT 229

RESULT 17

CW773364

LOCUS

DEFINITION

5', genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza glaberrima (African rice)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartioideae; Oryzoaceae; Oryza.

1 (bases 1 to 308)

AUTHORS Kim, H., Yu, Y., Wlassovski, M., Byrne, M., Stum, D., Smart, D., Rao, K.,

Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C.

and Wing, R.

OMAP

Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Plate: 0091 row: C column: 22

Seq primer: TAA TAC GAC TCA CTA TAG GG

Class: BAC ends.

Location/Qualifiers

1. .308

/organism="Oryza glaberrima"

/mol_type="genomic DNA"

/db_xref="taxon:4538"

/clone="OG_BBa0091C22"

/tissue_type="young leaves"

/lab_host="DH10B T1 phage resistant"

/clone_lib="OG_BBa"

/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 85.5%; Score 18.8; DB 10; Length 308;

Best Local Similarity 90.9%; Pred. No. 8.1e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22

Db 186 CCATCTCCAAGGATCGAGTT 207

RESULT 18

CV836743

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)

Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 312)

AUTHORS Sabater-Munoz, B., Legeai, F., Bonhomme, J., Dang, P., Dossat, C.,

Duclet, A., Gauthier, J.P., Hunter, W., Martinez-Torres, D., Moya, A.,

Nakabachi, A., Prunier-Leterme, N., Rabhe, Y., Shigenobu, S.,

Simon, J.C., Stern, D., Wincker, P. and Tagu, D.

TITLE Annotated ESTs of the pea aphid
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 3A row: G column: 6.
Location/Qualifiers

FEATURES
source

1. 312
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"
/db_xref="taxon:7029"
/clone="ID0ACC3AG06"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 312;
Best Local Similarity 90.9%; Pred. NO. 8.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 212 CCARAGCCCAAGGAGATCGAGCT 233

RESULT 19
CV837906

LOCUS ID0ACC6BH10M1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC6BH10
DEFINITION 5', mRNA sequence. EST 17-NOV-2004

ACCESSION CV837906.1 GI:55803589
VERSION CV837906
KEYWORDS EST

SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 312)

REFERENCE Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
AUTHORS Duclert,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

Unannotated ESTs of the pea aphid
Unpublished (2004)
Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 6B row: H column: 10.
Location/Qualifiers

FEATURES
source

1. 312
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"

/db_xref="taxon:7029"
/clone="ID0ACC6BH10"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 312;
Best Local Similarity 90.9%; Pred. No. 8.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 212 CCARAGCCCAAGGAGATCGAGCT 233

RESULT 20
CN764328

LOCUS ID0AAA9CD12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA9CD12 5',
DEFINITION mRNA sequence. EST 20-MAY-2004

ACCESSION CN764328.1 GI:47538251
VERSION CN764328
KEYWORDS EST

SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 316)

REFERENCE Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
AUTHORS Stern,D., Tagu,D. and Wincker,P.

An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
Unpublished (2004)
Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 9 row: D column: 12.
Location/Qualifiers

1. 316
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA9CD12"

FEATURES
source

/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

1 (bases 1 to 319)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.

AUTHORS

An expressed sequence tags database for the pea aphid *Acyrthosiphon pisum*

TITLE

Unpublished (2004)

JOURNAL

Contact: D. Tagu

COMMENT

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope

PCR Primers
FORWARD: CAGGAACAGCTATGACC

Plate: 15 row: H column: 11.

Location/Qualifiers

1. .319

/organism="Acyrthosiphon pisum"

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/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA15BH11"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ;

Soil conditions: Soil ; Sowing date: 01/06/1999 ;

Harvesting date: 01/06/1999 ; Stress date: no stress ;

Description: Aphids inoculated on one-week old *Vicia faba* under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 85.5%; Score 18.8; DB 7; Length 319;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

Qy 1 CCATCGCCAGGAGATCGAGCT 22

Db 219 CCAAGCCAGGAGATCGAGCT 240

RESULT 24

CN755404

LOCUS

DEFINITION

CN755404 319 bp mRNA linear EST 19-MAY-2004

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 319)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid *Acyrthosiphon*

pisum

Unpublished (2004)

Contact: D. Tagu

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 15 row: A column: 7.

Location/Qualifiers

1. .319

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/clone="ID0AAA15DA07"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ;

Soil conditions: Soil ; Sowing date: 01/06/1999 ;

Harvesting date: 01/06/1999 ; Stress date: no stress ;

Description: Aphids inoculated on one-week old *Vicia faba* under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 85.5%; Score 18.8; DB 7; Length 319;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCAGGAGATCGAGCT 22

Db 219 CCAAGCCAGGAGATCGAGCT 240

RESULT 25

CZ112870

LOCUS

DEFINITION

OM_Ba0154L01.f OM_Ba Oryza minuta genomic clone OM_Ba0154L01 5',

genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza minuta

Oryza minuta

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzaceae; Oryza.

1 (bases 1 to 323)

Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,

Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and

Wing, R.

OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute

Unpublished (2005)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

Plate: 0154 row: L column: 01

Class: BAC ends.

Location/Qualifiers

1. .323

FEATURES

source

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/clone_lib="OM_Ba"
/notes="Vector: pCUGIBAC1; Site_1: HindIII; Site_2: HindIII"

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Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 160 CCATCTCCAAGGAGATCGAGTT 181

RESULT 26
CV828800
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC10DH01RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC10DH01
5', mRNA sequence.
ACCESSION      CV828800
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE      1 (bases 1 to 332)
AUTHORS
Sabater-Munoz,B., Leggai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rabbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
Unpublished (2004)
CONTACT: D. Tagu
INRA Rennes
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Reverse: CAGGAAACAGCTATGACC
Plate: 10D row: H column: 1.
Location/Qualifiers
1. .332
/organism="Acyrtosiphon pisum"
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/clone="ID0ACC10DH01"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"
/notes="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

FEATURES
source
ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 232 CCAAGCCCAAGGAGATCGAGCT 253

RESULT 28
CV830911
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC16DD11RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC16DD11
5', mRNA sequence.
ACCESSION      CV830911
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE      1 (bases 1 to 332)
AUTHORS
Sabater-Munoz,B., Leggai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rabbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
Unpublished (2004)
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Reverse: CAGGAAACAGCTATGACC
Plate: 10D row: H column: 1.
Location/Qualifiers
1. .332
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
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BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

FEATURES
source
ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 232 CCAAGCCCAAGGAGATCGAGCT 253

RESULT 27
CV829374
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC12CC01RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC12CC01
5', mRNA sequence.
ACCESSION      CV829374
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE      1 (bases 1 to 332)
AUTHORS
Sabater-Munoz,B., Leggai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rabbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
Unpublished (2004)
CONTACT: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Reverse: CAGGAAACAGCTATGACC
Plate: 12C row: C column: 1.
Location/Qualifiers
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/lab_host="XLI-Blue"
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Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

FEATURES
source
ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 232 CCAAGCCCAAGGAGATCGAGCT 253

RESULT 28
CV830911
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC16DD11RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC16DD11
5', mRNA sequence.
ACCESSION      CV830911
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE      1 (bases 1 to 332)
AUTHORS
Sabater-Munoz,B., Leggai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
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Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
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PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Reverse: CAGGAAACAGCTATGACC
Plate: 12C row: C column: 1.
Location/Qualifiers
1. .332
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"
/db_xref="taxon:7029"
/clone="ID0ACC12CC01"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"
/notes="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

FEATURES
source
ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

AUTHORS

1 (bases 1 to 332)
Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

TITLE

JOURNAL

Unpublished (2004)

COMMENT

Annotated ESTs of the pea aphid

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 16D row: D column: 11.

FEATURES

source

Location/Qualifiers

1..332

/organism="Acyrthosiphon pisum"

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/clone="ID0ACCI6DD11"

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/dev_stage="larvae L3 (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ID0ACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0ACC; Plant growth place: INRA Rennes, UMR

BIO3P, 35327, 35653 Le Rheu Cedex France; Soil

conditions: Soil; Sowing date: 01/10/2003; Harvesting

date: 17/10/2003; Description: aphids inoculated on

one-week old Vicia faba germinations under non sterile

conditions experimental condition: long photoperiod (16-hr

light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 CCATCGCCCAAGGAGATCGAGCT 22

|||||

232 CCAAGGCCAAGGAGATCGAGCT 253

|||||

CV831091

332 bp mRNA linear EST 17-NOV-2004

ID0ACCI7BE01RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACCI7BE01

5', mRNA sequence.

CV831091

GI:55796774

CV831091

Acyrthosiphon pisum (pea aphid)

Acyrthosiphon pisum

Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 332)

Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,

Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,

Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,

Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

Annotated ESTs of the pea aphid

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 17B row: E column: 1.

FEATURES

source

Location/Qualifiers

1..332

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

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/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0ACC; Plant growth place: INRA Rennes, UMR

BIO3P, 35327, 35653 Le Rheu Cedex France; Soil

conditions: Soil; Sowing date: 01/10/2003; Harvesting

date: 17/10/2003; Description: aphids inoculated on

one-week old Vicia faba germinations under non sterile

conditions experimental condition: long photoperiod (16-hr

light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 CCATCGCCCAAGGAGATCGAGCT 22

|||||

232 CCAAGGCCAAGGAGATCGAGCT 253

|||||

CV832760

332 bp mRNA linear EST 17-NOV-2004

ID0ACC20DH09RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC20DH09

5', mRNA sequence.

CV832760

GI:55798443

CV832760.1

Acyrthosiphon pisum (pea aphid)

Acyrthosiphon pisum

Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 332)

Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,

Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,

Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,

Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

Annotated ESTs of the pea aphid

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INRA Rennes

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Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Location/Qualifiers

1..332

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

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/clone="ID0ACC20DH09"

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Sample name: IDOACC ; Plant growth place: INRA Rennes, UMR Bio3P, 35327, 35653 Le Rheu Cedex France ; Soil conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting date: 17/10/2003 ; Description: aphids inoculated on one-week old *Vicia faba* germinations under non sterile conditions experimental condition: long photoperiod (16-hr light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
|||||

Db 232 CCAAAGCCAAGGAGATCGAGCT 253
|||||

RESULT 31
CV838428
LOCUS
DEFINITION
IDOACC7DG09RM1 IDOACC Acyrthosiphon pisum cDNA clone IDOACC7DG09
5', mRNA sequence.
CV838428 332 bp mRNA linear EST 17-NOV-2004

ACCESSION
CV838428 1 GI:55804111

KEYWORDS
EST.

SOURCE
Acyrtosiphon pisum (pea aphid)

ORGANISM
Acyrtosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE
AUTHORS
1 (bases 1 to 332)
Sabater-Munoz, B., Legai, F., Bonhomme, J., Dang, P., Dossat, C.,
Duclert, A., Gauthier, J.P., Hunter, W., Martinez-Torres, D., Moya, A.,
Nakabachi, A., Prunier-Leterme, N., Rahbe, Y., Shigenobu, S.,
Simon, J.C., Stern, D., Wincker, P. and Tagu, D.

TITLE
JOURNAL
COMMENT
Annotated ESTs of the pea aphid
Unpublished (2004)
Contact: D. Tagu

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Tel: +33.2.23.23.48.51.65
Fax: +33.2.23.48.51.50

PCR Primers
FORWARD: CAGGAACACGTATGACC
Plate: 7D row: G column: 9.

FEATURES
source
1. .332
Location/Qualifiers
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
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/lab_host="XLI-Blue"
/clone_lib="IDOACC"
/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: IDOACC ; Plant growth place: INRA Rennes, UMR
Bio3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old *Vicia faba* germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
|||||

Db 232 CCAAAGCCAAGGAGATCGAGCT 253

RESULT 32

CN764316

LOCUS

DEFINITION

ACCESSION

CN764316 1 GI:47538239

KEYWORDS

SOURCE

ORGANISM

Acyrtosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

AUTHORS

1 (bases 1 to 340)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.

TITLE

JOURNAL

COMMENT

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACACGTATGACC

Plate: 9 Location/Qualifiers

1. .340

/organism="Acyrtosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA9CC12"

/issue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: IDOAAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old *Vicia faba*
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 340;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
|||||

Db 240 CCAAAGCCAAGGAGATCGAGCT 261
|||||

RESULT 33

CN750782

LOCUS

DEFINITION

ACCESSION

CN750782 1 GI:47515779

KEYWORDS

SOURCE

ORGANISM

Acyrtosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

AUTHORS

1 (bases 1 to 407)
ApDt-XXVI-D10 ApDt Acyrthosiphon pisum cDNA clone ApDTXXVI-D10 5',
mRNA sequence.

CN750782

CN750782 1 GI:47515779

EST.
 Acyrthosiphon pisum (pea aphid)
 Acyrthosiphon pisum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
 1 (bases 1 to 407)
 Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
 Stern, D., Tagu, D. and Wincker, P.
 An expressed sequence tags database for the pea aphid *Acyrthosiphon*
 pisum
 Unpublished (2004)
 Contact: D. Tagu
 INRA Rennes
 UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
 Tel: +33.2.23.48.51.65
 Fax: +33.2.23.48.51.50
 Risk of contamination by bacterial sequences from obligatory
 (Buchnera) or facultative endosymbionts.
 PCR Primers
 FORWARD: GCGCATACCTTCGTATAGCA
 Plate: XXVI row: D column: 10.
 Location/Qualifiers
 1..407
 /organism="Acyrthosiphon pisum"
 /mol_type="mRNA"
 /cultivar="inra-lyon-bf2i 1101"
 /db_xref="taxon:7029"
 /clone="ApDfXXVID10"
 /tissue_type="digestive track"
 /dev_stage="adults, parthenogenetic females"
 /lab_host="TOP10"
 /clone_lib="ApDf"
 /notes="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
 Sample name: ApDT; Plant growth place: UMR INRA-INSA BF2I
 ; Sowing date: 03/04/2003 ; Harvesting date: 12/06/2003 ;
 Description: Long photoperiod 16-hr light/8-hr dark at 20
 C; no overcrowding; grown on *Vicia faba* 3-wk old seedlings
 sown under non sterile condition. ; experimental
 condition: standard, see description"

ORIGIN
 Query Match 85.5%; Score 18.8; DB 7; Length 407;
 Best Local Similarity 90.9%; Pred. No. 8.3e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCATCGCCAGGAGATCGAGCT 22
 ||| ||||| ||||| |||||
 Db 240 CCAAGCCAGGAGATCGAGCT 261

RESULT 34
 CA999580
 LOCUS
 DEFINITION
 S345P G03 Rice cold stress germination cDNA library Oryza sativa
 (japonica cultivar-group) cDNA 5', mRNA sequence.
 CA999580
 VERSION
 CA999580.1 GI:27576886
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 414)
 de los Reyes, B.G., Morsy, M., Gibbons, J., Varma, T.S.N., Antoine, W.,
 Redus, M., McGrath, J.M. and Halgren, R.
 Development of a chilling stress EST library of germinating rice
 (Oryza sativa L. subsp. japonica) enriched with stress-related and
 novel genes
 Unpublished (2002)
 Contact: Benito G. de los Reyes
 Plant Genomics Lab., Department of Crop, Soil and Environmental

```

Sciences
University of Arkansas
115 Plant Science Building, Fayetteville, AR 72701, USA
Tel: (479)-575-7465
Fax: (479)-575-8435
Email: breyes@ark.edu
Plate: S345P row: G column: 03
Seq primer: T3.

FEATURES             Location/Qualifiers
     1..414
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /catalvar="PI560247"
     /db_xref="taxon:39947"
     /tissue_type="coleotile, radicle, prophyll, immature leaf"
     /dev_stage="embryo at different stages of germination and
     shoots of germinated seeds under chilling stress
     (130C/100C)"
     /lab_host="SOLR"
     /clone_lib="Rice cold stress germination cDNA library"
     /notes="Organ: seedlings; Vector: Lambda Uni-Zap XR excised
     as pBluescript; Site_1: EcoRI; Site_2: XhoI; The cDNAs
     were derived from reverse transcription of mRNA samples
     from seeds at different stages of germination and
     seedlings at early phase of growth under chilling stress
     (130C/100C). The mRNA pool was used as template for double
     stranded cDNA synthesis using the Stratagene Uni-Zap XR
     cDNA synthesis and library kit. A total of 150,000 phages
     were excised from the primary library as pBluescript
     phagemid clones. Enrichment of the primary excised library
     with chilling-induced transcripts was performed by
     hybridizing the primary excised library colony lifts with
     the PCR-select subtraction product, with cold germinated
     cDNA as tester and control temperature-germinated cDNA as
     driver."

ORIGIN
Query Match      85.5%;   Score 18.8;   DB 6;   Length 414;
Best Local Similarity 90.9%;   Pred. No. 8.3e+02;
Matches 20;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      1  CCATCGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      113 CCATCTCCAAGGAGATCGAGTT 134

RESULT 35
LOCUS      CN583674
DEFINITION  USDA-FP 126739 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum
            cDNA clone WHAP041_C03, mRNA sequence.
ACCESSION  CN583674
VERSION    CN583674.1 GI:46995397
KEYWORDS   EST.
SOURCE     Acyrthosiphon pisum (pea aphid)
ORGANISM   Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrotriphini; Acyrthosiphon.
REFERENCE  1 (bases 1 to 424)
            Hunter,W.B., Dang,P.M., Stern,D. and Lapointe,S.L.
            Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
            Unpublished (2004)
CONTACT    Wayne Hunter; Phat Dang
            US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS
2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ushrl.ars.usda.gov.
            Location/Qualifiers
            1..424
            /organism="Acyrthosiphon pisum"

```


[illegible]

```

FEATURES
  source
    Location/Qualifiers
      1. .484
        /organism="Acyrthosiphon pisum"
        /mol_type="mRNA"
        /cultivar="yr2"
        /db_xref="taxon:7029"
        /clone="ApAL3SDIVF8"
        /tissue_type="antennae"
        /dev_stage="third instar nymph (L3)"
        /lab_host="TOP10"
        /clone_lib="ApAL3SD"
        /notes="Vector: pDNR-LIB; Site_1: SfIIA; Site_2: SfiIB;
        Sample name: ApAL3SD ; Plant growth place: INRA-Rennes,
        UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
        conditions: peat ; Sowing date: 25/03/2003 ; Harvesting
        date: 10/04/2003 ; Stress date: no stress ; Description:
        aphids inoculated on one-week old Vicia faba germinations
        under non sterile conditions. ; experimental condition:
        short photoperiod (12-hr light/12-hr dark at 18 c)"

ORIGIN
  Query Match      85.5%; Score 18.8; DB 7; Length 484;
  Best Local Similarity 90.9%; Pred. No. 8.4e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCGCCAAGGAGATCGAGCT 22
    ||| ||||| ||||| |||||
Db 5 CCAAGGCCAAGGAGATCGAGCT 26

RESULT 40
CD451510
LOCUS
DEFINITION
  CD451510 492 bp mRNA linear EST 03-JUN-2003
  cDNA clone WHWTC-47_E03 5', mRNA sequence.
CD451510
CD451510.1 GI:31366250
EST.
Toxoptera citricida (brown citrus aphid)
Toxoptera citricida
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Aphidini; Toxoptera.
1 (bases 1 to 492)
Hunter, W.B., Dang, P.M., Bausher, M.G., Chaparro, J.X., McKendree, W.,
Shatters, R.G. Jr., McKenzie, C.L. and Sinisterra X.H.
Aphid biology: Expressed genes from alate Toxoptera citricida, the
brown citrus aphid
J. Insect Sci. 3 (23), 1-7 (2003)
Contact: Wayne B. Hunter
US Horticultural Research Laboratory
USDA - ARS
2001 South Rock Rd., Fort Pierce, FL 34945, USA
Tel: (772) 462-5898
Fax: (772) 462-5960
Email: whunter@usrl.ars.usda.gov
Seq primer: T3 Primer.
Location/Qualifiers
  1. .492
    /organism="Toxoptera citricida"
    /mol_type="mRNA"
    /db_xref="taxon:223852"
    /clone="WHWTC-47_E03"
    /sex="Mixed population"
    /issue_type="Entire insect"
    /dev_stage="Adult Alate"
    /lab_host="XLI-Blue"
    /clone_lib="Adult Alate Brown Citrus Aphid"
    /notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
    XhoI; Toxoptera citricida (Kirkaldy); A high quality EST
    with at least 100 contiguous bases at Trace Tuner score of
    20 or better."
FEATURES
  source
    Location/Qualifiers

```

ORIGIN


```

/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP079_F04"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="XLI-Blue"
/clone_lib="Acyrtosiphon pisum, Pea Aphid"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; Acyrthosiphon pisum colonies. Library by Srin-
kambampati; Peter Dearnden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at Trace Tuner score of 20 or better.
Sequencing of clones by Dr. PW Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."

ORIGIN
Query Match      85.5%; Score 18.8; DB 7; Length 572;
Best Local Similarity 90.9%; Pred. No. 8.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 80 CCAAGCCCAAGGAGATCGAGCT 101

RESULT 47
CB087986
LOCUS
DEFINITION
hkl0g08.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
centranthoides cDNA clone hkl0g08, mRNA sequence.
ACCESSION
CB087986
VERSION
CB087986.1 GI:27912178
KEYWORDS
EST.
SOURCE
Hedyotis centranthoides
ORGANISM
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;
Spermacoceae; Hedyotis.
REFERENCE
1 (bases 1 to 581)
Levesque M.P., Twigg R.W., Motley T., Katari M.S., Dedhia N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P. and Stevenson, D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hkl0 row: g column: 08
Seq primer: -21M13UnivRev
High quality sequence stop: 581.
Location/Qualifiers
1. .581
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone="hkl0g08"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/notes="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 599;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 229 CCAAGCCCAAGGAGATCGAGCT 250

RESULT 49
CN584119
LOCUS
DEFINITION
USDA-FP 127186 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum
cDNA clone WHAP055_A09, mRNA sequence.
ACCESSION
CN584119
VERSION
CN584119.1 GI:46995842
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)

```

```

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 581;
Best Local Similarity 90.9%; Pred. No. 8.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 234 CCAAGCCCAAGGAGATCGAGCT 255

RESULT 48
CD450119
LOCUS
DEFINITION
USDA-FP 102080 Adult Alate Brown Citrus Aphid Toxoptera citricida
cDNA clone WHWTC-28_H10 5', mRNA sequence.
ACCESSION
CD450119
VERSION
CD450119.1 GI:31364853
KEYWORDS
EST.
SOURCE
Toxoptera citricida (brown citrus aphid)
ORGANISM
Toxoptera citricida
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Aphidini; Toxoptera.
REFERENCE
1 (bases 1 to 599)
Hunter W.B., Dang, P.M., Bausher, M.G., Chaparro, J.X., McKendree, W.,
Shatters, R.G. Jr., McKenzie, C.L. and Sinisterza, X.H.
Aphid biology: Expressed genes from alate Toxoptera citricida, the
brown citrus aphid
J. Insect Sci. 3 (23), 1-7 (2003)
Contact: Wayne B. Hunter
US Horticultural Research Laboratory
USDA - ARS
2001 South Rock Rd., Fort Pierce, FL 34945, USA
Tel: (772) 462-5898
Fax: (772) 462-5960
Email: whunter@uehrl.ars.usda.gov
Seq primer: T3 Primer.
Location/Qualifiers
1. .599
/organism="Toxoptera citricida"
/mol_type="mRNA"
/db_xref="taxon:223852"
/clone="WHWTC-28_H10"
/sex="Mixed population"
/tissue_type="Entire insect"
/dev_stage="Adult Alate"
/lab_host="XLI-Blue"
/clone_lib="Adult Alate Brown Citrus Aphid"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; Toxoptera citricida (Kirkaldy); A high quality EST
with at least 100 contiguous bases at Trace Tuner score of
20 or better."

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 599;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 229 CCAAGCCCAAGGAGATCGAGCT 250

RESULT 49
CN584119
LOCUS
DEFINITION
USDA-FP 127186 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum
cDNA clone WHAP055_A09, mRNA sequence.
ACCESSION
CN584119
VERSION
CN584119.1 GI:46995842
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)

```

```
ORGANISM      Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE
1 (bases 1 to 612)
AUTHORS      Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
TITLE        Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
JOURNAL      Unpublished (2004)
COMMENT      Contact: Wayne Hunter; Phat Dang
US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS
2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ushrl.ars.usda.gov.

FEATURES
source
1..612
Location/Qualifiers
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP055_A09"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="Xkl-Blue"
/clone_lib="Acyrthosiphon pisum, Pea Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Acyrthosiphon pisum colonies. Library by Srin
Kambhampati; Peter Dearden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at trace tuner score of 20 or better.
Sequencing of clones by Dr. PM Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."

ORIGIN
Query Match      85.5%; Score 18.8; DB 7; Length 612;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB      156 CCAGAGCCCAAGGAGATCGAGCT 177
|||||

RESULT 50
CL612592
LOCUS      CL612592
DEFINITION      OR_BB0003013.r OR_BBa Oryza nivara genomic clone OR_BB0003013 3',
genomic survey sequence.
ACCESSION      CL612592
VERSION        CL612592.1 GI:49101070
KEYWORDS       GSS
SOURCE         Oryza nivara
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoae; Oryza.
REFERENCE      1 (bases 1 to 629)
AUTHORS       Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
TITLE         OMAP Project
JOURNAL       Unpublished (2004)
COMMENT       Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161 Std Error: 0.00
Plate: 0003 row: O column: 13
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1..629
Location/Qualifiers
/organism="Oryza nivara"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BB0003013"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      85.5%; Score 18.8; DB 10; Length 629;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB      314 CCATCTCCCAAGGAGATCGAGTT 335
|||||

RESULT 51
CB690026
LOCUS      CB690026
DEFINITION      CEST-57-H-12 Mixed source, strain EP155 and EP155 infected with
hypovirus CHV1-EP713 Cryphonectria parasitica cDNA clone EP155,
EP155-CHV1-EP713 5-prime, mRNA sequence.
ACCESSION      CB690026
VERSION        CB690026.1 GI:34450895
KEYWORDS       EST.
SOURCE         Cryphonectria parasitica
ORGANISM       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Diaporthales; Valsaceae; Cryphonectria-Endothia
complex; Cryphonectria.
REFERENCE      1 (bases 1 to 640)
AUTHORS       Dawe, A.L., McMains, V.C., Panglao, M., Kasahara, S., Chen, B. and
Nuss, D.L.
TITLE         An ordered collection of expressed sequences from Cryphonectria
parasitica and evidence of genomic microsynteny with Neurospora
crassa and Magnaporthe grisea
JOURNAL       Microbiology 149 (9), 2373-2384 (2003)
PUBMED       12949163
COMMENT       Contact: Dawe AL, Nuss DL
Center for Biosystems Research
University of Maryland Biotechnology Institute
5115 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301-405-7661 or 5111
Fax: 301-314-9075
Email: dawe@umbi.umd.edu
Cryphonectria parasitica EST derived from mixed samples of cDNA
from wild-type (strain EP155) and hypovirus-infected cultures.
Seq primer: M13-reverse.

FEATURES
source
1..640
Location/Qualifiers
/organism="Cryphonectria parasitica"
/mol_type="mRNA"
/strain="EP155"
/db_xref="ATCC (inhost):38755 and 52571"
/db_xref="taxon:5116"
/clone="EP155, EP155-CHV1-EP713"
/clone_lib="Mixed source, strain EP155 and EP155 infected
with hypovirus CHV1-EP713"
/note="Cryphonectria parasitica EST derived from mixed
samples of cDNA from wild-type (strain EP155) and
hypovirus-infected cultures"

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 640;
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Best Local Similarity 90.9%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAGGAGATCGAGCT 22
 |||||
 Db 158 CCATCGCCAGGAGATCGAGCT 179

RESULT 52

CF587912
 LOCUS
 DEFINITION USDA-FP 121300-059 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum cDNA clone WHAP-010_H06 5', mRNA sequence.

ACCESSION CF587912
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Acyrthosiphon pisum (pea aphid)

Acyrthosiphon pisum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 646)
 AUTHORS Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
 TITLE Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
 JOURNAL Unpublished (2004)

COMMENT Contact: Wayne Hunter; Phat Dang

US. Horticultural Research Lab, Ft. Pierce, FL

USDA-ARS

2001 South Rock Rd., Ft. Pierce, FL 34945, USA

Tel: (772) 462-5898, (772) 462-5940

Fax: (772) 462-5986

Email: Whunter@ushrl.ars.usda.gov

Seq primer: T3 Primer.

FEATURES

source

1..646
 /location/Qualifiers
 /organism="Acyrthosiphon pisum"
 /mol_type="mRNA"
 /db_xref="taxon:7029"
 /clone="WHAP-010_H06"
 /sex="Mixed population"
 /tissue_type="whole body, nymphs and adults"
 /dev_stage="All"
 /lab_host="X11-Blue"
 /clone_lib="Acyrthosiphon pisum, Pea Aphid"
 /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; Acyrthosiphon pisum colonies. Library by Srini Kambhampati; Peter Dearaden; David Stern, Department of Ecology and Evolutionary Biology, Princeton University, NJ. (609) 258-0759. A high quality EST with at least 100 contiguous bases at Trace Tumor score of 20 or better. Sequencing of clones by Dr. PW Dang, US. Horticultural Research Lab, Ft. Pierce, FL. (772) 462-5940."

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 646;
 Best Local Similarity 90.9%; Pred. No. 8.6e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAGGAGATCGAGCT 22
 |||||
 Db 213 CCAAGGCCAAGGAGATCGAGCT 234

RESULT 53

AQ257000
 LOCUS
 DEFINITION nxb0017E16f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nxb0017E16f, genomic survey sequence.

ACCESSION AQ257000
 VERSION AQ257000.1
 KEYWORDS GSS.
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 656)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGGG

Class: BAC ends

High quality sequence stop: 397.

FEATURES

source

1..656

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="japonica"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="nxb0017E16f"

/tissue_type="Leaf"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice BAC Library"

/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 656;
 Best Local Similarity 90.9%; Pred. No. 8.6e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22

|||||

Db 314 CCATCTCCAGGAGATCGAGTT 335

RESULT 54

CB000900/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

CB000900 665 bp mRNA linear EST 10-JAN-2003
 S345K_B05 Rice cold stress germination cDNA library Oryza sativa (japonica cultivar-group) cDNA 5', mRNA sequence.

CB000900
 CB000900.1 GI:27578205
 EST.
 Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 665)


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1. .671
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/mol_type="genomic DNA"
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0089B04f"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CGI Rice BAC Library"
/notes="Vector: pBelOBAC1; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN
Query Match 85.5%; Score 18.8; DB 9; Length 671;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
Db 314 CCATCTCCAAGGAGATCGAGTT 335

RESULT 57
CW775708 672 bp DNA linear GSS 15-NOV-2004
LOCUS OP_Ba0075J13.r OP_Ba Oryza punctata genomic clone OP_Ba0075J13
DEFINITION 3', genomic survey sequence.
VERSION CW775708.1 GI:55744089
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 672)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19s.
Bases 163-840 of the raw sequence (length 1008) were retained after
clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0006 row: N column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

REFERENCE
AUTHORS SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
TITLE OMAP Project - Purdue University
JOURNAL Unpublished (2004)
COMMENT Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19s.
Bases 163-840 of the raw sequence (length 1008) were retained after
clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0006 row: N column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1. .673
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0006N04"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/notes="Vector: PAGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 673;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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FEATURES
source
1. .672
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0075J13"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/notes="Vector: PAGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 672;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
Db 255 CCATCTCCAAGGAGATCGAGTT 276

RESULT 58
CW506965 673 bp DNA linear GSS 06-OCT-2004
LOCUS OP_Ba0006N04.r OP_Ba Oryza punctata genomic clone OP_Ba0006N04
DEFINITION 3', genomic survey sequence.
ACCESSION CW506965
VERSION CW506965.1 GI:53836470
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 673)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19s.
Bases 193-865 of the raw sequence (length 1400) were retained after
clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0006 row: N column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
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/organism="Oryza punctata"
/mol_type="genomic DNA"
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/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/notes="Vector: PAGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 673;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCATGCCAAGGAGATCGAGCT 22
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 Db 235 CCATCTCCAAGGAGATCGAGTT 256

RESULT 59
 AQ287315

LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) genomic clone nbxb0029K22f, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AQ287315 684 bp DNA linear GSS 03-DEC-1998
 nbxb0029K22f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0029K22f, genomic survey sequence.

AQ287315 1 GI:3949057
 GSS.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoideae; Oryza.
 1 (bases 1 to 684)
 Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: TAATACGACTCATATAGGG
 Class: BAC ends
 High quality sequence stop: 460.

FEATURES
 source
 1..684
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
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 /cultivar="Nipponbare"
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 /tissue_type="Leaf"
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 /clone_lib="CUGI Rice BAC Library"
 /note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 684;
 Best Local Similarity 90.9%; Pred. No. 8.6e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22
 ||||| ||||| ||||| ||||| |||||
 Db 313 CCATCTCCAAGGAGATCGAGTT 334

RESULT 60
 CF588105

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source
 1..696
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 /organism="Acyrtosiphon pisum"
 /mol_type="mRNA"
 /db_xref="taxon:7029"
 /clone="WHAP-007_B07"
 /sex="Mixed population"
 /tissue_type="whole body, nymphs and adults"
 /dev_stage="All"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; Acyrtosiphon pisum colonies, Library by Srinil Kambampati; Peter Dearaden; David Stern, Department of Ecology and Evolutionary Biology, Princeton University, NJ. (609) 258-0759. A high quality EST with at least 100 contiguous bases at Trace Tuner score of 20 or better. Sequencing of clones by Dr. PM Dang, US. Horticultural Research Lab, Ft. Pierce, FL. (772) 462-5940."

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 696;
 Best Local Similarity 90.9%; Pred. No. 8.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22
 ||||| ||||| ||||| ||||| |||||
 Db 283 CCAAAGCCAGGAGATCGAGCT 304

Search completed: April 2, 2006, 00:09:35
 Job time : 308.022 secs

CF588105 696 bp mRNA linear EST 25-SEP-2003
 USDA-FP_121000-060 Acyrtosiphon pisum, Pea Aphid Acyrtosiphon pisum cDNA clone WHAP-007_B07 5', mRNA sequence.

CF588105
 CF588105.1 GI:35509039
 EST.
 Acyrtosiphon pisum (pea aphid)
 Acyrtosiphon pisum
 Acyrtosiphon pisum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrtosiphon.

1 (bases 1 to 696)
 Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
 Gene expression in Acyrtosiphon pisum (Hemiptera: Aphididae)
 Unpublished (2004)
 Contact: Wayne Hunter; Phat Dang
 US. Horticultural Research Lab, Ft. Pierce, FL
 USDA-ARS
 2001 South Rock Rd., Ft. Pierce, FL 34945, USA
 Tel: (772) 462-5898, (772) 462-5940
 Fax: (772) 462-5986
 Email: Whunter@ushrl.ars.usda.gov
 Seq primer: T3 Primer.

USDA-ARS
 2001 South Rock Rd., Ft. Pierce, FL 34945, USA
 Tel: (772) 462-5898, (772) 462-5940
 Fax: (772) 462-5986
 Email: Whunter@ushrl.ars.usda.gov
 Seq primer: T3 Primer.

1..696
 Location/Qualifiers
 /organism="Acyrtosiphon pisum"
 /mol_type="mRNA"
 /db_xref="taxon:7029"
 /clone="WHAP-007_B07"
 /sex="Mixed population"
 /tissue_type="whole body, nymphs and adults"
 /dev_stage="All"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; Acyrtosiphon pisum colonies, Library by Srinil Kambampati; Peter Dearaden; David Stern, Department of Ecology and Evolutionary Biology, Princeton University, NJ. (609) 258-0759. A high quality EST with at least 100 contiguous bases at Trace Tuner score of 20 or better. Sequencing of clones by Dr. PM Dang, US. Horticultural Research Lab, Ft. Pierce, FL. (772) 462-5940."

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:17:36 ; Search time 59.2198 Seconds
(without alignments)
3072.051 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22
Sequence: 1 ccacgcgaagagatcgagct 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : Published Applications_NA_Main:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	US-10-824-527-1	Sequence 1, Appl
2	22	100.0	647	US-09-880-505-115	Sequence 115, App
3	22	100.0	647	US-10-051-643-115	Sequence 115, App
4	22	100.0	647	US-10-205-979-15	Sequence 32, Appl
5	22	100.0	888	US-10-267-311-32	Sequence 32, Appl
6	22	100.0	888	US-10-679-956-32	Sequence 113, App
7	22	100.0	1569	US-09-880-505-113	Sequence 113, App
8	22	100.0	1569	US-10-051-643-113	Sequence 26142, A
9	22	100.0	1620	US-10-282-122A-26142	Sequence 23, Appl
10	22	100.0	1623	US-09-712-363-23	Sequence 3, Appl
11	22	100.0	1623	US-10-267-311-3	Sequence 3, Appl
12	22	100.0	1623	US-10-156-761-3915	Sequence 3915, Ap
13	22	100.0	1623	US-10-282-122A-25595	Sequence 25595, A
14	22	100.0	1623	US-10-282-122A-28196	Sequence 28196, A
15	22	100.0	1623	US-10-679-956-3	Sequence 3, Appl
16	22	100.0	1626	US-09-880-505-159	Sequence 159, App
17	22	100.0	1626	US-10-051-643-159	Sequence 159, App
18	22	100.0	1626	US-10-205-979-14	Sequence 14, Appl
19	22	100.0	1626	US-10-282-122A-27502	Sequence 27502, A
20	22	100.0	1626	US-10-491-300-1	Sequence 1, Appl
21	22	100.0	1632	US-10-369-493-44560	Sequence 44560, A
22	22	100.0	1701	US-10-501-127A-21	Sequence 21, Appl
23	22	100.0	1761	US-10-635-211-1	Sequence 1, Appl

24	22	100.0	1920	5	US-10-267-311-16	Sequence 16, Appl
25	22	100.0	1920	5	US-10-679-956-16	Sequence 16, Appl
26	22	100.0	1947	5	US-10-267-311-28	Sequence 28, Appl
27	22	100.0	1947	5	US-10-679-956-28	Sequence 28, Appl
28	22	100.0	2073	5	US-10-068-059-9	Sequence 9, Appl
29	22	100.0	2073	5	US-10-941-049-9	Sequence 9, Appl
30	22	100.0	2130	5	US-10-068-059-7	Sequence 7, Appl
31	22	100.0	2130	5	US-10-941-049-7	Sequence 7, Appl
32	22	100.0	2175	5	US-10-068-059-11	Sequence 11, Appl
33	22	100.0	2175	5	US-10-941-049-11	Sequence 11, Appl
34	22	100.0	2241	5	US-10-068-059-5	Sequence 5, Appl
35	22	100.0	2241	5	US-10-941-049-5	Sequence 5, Appl
36	22	100.0	2847	5	US-10-267-311-20	Sequence 20, Appl
37	22	100.0	2847	9	US-10-679-956-20	Sequence 20, Appl
38	22	100.0	86114	6	US-10-080-170-648	Sequence 648, App
39	22	100.0	86114	7	US-10-080-170-648	Sequence 648, App
40	22	100.0	86114	8	US-10-468-356-648	Sequence 648, App
41	22	100.0	9025608	6	US-10-156-761-1	Sequence 1, Appl
42	20.4	92.7	1728	6	US-10-369-493-32009	Sequence 32009, A
43	20.4	92.7	99090	8	US-10-656-394A-13	Sequence 13, Appl
44	20	90.9	20	8	US-10-500-586-55	Sequence 55, Appl
45	19	86.4	4134	3	US-09-975-553-17	Sequence 17, Appl
46	19	86.4	4134	5	US-10-125-792-1	Sequence 1, Appl
47	19	86.4	4134	5	US-10-125-778-1	Sequence 1, Appl
48	19	86.4	4134	5	US-10-270-795-17	Sequence 17, Appl
49	19	86.4	4134	5	US-10-270-876-17	Sequence 17, Appl
50	19	86.4	4134	6	US-10-268-051-7	Sequence 7, Appl
51	19	86.4	4134	6	US-10-125-772-1	Sequence 1, Appl
52	19	86.4	4134	6	US-10-016-496-1	Sequence 1, Appl
53	19	86.4	4134	6	US-10-411-076-23	Sequence 23, Appl
54	19	86.4	4134	6	US-10-410-872-17	Sequence 17, Appl
55	19	86.4	4134	6	US-10-410-885-1	Sequence 1, Appl
56	19	86.4	4134	8	US-10-851-047-7	Sequence 7, Appl
57	19	86.4	4134	8	US-10-626-115-17	Sequence 17, Appl
58	19	86.4	4134	10	US-11-057-660-23	Sequence 23, Appl
59	19	86.4	4134	10	US-11-085-364-1	Sequence 1, Appl
60	19	86.4	4134	10	US-11-086-550-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-824-527-1
; Sequence 1, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-0000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer

US-10-824-527-1

Query Match 100.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 1 CCATGCCCAAGGAGATCGAGCT 22

RESULT 2

US-09-880-505-115
; Sequence 115, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.100762
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-115

Query Match 100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 3

US-10-051-643-115
; Sequence 115, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.10082
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-115

Query Match 100.0%; Score 22; DB 5; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 4

US-10-205-979-15
; Sequence 15, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.10630
; CURRENT APPLICATION NUMBER: US/10/205,979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-205-979-15

Query Match 100.0%; Score 22; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 5

US-10-267-311-32
; Sequence 32, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match 100.0%; Score 22; DB 5; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 6

US-10-679-956-32
; Sequence 32, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2006-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(885)
US-10-679-956-32

Query Match 100.0%; Score 22; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 7

US-09-880-505-113
; Sequence 113, Application US/09880505
; Publication No. US20030007876A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-113

Query Match 100.0%; Score 22; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 8

US-10-051-643-113
; Sequence 113, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-113

Query Match 100.0%; Score 22; DB 5; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 9

US-10-282-122A-26142
; Sequence 26142, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

US-10-282-122A-26142

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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26142
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-26142

Query Match          100.0%; Score 22; DB 7; Length 1620;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
        ||||||||||||||||||
Db      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 10
US-09-712-363-23
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match          100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
        ||||||||||||||||||
Db      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 11
US-10-267-311-3
; Sequence 3, Application US/10267311
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; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match          100.0%; Score 22; DB 5; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
        ||||||||||||||||||
Db      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 12
US-10-156-761-3915
; Sequence 3915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3915
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
US-10-156-761-3915

Query Match          100.0%; Score 22; DB 6; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
        ||||||||||||||||||
Db      161 CCATGCCCAAGGAGATCGAGCT 182
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RESULT 13
US-10-282-122A-25595
; Sequence 25595, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25595
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25595

Query Match      100.0%; Score 22; DB 7; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 14
US-10-282-122A-28196
; Sequence 28196, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25595
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25595

Query Match      100.0%; Score 22; DB 7; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 15
US-10-679-956-3
; Sequence 3, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
```

US-10-679-956-3

Query Match 100.0%; Score 22; DB 9; Length 1623;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 16

US-09-880-505-159
 ; Sequence 159, Application US/09880505
 ; Publication No. US2003000796A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; APPLICANT: Prestidge, Ross
 ; TITLE OF INVENTION: Methods and Compounds for the Treatment
 ; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
 ; FILE REFERENCE: 11000.100762
 ; CURRENT APPLICATION NUMBER: US/09/880,505
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: US 08/997,080
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 194
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0
 ; SEQ ID NO 159
 ; LENGTH: 1626
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-09-880-505-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 17

US-10-051-643-159
 ; Sequence 159, Application US/10051643
 ; Publication No. US20020197265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; TITLE OF INVENTION: Methods and Compounds for the Treatment
 ; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
 ; TITLE OF INVENTION: System using Mycobacterium Vaccae
 ; FILE REFERENCE: 11000.1008c2
 ; CURRENT APPLICATION NUMBER: US/10/051,643
 ; CURRENT FILING DATE: 2002-01-18
 ; PRIOR FILING DATE: US09/156,181
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: US 08/996,624
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0
 ; SEQ ID NO 159
 ; LENGTH: 1626
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-10-051-643-159

Query Match 100.0%; Score 22; DB 5; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 18

US-10-205-979-14
 ; Sequence 14, Application US/10205979
 ; Publication No. US20030147861A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; APPLICANT: Abernethy, Nevin
 ; TITLE OF INVENTION: Compounds and Methods for the Modulation
 ; TITLE OF INVENTION: of Immune Responses
 ; FILE REFERENCE: 11000.1063U
 ; CURRENT APPLICATION NUMBER: US/10/205,979
 ; CURRENT FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/308,446
 ; PRIOR FILING DATE: 2001-07-26
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 1626
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-10-205-979-14

Query Match 100.0%; Score 22; DB 6; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 19

US-10-282-122A-27502
 ; Sequence 27502, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27

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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27502
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-282-122A-27502

Query Match      100.0%; Score 22; DB 7; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 20
US-10-491-300-1
; Sequence 1, Application US/10491300
; Publication No. US2005063984A1
; GENERAL INFORMATION:
; APPLICANT: MEDVET SCIENCE PTY LTD
; APPLICANT: KURAL INDUSTRIES RESEARCH AND DEVELOPMENT CORPORATION
; TITLE OF INVENTION: GroEL Chimeric Protein and Vaccine
; FILE REFERENCE: A20-061
; CURRENT APPLICATION NUMBER: US/10/491,300
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rhodococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
; OTHER INFORMATION: groEL gene
US-10-491-300-1

Query Match      100.0%; Score 22; DB 9; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 21
US-10-369-493-44560
; Sequence 44560, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
```

```
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44560
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-10-369-493-44560

Query Match      100.0%; Score 22; DB 6; Length 1632;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 22
US-10-501-127A-21
; Sequence 21, Application US/10501127A
; Publication No. US20050232937A1
; GENERAL INFORMATION:
; APPLICANT: ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid.
; TITLE OF INVENTION: Paramycobacterial diagnostics and vaccines
; FILE REFERENCE: 2002-032-US
; CURRENT APPLICATION NUMBER: US/10/501,127A
; CURRENT FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: mycobacterium avium paratuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1701)
US-10-501-127A-21

Query Match      100.0%; Score 22; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 236 CCATGCCCAAGGAGATCGAGCT 257

RESULT 23
US-10-635-211-1
; Sequence 1, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
; NAME/KEY: CDS
; LOCATION: (1)..(1761)
US-10-635-211-1

Query Match      100.0%; Score 22; DB 8; Length 1761;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 24
US-10-267-311-16
; Sequence 16, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 22; DB 5; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 25
US-10-679-956-16
; Sequence 16, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-679-956-16

Query Match 100.0%; Score 22; DB 5; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 26
US-10-267-311-28
; Sequence 28, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-267-311-28

Query Match 100.0%; Score 22; DB 5; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 27
US-10-679-956-28
; Sequence 28, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
```

```
; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match      100.0%; Score 22; DB 9; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
Db 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-068-059-9
; Sequence 9, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      100.0%; Score 22; DB 5; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
Db 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 29
US-10-941-049-9
; Sequence 9, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-9

; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match      100.0%; Score 22; DB 9; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
Db 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-068-059-9
; Sequence 9, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      100.0%; Score 22; DB 5; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
Db 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 29
US-10-941-049-9
; Sequence 9, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-9

Query Match      100.0%; Score 22; DB 9; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
Db 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 30
US-10-068-059-7
; Sequence 7, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-7

Query Match      100.0%; Score 22; DB 5; Length 2130;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
   |||||
Db 668 CCATGCCCAAGGAGATCGAGCT 689

RESULT 31
US-10-941-049-7
; Sequence 7, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-7
```

Query Match 100.0%; Score 22; DB 9; Length 2130;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 668 CCATGCCCAAGGAGATCGAGCT 689

RESULT 32
US-10-068-059-11
; Sequence 11, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 22; DB 5; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 713 CCATGCCCAAGGAGATCGAGCT 734

RESULT 33
US-10-941-049-11
; Sequence 11, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-11

Query Match 100.0%; Score 22; DB 9; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 713 CCATGCCCAAGGAGATCGAGCT 734

RESULT 34
US-10-068-059-5
; Sequence 5, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 22; DB 5; Length 2241;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 779 CCATGCCCAAGGAGATCGAGCT 800

RESULT 35
US-10-941-049-5
; Sequence 5, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-5

Query Match 100.0%; Score 22; DB 9; Length 2241;

```
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
    |||||
Db 779 CCATCGCCAAGGAGATCGAGCT 800

RESULT 36
US-10-267-311-20
; Sequence 20, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match 100.0%; Score 22; DB 5; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
    |||||
Db 221 CCATCGCCAAGGAGATCGAGCT 242

RESULT 37
US-10-679-956-20
; Sequence 20, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)

US-10-679-956-20

Query Match 100.0%; Score 22; DB 9; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
    |||||
Db 221 CCATCGCCAAGGAGATCGAGCT 242

RESULT 38
US-10-080-170-648
; Sequence 648, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-648

Query Match 100.0%; Score 22; DB 6; Length 86114;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
    |||||
Db 15365 CCATCGCCAAGGAGATCGAGCT 15386

RESULT 39
US-10-080-170-648
; Sequence 648, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-648

Query Match 100.0%; Score 22; DB 7; Length 86114;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
    |||||
Db 15365 CCATCGCCAAGGAGATCGAGCT 15386
```

RESULT 40

US-10-468-356-648
 ; Sequence 648, Application US/10468356
 ; Publication No. US20040197896A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COLE, STEWART
 ; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
 ; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
 ; TREATMENT OF MYCOBACTERIOSES
 ; FILE REFERENCE: 05394.0019
 ; CURRENT APPLICATION NUMBER: US/10/468,356
 ; CURRENT FILING DATE: 2003-08-19
 ; PRIOR APPLICATION NUMBER: 10/080,170
 ; PRIOR FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: 60/270,123
 ; PRIOR FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 655
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 648
 ; LENGTH: 86114
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 US-10-468-356-648

Query Match 100.0%; Score 22; DB 8; Length 86114;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 DB 15365 CCATCGCCCAAGGAGATCGAGCT 15386

RESULT 41

US-10-156-761-1/c
 ; Sequence 1, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1
 ; LENGTH: 9025608
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermitilis
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4187715)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-156-761-1

Query Match 100.0%; Score 22; DB 6; Length 9025608;
 Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 DB 4855659 CCATCGCCCAAGGAGATCGAGCT 4855638

RESULT 42

US-10-369-493-32009
 ; Sequence 32009, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 32009
 ; LENGTH: 1728
 ; TYPE: DNA
 ; ORGANISM: Thermobifida fusca
 US-10-369-493-32009

Query Match 92.7%; Score 20.4; DB 6; Length 1728;
 Best Local Similarity 95.5%; Pred. No. 7.2; Indels 1; Gaps 0;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 DB 269 CCATCGCTAAGGAGATCGAGCT 290

RESULT 43

US-10-656-394A-13/c
 ; Sequence 13, Application US/10656394A
 ; Publication No. US20040210957A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang et al.
 ; TITLE OF INVENTION: Cloning and Characterization of the
 ; FILE REFERENCE: 035718/252062
 ; CURRENT APPLICATION NUMBER: US/10/656,394A
 ; CURRENT FILING DATE: 2003-09-05
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PASCSEQ for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 99090
 ; TYPE: DNA
 ; ORGANISM: Oryza minuta
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 23216
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-656-394A-13

Query Match 92.7%; Score 20.4; DB 8; Length 99090;
 Best Local Similarity 95.5%; Pred. No. 6.8; Indels 1; Gaps 0;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
 |||||
 DB 38860 CCATCGCCCAAGGAGATCGAGCT 38839

RESULT 44

US-10-500-586-55
 ; Sequence 55, Application US/10500586
 ; Publication No. US20050014157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIM, Bum-Joon
 ; APPLICANT: BIOMEDLAB CORPORATION
 ; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HS

```
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIES
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSPF3
US-10-500-586-55

Query Match          90.4%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATCGCCCAAGGAGATCGAGCT 22
Db 1 ATCGCCCAAGGAGATCGAGCT 20

RESULT 45
US-09-975-553-17
; Sequence 17, Application US/09975553
; Patent No. US20020152968A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; FILE REFERENCE: 2213.1004-001
; CURRENT APPLICATION NUMBER: US/09/975,553
; CURRENT FILING DATE: 2001-10-11
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,477
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,476
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-975-553-17

Query Match          86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAG 20
Db 2256 CATCGCCCAAGGAGATCGAG 2274

RESULT 46
US-10-125-792-1
; Sequence 1, Application US/10125792
; Publication No. US20030051269A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
```

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; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-007
; CURRENT APPLICATION NUMBER: US/10/125,792
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-792-1

Query Match          86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAG 20
Db 2256 CATCGCCCAAGGAGATCGAG 2274

RESULT 47
US-10-125-778-1
; Sequence 1, Application US/10125778
; Publication No. US20030082574A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005
; CURRENT APPLICATION NUMBER: US/10/125,778
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-778-1

Query Match          86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAG 20
Db 2256 CATCGCCCAAGGAGATCGAG 2274

RESULT 48
US-10-270-795-17
; Sequence 17, Application US/10270795
; Publication No. US20030084855A1
; GENERAL INFORMATION:
```

```
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/10/270,795
; CURRENT FILING DATE: 2002-10-11
; PRIOR FILING DATE: US/09/687,372
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match      86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 49
US-10-270-876-17
; Sequence 17, Application US/10270876
; Publication No. US20030116096A1
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17

Query Match      86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 50
US-10-268-051-7
; Sequence 7, Application US/10268051
; Publication No. US20030124090A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Species and Methods of Use Thereof

; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-268-051-7

Query Match      86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 51
US-10-125-772-1
; Sequence 1, Application US/10125772
; Publication No. US20030124657A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-006
; CURRENT APPLICATION NUMBER: US/10/125,772
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-772-1

Query Match      86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 52
US-10-016-496-1
; Sequence 1, Application US/10016496
; Publication No. US20030166908A1
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
```

; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/10/016,496
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalas acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439)...(3522)
US-10-016-496-1

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
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DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 53
US-10-411-076-23
; Sequence 23, Application US/10411076
; Publication No. US20030226516A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Growing Marine Fish in Freshwater
; FILE REFERENCE: 2213.1003007
; CURRENT APPLICATION NUMBER: US/10/411,076
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US01/31625
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,373
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Mustelus canis
US-10-411-076-23

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 54
US-10-410-872-17
; Sequence 17, Application US/10410872
; Publication No. US20030230247A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous

; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-001
; CURRENT APPLICATION NUMBER: US/10/410,872
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/975,553
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,477
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,476
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-410-872-17

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 55
US-10-410-885-1
; Sequence 1, Application US/10410885
; Publication No. US20030232366A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Betka, Marlies
; APPLICANT: Nearing, Jacqueline A.
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-008
; CURRENT APPLICATION NUMBER: US/10/410,885
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/125,778
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,772
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,792
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-410-885-1

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 56


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RESULT 60
US-11-086-550-1
; Sequence 1, Application US/11086550
; Publication No. US20050181426A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005
; CURRENT APPLICATION NUMBER: US/11/086,550
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: US/10/125,778
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-11-086-550-1

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Query Match      86.4%; Score 19; DB 10; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 CATCGCCAGGAGATCGAG 20
Db      2256 CATCGCCAGGAGATCGAG 2274

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Job time : 64.2198 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccacgcgaaggatcgagct 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : Published Applications NA New.*

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- 2: /SID85/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SID85/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SID85/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SID85/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 8: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq.1*
- 9: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq.2*
- 10: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq.3*
- 11: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq.2*
- 13: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq.3*
- 14: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq.4*
- 15: /SID85/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	45	14	US-11-099-683-70
2	17.8	80.9	997	10	US-10-301-480-592106
3	17.8	80.9	997	10	US-10-301-480-1205515
4	17.8	80.9	1481	6	US-09-925-065A-673455
5	17.4	79.1	2430	14	US-11-024-959-133
6	17.2	78.2	25	9	US-10-932-182A-33211
7	17.2	78.2	25	9	US-10-932-182A-33211
8	17.2	78.2	486	9	US-10-932-182A-2466
9	17.2	78.2	486	9	US-10-932-182A-2466
10	17.2	78.2	2035	11	US-11-077-619-107
11	16.8	76.4	626	6	US-09-925-065A-913133
12	16.8	76.4	634	6	US-09-925-065A-909976
13	16.8	76.4	634	6	US-09-925-065A-911013
14	16.4	74.5	256	8	US-10-802-796-212
15	16.4	74.5	256	11	US-11-221-284-212
16	16.4	74.5	315	8	US-10-802-796-407
17	16.4	74.5	315	11	US-11-221-284-407
18	16.4	74.5	978	10	US-10-301-480-553257

19	16.4	74.5	978	10	US-10-301-480-1166666	Sequence 1166666,
20	16.4	74.5	6510	8	US-10-775-169-320	Sequence 320, App
21	16.2	73.6	25	14	US-11-136-527-262340	Sequence 262340,
22	16.2	73.6	415	9	US-10-504-389A-46	Sequence 46, Appl
23	16.2	73.6	478	6	US-09-925-065A-564483	Sequence 564483,
24	16.2	73.6	512	6	US-09-925-065A-804140	Sequence 804140,
25	16.2	73.6	512	6	US-09-925-065A-857058	Sequence 857058,
26	16.2	73.6	516	10	US-10-301-480-267847	Sequence 267847,
27	16.2	73.6	516	10	US-10-301-480-881256	Sequence 881256,
28	16.2	73.6	523	6	US-09-925-065A-176640	Sequence 176640,
29	16.2	73.6	544	11	US-11-096-568A-13286	Sequence 13286, A
30	16.2	73.6	557	6	US-09-925-065A-423193	Sequence 423193,
31	16.2	73.6	562	10	US-10-301-480-487545	Sequence 487545,
32	16.2	73.6	562	10	US-10-301-480-1100954	Sequence 1100954,
33	16.2	73.6	592	6	US-09-925-065A-497702	Sequence 497702,
34	16.2	73.6	606	6	US-09-925-065A-28876	Sequence 28876, A
35	16.2	73.6	606	9	US-10-301-480-130114	Sequence 130114,
36	16.2	73.6	606	10	US-10-301-480-130123	Sequence 130123,
37	16.2	73.6	607	6	US-09-925-065A-443435	Sequence 443435,
38	16.2	73.6	611	6	US-09-925-065A-193825	Sequence 193825,
39	16.2	73.6	617	10	US-10-301-480-896622	Sequence 896622,
40	16.2	73.6	617	10	US-10-301-480-896622	Sequence 896622,
41	16.2	73.6	627	9	US-10-301-480-71948	Sequence 71948, A
42	16.2	73.6	627	10	US-10-301-480-885357	Sequence 885357,
43	16.2	73.6	629	10	US-10-301-480-264567	Sequence 264567,
44	16.2	73.6	629	10	US-10-301-480-877976	Sequence 877976,
45	16.2	73.6	631	10	US-10-301-480-503870	Sequence 503870,
46	16.2	73.6	631	10	US-10-301-480-1117279	Sequence 1117279,
47	16.2	73.6	633	6	US-09-925-065A-172956	Sequence 172956,
48	16.2	73.6	633	6	US-09-925-065A-339781	Sequence 339781,
49	16.2	73.6	633	10	US-10-301-480-412794	Sequence 412794,
50	16.2	73.6	633	10	US-10-301-480-1026203	Sequence 1026203,
51	16.2	73.6	674	6	US-09-925-065A-942839	Sequence 942839,
52	16.2	73.6	674	6	US-09-925-065A-942840	Sequence 942840,
53	16.2	73.6	730	14	US-11-136-527-1439	Sequence 1439, Ap
54	16.2	73.6	730	14	US-11-136-527-5535	Sequence 5535, Ap
55	16.2	73.6	734	10	US-10-301-480-599819	Sequence 599819,
56	16.2	73.6	734	10	US-10-301-480-1213228	Sequence 1213228,
57	16.2	73.6	846	11	US-11-096-568A-8351	Sequence 8351, Ap
58	16.2	73.6	982	10	US-10-301-480-590859	Sequence 590859,
59	16.2	73.6	982	10	US-10-301-480-1204268	Sequence 1204268,
60	16.2	73.6	1989	14	US-11-183-136-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-11-099-683-70
; Sequence 70, Application US/11099683
; Publication No. US20060019916A1
; GENERAL INFORMATION:
; APPLICANT: Krueger, Arthur
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
; FILE REFERENCE: C1037.70047US01
; CURRENT APPLICATION NUMBER: US/11/099.683
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/558,951
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-099-683-70

Query Match 100.0%; Score 22; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 673455
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-673455

Query Match      80.9%; Score 17.8; DB 6; Length 1481;
Best Local Similarity 90.5%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 2; Indels 0;

QY      2 CATCGCCCAAGGAGATCGAGCT 22
Db      683 CATGCGCAAGGAGATCGAGTT 703

RESULT 5
US-11-024-959-133
; Sequence 133, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 04463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 133
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Pinus radiata
US-11-024-959-133

Query Match      79.1%; Score 17.4; DB 14; Length 2430;
Best Local Similarity 94.7%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 1; Indels 0;

QY      2 CATCGCCCAAGGAGATCGAG 20
Db      339 CATGCGCAAGGAGATCGAG 357

RESULT 6
US-10-932-182A-33211/c

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; Sequence 33211, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-33211

Query Match      78.2%; Score 17.2; DB 9; Length 25;
Best Local Similarity 86.4%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 22 CCATGCCCATCGAGATCGAACT 1

RESULT 7
US-10-932-182A-33211/c
; Sequence 33211, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-33211

Query Match      78.2%; Score 17.2; DB 9; Length 25;
Best Local Similarity 86.4%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 22 CCATGCCCATCGAGATCGAACT 1

RESULT 8
US-10-932-182A-2466/c
; Sequence 2466, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
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; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2466
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2466

Query Match      78.2%; Score 17.2; DB 9; Length 486;
Best Local Similarity 86.4%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 440 CCATGCCCATCGAGATCGAACT 419

RESULT 9
US-10-932-182A-2466/c
; Sequence 2466, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2466
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2466

Query Match      78.2%; Score 17.2; DB 9; Length 486;
Best Local Similarity 86.4%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 440 CCATGCCCATCGAGATCGAACT 419

RESULT 10
US-11-077-619-107
; Sequence 107, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107
; LENGTH: 2035
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; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2035)
; OTHER INFORMATION: groEL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1835)
US-11-077-619-107

Query Match 78.2%; Score 17.2; DB 11; Length 2035;
Best Local Similarity 86.4%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
||||| ||||| ||||| ||||| |||||
Db 361 CCATCGCGAAAGAAATCGAGCT 382

RESULT 11

US-09-925-065A-913133
; Sequence 913133, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 913133
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-913133

Query Match 76.4%; Score 16.8; DB 6; Length 626;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCGCCCAAGGAGATCGAGCT 22
||||| ||||| ||||| ||||| |||||
Db 581 ATCGCCCAAGGAGATCGAGCT 600

RESULT 12

US-09-925-065A-909976/c
; Sequence 909976, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 909976
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-909976

Query Match 76.4%; Score 16.8; DB 6; Length 634;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCGCCCAAGGAGATCGAGCT 22
||||| ||||| ||||| ||||| |||||
Db 55 ATCGCCCAAGGAGATCGAGCT 36

RESULT 13

US-09-925-065A-911013
; Sequence 911013, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 911013
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-911013

Query Match 76.4%; Score 16.8; DB 6; Length 634;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCGCCCAAGGAGATCGAGCT 22
||||| ||||| ||||| ||||| |||||
Db 581 ATCGCCCAAGGAGATCGAGCT 600

RESULT 14

US-10-802-796-212/c
; Sequence 212, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESEN-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF

```
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 212
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-212

Query Match          74.5%; Score 16.4; DB 8; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGCTCGA 19
        |||||
Db      67 CATGCCCAAGGAGCTCGA 50

RESULT 15
US-11-221-284-212/c
; Sequence 212, Application US/11221284
; Publication No. US20060063182A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/11/221,284
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: US/09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-11-221-284-212

Query Match          74.5%; Score 16.4; DB 11; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGCTCGA 19
        |||||
Db      67 CATGCCCAAGGAGCTCGA 50

RESULT 16
US-10-802-796-407/c
; Sequence 407, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
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; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 407
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-407

Query Match          74.5%; Score 16.4; DB 8; Length 315;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGCTCGA 19
        |||||
Db      64 CATGCCCAAGGAGCTCGA 47

RESULT 17
US-11-221-284-407/c
; Sequence 407, Application US/11221284
; Publication No. US20060063182A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/11/221,284
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: US/09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 407
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-11-221-284-407

Query Match          74.5%; Score 16.4; DB 11; Length 315;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGCTCGA 19
        |||||
Db      64 CATGCCCAAGGAGCTCGA 47

RESULT 18
US-10-301-480-553257
; Sequence 553257, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
```

; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553257
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-553257

Query Match 74.5%; Score 16.4; DB 10; Length 978;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCG 18
||||| |||||||
Db 51 CCATCGCCAAGGAGATCG 68

RESULT 19

US-10-301-480-1166666
; Sequence 1166666, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166666
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166666

Query Match 74.5%; Score 16.4; DB 10; Length 978;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCG 18
||||| |||||||
Db 51 CCATCGCCAAGGAGATCG 68

RESULT 20

US-10-775-169-320
; Sequence 320, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 320
; LENGTH: 6510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-320

Query Match 74.5%; Score 16.4; DB 8; Length 6510;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCG 18
||||| |||||||
Db 2141 CCATCGCCAAGGAGATCG 2158

RESULT 21

US-11-136-527-262340
; Sequence 262340, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 262340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-262340

Query Match 73.8%; Score 16.2; DB 14; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCAAGGAGATCGAGCT 22
||||| |||||||
Db 5 CAACGCCCTGGAGATCGAGCT 25

RESULT 22

US-10-504-389A-46
; Sequence 46, Application US/10504389A
; Publication No. US20060045876A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: LUD 5821
; CURRENT APPLICATION NUMBER: US/10/504,389A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/04243
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 46
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: nucleotide sequence for murine light chain variable region
US-10-504-389A-46

Query Match 73.6%; Score 16.2; DB 9; Length 415;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCAAGGAGATCGAGCT 22
||||| |||||||
Db 71 CAGCGCCATGGACATCGAGCT 91

RESULT 23
US-09-925-065A-564483
; Sequence 564483, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564483
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-564483

Query Match 73.6%; Score 16.2; DB 6; Length 478;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
DB 10 CATCCCAAGGAGATCGTCT 30

RESULT 24
US-09-925-065A-804140
; Sequence 804140, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 804140
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-804140

Query Match 73.6%; Score 16.2; DB 6; Length 512;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22

DB 38 CATCCCAAGGAGATCGTCT 58
RESULT 25
US-09-925-065A-857058
; Sequence 857058, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 857058
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-857058

Query Match 73.6%; Score 16.2; DB 6; Length 512;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
DB 38 CATCCCAAGGAGATCGTCT 58

RESULT 26
US-10-301-480-267847
; Sequence 267847, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267847
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-267847

Query Match 73.6%; Score 16.2; DB 10; Length 516;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
DB 4 CATCCCAAGGAGATCGTCT 24

RESULT 27
US-10-301-480-881256
; Sequence 881256, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 881256
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-881256

Query Match 73.6%; Score 16.2; DB 10; Length 516;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 4 CATCACCAAGGAGATGGTGCT 24
|||||

RESULT 28
US-09-925-065A-176640/c
; Sequence 176640, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176640
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-176640

Query Match 73.6%; Score 16.2; DB 6; Length 523;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 520 CATCACCAAGGAGATGGTGCT 500
|||||

RESULT 29
US-11-096-568A-13286

; Sequence 13286, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13286
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(544)
; OTHER INFORMATION: Ceres Seq. ID no. 15174132
US-11-096-568A-13286

Query Match 73.6%; Score 16.2; DB 11; Length 544;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 154 CGTCGTCACCAAGGAGATCGAGAT 174
|||||

RESULT 30
US-09-925-065A-423193/c
; Sequence 423193, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 423193
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-423193

Query Match 73.6%; Score 16.2; DB 6; Length 557;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 296 CATCACCAAGGAGATGGTGCT 276
|||||

RESULT 31
US-10-301-480-487545/c
; Sequence 487545, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487545
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-487545

Query Match          73.6%; Score 16.2; DB 10; Length 562;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      296 CATCACCACGAGATGCTGCT 276

RESULT 32
US-10-301-480-1100954/c
; Sequence 1100954, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1100954
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1100954

Query Match          73.6%; Score 16.2; DB 10; Length 562;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      296 CATCACCACGAGATGCTGCT 276

RESULT 33
US-09-925-065A-497702
; Sequence 497702, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497702
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-497702

Query Match          73.6%; Score 16.2; DB 6; Length 592;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCGCCAAGGAGATCGAGC 21
      ||||| ||||| ||||| |||||
Db      111 CCATCTCCAAAGAGGTGCGAGC 131

RESULT 34
US-09-925-065A-28876
; Sequence 28876, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28876
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-28876

Query Match          73.6%; Score 16.2; DB 6; Length 606;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      332 CATCACCACGAGATGCTGCT 352

RESULT 35
US-10-301-480-130114
; Sequence 130114, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
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; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130114
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-130114

Query Match      73.6%; Score 16.2; DB 9; Length 606;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      332 CATCACCACGAGATCGTGCT 352

RESULT 36
US-10-301-480-743523
; Sequence 743523, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743523
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-743523

Query Match      73.6%; Score 16.2; DB 10; Length 606;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      332 CATCACCACGAGATCGTGCT 352

RESULT 37
US-09-925-065A-443435
; Sequence 443435, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
```

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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 443435
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-443435

Query Match      73.6%; Score 16.2; DB 6; Length 607;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      119 CATCACCACGAGATCGTGCT 139

RESULT 38
US-09-925-065A-193825/c
; Sequence 193825, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193825
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-193825

Query Match      73.6%; Score 16.2; DB 6; Length 611;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      387 CATCACCACGAGATCGAGCT 367

RESULT 39
US-10-301-480-283213/c
; Sequence 283213, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283213
```

```
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-283213

Query Match      73.6%; Score 16.2; DB 10; Length 617;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 387 CATCACCAGGAGATCGAGCT 367

RESULT 40
US-10-301-480-896622/c
; Sequence 896622, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896622
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-896622

Query Match      73.6%; Score 16.2; DB 10; Length 617;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 387 CATCACCAGGAGATCGAGCT 367

RESULT 41
US-10-301-480-71948
; Sequence 71948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71948
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-71948

Query Match      73.6%; Score 16.2; DB 9; Length 627;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 387 CATCACCAGGAGATCGAGCT 367

RESULT 42
US-10-301-480-685357
; Sequence 685357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685357
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-685357

Query Match      73.6%; Score 16.2; DB 10; Length 627;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 347 CATCACCAGGAGATCGGTGCT 367

RESULT 43
US-10-301-480-264567
; Sequence 264567, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264567
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-264567

Query Match      73.6%; Score 16.2; DB 10; Length 629;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 492 CATCACCAGGAGATCGGTGCT 512

RESULT 44
US-10-301-480-877976
; Sequence 877976, Application US/10301480
; Publication No. US20060057564A1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 877976
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-877976

Query Match      73.6%; Score 16.2; DB 10; Length 629;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      492 CATCACCAGGAGATGGTGCT 512

RESULT 45
US-10-301-480-503870/c
; Sequence 503870, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 503870
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-503870

Query Match      73.6%; Score 16.2; DB 10; Length 631;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      513 CATCACCAGGAGATGGTGCT 493

RESULT 46
US-10-301-480-1117279/c
; Sequence 1117279, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
```

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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 172956
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-172956

Query Match      73.6%; Score 16.2; DB 6; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      496 CATCACCAGGAGATGGTGCT 516

RESULT 47
US-09-925-065A-172956
; Sequence 172956, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 172956
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-172956

Query Match      73.6%; Score 16.2; DB 10; Length 631;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      513 CATCACCAGGAGATGGTGCT 493

RESULT 48
US-09-925-065A-339781/c
; Sequence 339781, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
```

```
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339781
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-339781

Query Match      73.6%; Score 16.2; DB 6; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      273 CATCACCAAGGAGATGCTGCT 253

RESULT 49
US-10-301-480-412794
; Sequence 412794, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412794
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-412794

Query Match      73.6%; Score 16.2; DB 10; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      361 CATCACCAAGGAGATGCTGCT 381

RESULT 50
US-10-301-480-1026203
; Sequence 1026203, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1026203
; LENGTH: 633
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-1026203

Query Match      73.6%; Score 16.2; DB 10; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      361 CATCACCAAGGAGATGCTGCT 381

RESULT 51
US-09-925-065A-942839
; Sequence 942839, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942839
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-942839

Query Match      73.6%; Score 16.2; DB 6; Length 674;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      368 CATCACCAAGGAGATGCTGCT 388

RESULT 52
US-09-925-065A-942840
; Sequence 942840, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 942840
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-942840

Query Match      73.6%; Score 16.2; DB 6; Length 674;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 368 CATCACCAAGGAGATAGTGCT 388

RESULT 53
US-11-136-527-1439/c
; Sequence 1439, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1439
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-1439

Query Match      73.6%; Score 16.2; DB 14; Length 730;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 704 CAACGCCCTGGAGATCGAGCT 684

RESULT 54
US-11-136-527-5535
; Sequence 5535, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5535
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-5535

Query Match      73.6%; Score 16.2; DB 14; Length 730;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
```

```
Db 27 CAACGCCCTGGAGATCGAGCT 47

RESULT 55
US-10-301-480-599819/c
; Sequence 599819, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 599819
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-599819

Query Match      73.6%; Score 16.2; DB 10; Length 734;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 123 CATCACCAAGGAGATAGTGCT 103

RESULT 56
US-10-301-480-1213228/c
; Sequence 1213228, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1213228
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-1213228

Query Match      73.6%; Score 16.2; DB 10; Length 734;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 123 CATCACCAAGGAGATAGTGCT 103

RESULT 57
US-11-096-568A-8351
; Sequence 8351, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
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; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8351
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(846)
; OTHER INFORMATION: Ceres Seq. ID no. 15225168
US-11-096-568A-8351

Query Match 73.6%; Score 16.2; DB 11; Length 846;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
Db 436 CATCGCCCAAGGAGAAACGAGCT 456

RESULT 58
US-10-301-480-590859
; Sequence 590859, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590859
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-590859

Query Match 73.6%; Score 16.2; DB 10; Length 982;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
Db 960 CATCACCACCAAGGAGATGGTGCT 980

RESULT 59
US-10-301-480-1204268
; Sequence 1204268, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1204268
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1204268

Query Match 73.6%; Score 16.2; DB 10; Length 982;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
Db 960 CATCACCACCAAGGAGATGGTGCT 980

RESULT 60
US-11-183-136-3
; Sequence 3, Application US/11183136
; Publication No. US20060019896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Dean
; APPLICANT: Park, Kye Won
; TITLE OF INVENTION: NETRIN-RELATED COMPOSITIONS AND USES
; FILE REFERENCE: UUTH-P01-011
; CURRENT APPLICATION NUMBER: US/11/183,136
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: US 60/587,796
; PRIOR FILING DATE: 2004-07-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-183-136-3

Query Match 73.6%; Score 16.2; DB 14; Length 1989;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21
Db 684 CCATCACCACCAAGCAGAACGAGC 704

Search completed: April 1, 2006, 22:39:03
Job time : 57.3836 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:04:52 ; Search time 154.853 Seconds
(without alignments)
8075.738 Million cell updates/sec

Title: US-10-824-527-2
Perfect score: 21.6
Sequence: 1 tgaagtgccggatctgtt 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
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8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_av.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21.6	100.0	337	6	AR079996 Sequence
C 2	21.6	100.0	337	6	AR085922 Sequence
C 3	21.6	100.0	337	6	AR093308 Sequence
C 4	21.6	100.0	337	6	AR121888 Sequence
C 5	21.6	100.0	337	6	BD218097 Sequence
C 6	21.6	100.0	337	6	BD218097 Compositi
C 7	21.6	100.0	337	6	AR213734 Sequence
C 8	21.6	100.0	337	6	AR365966 Sequence
C 9	21.6	100.0	552	1	AF429652 Lactobaci
C 10	21.6	100.0	552	1	AY691245 Coryneb
C 11	21.6	100.0	552	1	AY691305 Streptomy
C 12	21.6	100.0	560	1	AY339132 Bifidobac
C 13	21.6	100.0	567	1	AY691243 Coryneb
C 14	21.6	100.0	590	1	AF240574 Bifidobac
C 15	21.6	100.0	590	1	AY004278 Bifidobac
C 16	21.6	100.0	590	1	AY004280 Bifidobac
C 17	21.6	100.0	590	1	AY166560 Bifidobac
C 18	21.6	100.0	590	1	AY166562 Bifidobac

C 19	21.6	100.0	591	1	AF240567
C 20	21.6	100.0	797	6	E10965
C 21	21.6	100.0	852	6	E11716
C 22	21.6	100.0	927	6	AR080019
C 23	21.6	100.0	927	6	AR085945
C 24	21.6	100.0	927	6	AR121711
C 25	21.6	100.0	927	6	BD218120
C 26	21.6	100.0	927	6	AR213757
C 27	21.6	100.0	927	6	AR365989
C 28	21.6	100.0	927	6	BD008542
C 29	21.6	100.0	985	6	AR080046
C 30	21.6	100.0	985	6	AR085972
C 31	21.6	100.0	985	6	AR121738
C 32	21.6	100.0	985	6	BD218147
C 33	21.6	100.0	985	6	AR213784
C 34	21.6	100.0	985	6	AR366016
C 35	21.6	100.0	1569	6	AR080017
C 36	21.6	100.0	1569	6	AR085943
C 37	21.6	100.0	1569	6	AR121709
C 38	21.6	100.0	1569	6	BD218118
C 39	21.6	100.0	1569	6	AR213755
C 40	21.6	100.0	1569	6	AR365987
C 41	21.6	100.0	1569	6	BD008540
C 42	21.6	100.0	1589	6	E11719
C 43	21.6	100.0	1620	1	TTU90204
C 44	21.6	100.0	1623	1	AF352578
C 45	21.6	100.0	1623	6	A46454
C 46	21.6	100.0	1623	6	CQ816174
C 47	21.6	100.0	1623	6	AR266836
C 48	21.6	100.0	1623	6	AR655543
C 49	21.6	100.0	1623	6	AX073911
C 50	21.6	100.0	1624	1	AF281650
C 51	21.6	100.0	1626	1	AF352577
C 52	21.6	100.0	1626	6	AR080045
C 53	21.6	100.0	1626	6	AR085971
C 54	21.6	100.0	1626	6	AR121737
C 55	21.6	100.0	1626	6	BD218146
C 56	21.6	100.0	1626	6	AR213783
C 57	21.6	100.0	1626	6	AR366015
C 58	21.6	100.0	1644	6	BD165187
C 59	21.6	100.0	1644	6	AX123070
C 60	21.6	100.0	1647	6	E10966

ALIGNMENTS

RESULT 1	AR079996/c	AR079996	Sequence 77 from patent US 5968524.	337 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR079996	Sequence 77 from patent US 5968524.					
DEFINITION	AR079996	Sequence 77 from patent US 5968524.					
ACCESSION	AR079996	Sequence 77 from patent US 5968524.					
VERSION	AR079996.1	GI:10006731					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 337)						
AUTHORS	Watson,J.D. and Tan,P.L.J.						
TITLE	Methods and compounds for the treatment of immunologically-mediated psoriasis						
JOURNAL	Patent: US 5968524-A 77 19-OCT-1999;						
FEATURES	Location/Qualifiers						
source	1..337						
ORIGIN	/organism="unknown"						
	/mol_type="unassigned DNA"						

Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGAAGTGCCRCGGATCTTGT 22

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Db      166 TGAAGTGCCCGGATCTTGT 145
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RESULT 2
AR085922/c
LOCUS      AR085922      337 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 77 from patent US 5985287.
ACCESSION  AR085922
VERSION     AR085922.1 GI:10012688
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Tan, P., Skinner, M. and Prestidge, R.
TITLE      Compounds and methods for treatment and diagnosis of mycobacterial
           infections
JOURNAL    Patent: US 5985287-A 77 16-NOV-1999;
FEATURES    Location/Qualifiers
             source
             1..337
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db      166 TGAAGTGCCCGGATCTTGT 145
|||||:|||||:|||||:|||||
RESULT 3
AR093308/c
LOCUS      AR093308      337 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 77 from patent US 6001361.
ACCESSION  AR093308
VERSION     AR093308.1 GI:10020058
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Tan, P., Hiyama, J., Visser, E., Skinner, M., Scott, L. and Prestidge, R.
TITLE      Mycobacterium vaccae antigens
JOURNAL    Patent: US 6001361-A 77 14-DEC-1999;
FEATURES    Location/Qualifiers
             source
             1..337
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db      166 TGAAGTGCCCGGATCTTGT 145
|||||:|||||:|||||:|||||
RESULT 4
AR121688/c
LOCUS      AR121688      337 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 77 from patent US 6160093.
ACCESSION  AR121688
VERSION     AR121688.1 GI:14105264
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Tan, P., Visser, E., Skinner, M.A. and Prestid, R.L.
TITLE      Compositions derived from mycobacterium vaccae and methods for
           their use.
JOURNAL    Patent: JP 2002514385-A 22 21-MAY-2002;
           GENESIS RESEARCH AND DEVELOPMENT CORP LTD
           OS Mycobacterium vaccae
           PN JP 2002514385-A/22
           PD 21-MAY-2002
           PF 23-DEC-1998 JP 2000525553
           PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
           23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
           17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
           TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
           PI L PRESTIDGE
           PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
           A61P17/00,
           PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
           C07K19/00,
           PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
           G01N33/68//
           PC C12N15/09, C12R1/32, C12N15/00, C12N5/00, (C12N15/00, C12R1/32)
           CC Compositions derived from mycobacterium
           vaccae and methods for
           their use
           FH Key Location/Qualifiers
           FT source 1..337
           /organism="Mycobacterium vaccae".
           FT Location/Qualifiers
           1..337
           /organism="Mycobacterium vaccae"
           /mol_type="genomic DNA"
           /db_xref="taxon:1810"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
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Db 166 TGAAGTGCCGCGGATCTTGTT 145

RESULT 6
LOCUS AR213734/c 337 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 77 from patent US 6406704.
ACCESSION AR213734
VERSION AR213734.1 GI:23311021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 337)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 77 18-JUN-2002;
Genensis Research and Development Corporation Limited;;
NZX;

FEATURES
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Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGTT 22
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Db 166 TGAAGTGCCGCGGATCTTGTT 145

RESULT 7
LOCUS AR365966/c 337 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 77 from patent US 6328978.
ACCESSION AR365966
VERSION AR365966.1 GI:34598219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 337)
AUTHORS Watson, J.D., Tan, P.L.J. and Prestidge, R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 77 11-DEC-2001;
Genensis Research & Development Corp. Ltd.; Parnell;
NZX;

FEATURES
source Location/Qualifiers
1..337
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Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGTT 22
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Db 166 TGAAGTGCCGCGGATCTTGTT 145

RESULT 8
LOCUS BD008519/c 337 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial infections.
ACCESSION BD008519

BD008519.1 GI:18636892
JP 2001503969-A/22.
unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 337)
AUTHORS Tan, P., Hiyaama, J., Visser, E.S., Skinner, M.A., Scott, L.M. and Prestidge, R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial infections
JOURNAL Patent: JP 2001503969-A 22 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
OS Unidentified
COMMENT PN JP 2001503969-A/22
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04, A61K35/74, C07K14/35, C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..337
/organism="Unidentified".

FEATURES
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1..337
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ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGTT 22
|||||:|||||
Db 166 TGAAGTGCCGCGGATCTTGTT 145

RESULT 9
LOCUS AF429652/c 552 bp DNA linear BCT 23-NOV-2004
DEFINITION Lactobacillus rhamnosus strain ATCC 21052 60 kDa heat shock protein (HSP60) gene, partial cds.
ACCESSION AF429652
VERSION AF429652.1 GI:33312999
KEYWORDS
SOURCE Lactobacillus rhamnosus
ORGANISM Lactobacillus rhamnosus
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
REFERENCE 1 (bases 1 to 552)
AUTHORS Dobson, C.M., Chaban, B., Deneer, H. and Ziola, B.
TITLE Lactobacillus casei, Lactobacillus rhamnosus, and Lactobacillus zeae isolates identified by sequence signature and immunoblot phenotype
JOURNAL Can. J. Microbiol. 50 (7), 482-488 (2004)
PUBMED 15381972
REFERENCE 2 (bases 1 to 552)
AUTHORS Dobson, M.C., Deneer, H., Lee, S., Hemmingsen, S., Hill, J. and Ziola, B.R.
TITLE Redefining speciation of Lactobacillus and Pediococcus based on phylogenetic analysis of the partial 16S rRNA gene, 16S-23S rRNA region and 60 kDa heat shock protein sequences
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 552)
AUTHORS Dobson, M.C. and Ziola, B.R.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) Microbiology and Immunology, University of Saskatchewan, 107 Wiggins Road, Saskatoon, Saskatchewan S7N 5E5,

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ORIGIN
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    Best Local Similarity 95.5%; Pred. No. 7.5;
    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

    QY      1 TGAAGGTGCCCGGATCTTGT 22
            |||||:|||||
    Db      538 TGAAGGTGCCCGGATCTTGT 517

RESULT 10
AY691245/c
LOCUS      552 bp      DNA      linear      BCT 17-AUG-2004
DEFINITION      Corynebacterium amycolatum 60 kDa chaperonin (cpn60) gene, partial
ACCESSION      AY691245
VERSION      AY691245.1 GI:51103778
KEYWORDS
SOURCE      Corynebacterium amycolatum
ORGANISM      Corynebacterium amycolatum
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
    AUTHORS      Hill,J.E., Penny,S.L., Crowell,K.G., Goh,S.H. and Hemmingsen,S.M.
    TITLE      cpnDB: a chaperonin sequence database
    JOURNAL      Genome Res. 14 (8), 1669-1675 (2004)
    PUBMED      15289485
REFERENCE
    2 (bases 1 to 552)
    AUTHORS      Hill,J.E., Van Kessel,A.G., Dumonceaux,T.J. and Hemmingsen,S.M.
    LOCUS      cpnDB - a chaperonin sequence database
    DEFINITION      Direct Submission
    TITLE      Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110
    JOURNAL      Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada
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    Best Local Similarity 95.5%; Pred. No. 7.5;
    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

    QY      1 TGAAGGTGCCCGGATCTTGT 22
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    Db      538 TGAAGGTGCCCGGATCTTGT 517

FEATURES
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ORIGIN
    Query Match      100.0%; Score 21.6; DB 1; Length 552;
    Best Local Similarity 95.5%; Pred. No. 7.5;
    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

    QY      1 TGAAGGTGCCCGGATCTTGT 22
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    Db      538 TGAAGGTGCCCGGATCTTGT 517

FEATURES
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            DVEGEALSTLVVNKIRGTFFKSVAV"
ORIGIN
    Query Match      100.0%; Score 21.6; DB 1; Length 552;
    Best Local Similarity 95.5%; Pred. No. 7.5;
    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

    QY      1 TGAAGGTGCCCGGATCTTGT 22
            |||||:|||||
    Db      538 TGAAGGTGCCCGGATCTTGT 517

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ORIGIN
    Query Match      100.0%; Score 21.6; DB 1; Length 552;
    Best Local Similarity 95.5%; Pred. No. 7.5;
    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

    QY      1 TGAAGGTGCCCGGATCTTGT 22
            |||||:|||||
    Db      538 TGAAGGTGCCCGGATCTTGT 517

RESULT 11
AY691305/c
LOCUS      552 bp      DNA      linear      BCT 17-AUG-2004
DEFINITION      Streptomyces thermoviolaceus subsp. thermoviolaceus
                chaperonin (cpn60) gene, partial cds.
ACCESSION      AY691305
VERSION      AY691305.1 GI:51103898
KEYWORDS
SOURCE      Streptomyces thermoviolaceus subsp. thermoviolaceus
ORGANISM      Streptomyces thermoviolaceus subsp. thermoviolaceus
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Streptomyceinae; Streptomycetaceae; Streptomyces.
REFERENCE
    1 (bases 1 to 552)
    AUTHORS      Hill,J.E., Penny,S.L., Crowell,K.G., Goh,S.H. and Hemmingsen,S.M.
    TITLE      cpnDB: a chaperonin sequence database
    JOURNAL      Genome Res. 14 (8), 1669-1675 (2004)
    PUBMED      15289485
REFERENCE
    2 (bases 1 to 552)
    AUTHORS      Hill,J.E., Van Kessel,A.G., Dumonceaux,T.J. and Hemmingsen,S.M.
    LOCUS      cpnDB - a chaperonin sequence database
    DEFINITION      Direct Submission
    TITLE      Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110
    JOURNAL      Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada
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        Location/Qualifiers
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    Query Match      100.0%; Score 21.6; DB 1; Length 552;
    Best Local Similarity 95.5%; Pred. No. 7.5;
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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||
Db 556 TGAAGGTGCGCGGATCTTGT 535

RESULT 16
AY004280/c
LOCUS
DEFINITION Bifidobacterium bifidum heat shock protein 60 (hsp60) gene, partial
cds.
ACCESSION AY004280
VERSION AY004280.1 GI:11999206
KEYWORDS
SOURCE
ORGANISM Bifidobacterium bifidum
Bifidobacterium bifidum
Bacteria: Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
AUTHORS Jian,W., Zhu,L. and Dong,X.
TITLE New approach to phylogenetic analysis of the genus Bifidobacterium
based on partial Hsp60 gene sequences
JOURNAL Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1633-1638 (2001)
PUBMED 11594590
REFERENCE
AUTHORS Jian,W., Zhu,L. and Dong,X.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2000) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
3 (bases 1 to 590)
Jian,W., Zhu,L. and Dong,X.
Direct Submission
Submitted (16-MAR-2001) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
Sequence update by submitter
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
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QY 1 TGAAGGTGCGCGGATCTTGT 22

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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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Db 557 TGAAGGTGCGCGGATCTTGT 536

RESULT 15
AY004278/c
LOCUS
DEFINITION Bifidobacterium pullorum heat shock protein 60 (hsp60) gene,
partial cds.
ACCESSION AY004278
VERSION AY004278.1 GI:11999202
KEYWORDS
SOURCE
ORGANISM Bifidobacterium pullorum
Bifidobacterium pullorum
Bacteria: Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
AUTHORS Jian,W., Zhu,L. and Dong,X.
TITLE New approach to phylogenetic analysis of the genus Bifidobacterium
based on partial Hsp60 gene sequences
JOURNAL Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1633-1638 (2001)
PUBMED 11594590
REFERENCE
AUTHORS Jian,W., Zhu,L. and Dong,X.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2000) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
3 (bases 1 to 590)
Jian,W., Zhu,L. and Dong,X.
Direct Submission
Submitted (16-MAR-2001) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
Sequence update by submitter
Location/Qualifiers
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ORIGIN
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Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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556 TGAAGTGCGCGGATCTTGT 535

Db

RESULT 17

AY166560/c

LOCUS

DEFINITION

shock protein 60 (hsp60) gene, partial cds.

ACCESSION

AY166560

VERSION

AY166560.1 GI:24850358

KEYWORDS

Source

ORGANISM

Bifidobacterium thermacidophilum subsp. porcinum

REFERENCE

AY166560

1 (bases 1 to 590)

AUTHORS

Species Identification of Genus Bifidobacterium Based on Partial

TITLE

Hsp60 Gene Sequences and Proposal of Bifidobacterium thermacidophilum subsp. suis subsp. nov.

JOURNAL

Submitted (18-OCT-2002) State Key Laboratory of Microbial

Resources, Institute of Microbiology, Chinese Academy of Sciences,

No. 13 North 1st Street, Zhongguancun, Beijing 100080, P. R. China

Location/Qualifiers

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Query Match 100.0%; Score 21.6; DB 1; Length 590;

Best Local Similarity 95.5%; Pred. No. 7.5;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCGCGGATCTTGT 22

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Db 556 TGAAGTGCGCGGATCTTGT 535

gene

CDS

RESULT 18

AY166562/c

LOCUS

DEFINITION

shock protein 60 (hsp60) gene, partial cds.

ACCESSION

AY166562

VERSION

AY166562.1 GI:24850362

KEYWORDS

Source

ORGANISM

Bifidobacterium boum

REFERENCE

AY166562

1 (bases 1 to 590)

AUTHORS

Species Identification of Genus Bifidobacterium Based on Partial

TITLE

Hsp60 Gene Sequences and Proposal of Bifidobacterium thermacidophilum subsp. suis subsp. nov.

JOURNAL

Submitted (18-OCT-2002) State Key Laboratory of Microbial

Resources, Institute of Microbiology, Chinese Academy of Sciences,

No. 13 North 1st Street, Zhongguancun, Beijing 100080, P. R. China

Location/Qualifiers

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LLIIVADVDGEALPTLIILNKIRGTFTNTCAVKAPGFG"

Query Match 100.0%; Score 21.6; DB 1; Length 590;

Best Local Similarity 95.5%; Pred. No. 7.5;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCGCGGATCTTGT 22

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Db 556 TGAAGTGCGCGGATCTTGT 535

gene

CDS

RESULT 19

AF240567/c

LOCUS

DEFINITION

shock protein 60 (hsp60) gene, partial cds.

ACCESSION

AF240567

VERSION

AF240567.1 GI:7243788

KEYWORDS

Source

ORGANISM

Bifidobacterium thermophilum

REFERENCE

AF240567

1 (bases 1 to 591)

AUTHORS

Species Identification of Genus Bifidobacterium Based on Partial

TITLE

Hsp60 Gene Sequences and Proposal of Bifidobacterium thermacidophilum subsp. suis subsp. nov.

JOURNAL

Submitted (18-OCT-2002) State Key Laboratory of Microbial

Resources, Institute of Microbiology, Chinese Academy of Sciences,

No. 13 North 1st Street, Zhongguancun, Beijing 100080, P. R. China

Location/Qualifiers

1. .590

/organism="Bifidobacterium thermophilum subsp. nov."

/mol_type="genomic DNA"

/strain="P3-11"

/sub_species="suis"

/db_xref="taxon:212365"

<1. .>590

/gene="hsp60"

<1. .>590

/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AAAG62544.1"

/db_xref="GI:24850359"

/translation="GDGTTTATVLAQSLVHGLKNVAGSNPIALRGIEKADEIVK

ELVSAKQVETKQIAATATISADPEVGEKIAELDKVQDGVTVEDNNRRLGLDIE

FTEGHRFDKVIAPFYFTNADDDQTAVLENPIYLLTSGKSSQQDIHLADLVNMGSRP

LLIIVADVDGEALPTLIILNKIRGTFTNTCAVKAPGFG"

Query Match 100.0%; Score 21.6; DB 1; Length 590;

Best Local Similarity 95.5%; Pred. No. 7.5;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 556 TGAAGTGCGCGGATCTTGT 535

gene

CDS

RESULT 20

AF240567/c

LOCUS

DEFINITION

shock protein 60 (hsp60) gene, partial cds.

ACCESSION

AF240567

VERSION

AF240567.1 GI:7243788

KEYWORDS

Source

ORGANISM

Bifidobacterium thermophilum

REFERENCE

AF240567

1 (bases 1 to 591)

AUTHORS

Species Identification of Genus Bifidobacterium Based on Partial

TITLE

Hsp60 Gene Sequences and Proposal of Bifidobacterium thermacidophilum subsp. suis subsp. nov.

JOURNAL

Submitted (18-OCT-2002) State Key Laboratory of Microbial

Resources, Institute of Microbiology, Chinese Academy of Sciences,

No. 13 North 1st Street, Zhongguancun, Beijing 100080, P. R. China

Location/Qualifiers

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/organism="Bifidobacterium thermophilum subsp. nov."

/mol_type="genomic DNA"

/strain="P3-11"

/sub_species="suis"

/db_xref="taxon:212365"

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/gene="hsp60"

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/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AAAG62544.1"

/db_xref="GI:24850359"

/translation="GDGTTTATVLAQSLVHGLKNVAGSNPIALRGIEKADEIVK

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LLIIVADVDGEALPTLIILNKIRGTFTNTCAVKAPGFG"

Query Match 100.0%; Score 21.6; DB 1; Length 590;

Best Local Similarity 95.5%; Pred. No. 7.5;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 556 TGAAGTGCGCGGATCTTGT 535

gene

CDS

RESULT 21

AF240567/c

LOCUS

DEFINITION

shock protein 60 (hsp60) gene, partial cds.

ACCESSION

AF240567

VERSION

AF240567.1 GI:7243788

KEYWORDS

Source

ORGANISM

Bifidobacterium thermophilum

REFERENCE

AF240567

1 (bases 1 to 591)

AUTHORS

Species Identification of Genus Bifidobacterium Based on Partial

TITLE

Hsp60 Gene Sequences and Proposal of Bifidobacterium thermacidophilum subsp. suis subsp. nov.

JOURNAL

Submitted (18-OCT-2002) State Key Laboratory of Microbial

Resources, Institute of Microbiology, Chinese Academy of Sciences,

No. 13 North 1st Street, Zhongguancun, Beijing 100080, P. R. China

Location/Qualifiers

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/organism="Bifidobacterium thermophilum subsp. nov."

/mol_type="genomic DNA"

/strain="P3-11"

/sub_species="suis"

/db_xref="taxon:212365"

<1. .>590

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/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AAAG62544.1"

/db_xref="GI:24850359"

/translation="GDGTTTATVLAQSLVHGLKNVAGSNPIALRGIEKADEIVK

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FTEGHRFDKVIAPFYFTNADDDQTAVLENPIYLLTSGKSSQQDIHLADLVNMGSRP

LLIIVADVDGEALPTLIILNKIRGTFTNTCAVKAPGFG"

Query Match 100.0%; Score 21.6; DB 1; Length 590;

Best Local Similarity 95.5%; Pred. No. 7.5;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCGCGGATCTTGT 22

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Db 556 TGAAGTGCGCGGATCTTGT 535

gene

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/db_xref="taxon:33905"
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/gene="hsp60"
/codon_start=2
/transl_table=11
/product="heat shock protein 60"
/protein_id="AAP43452.1"
/db_xref="GI:7243789"
/translation="GGGTTATVLAQSLVHEGLKVVAGSNPIALRGGIEKADEIVK
ELVASAKDVEKQIAATATISAADPEVGEKIAELDKVGQGVVTVENNRPLGLE
FTGMRFDKGYIAPYFVTWADQTAVENTPYILLTSGRVSSQDVIHLADLVKMSGR
LLIIVAEVDGEALPTLILKIRGTFTNTCAVKAPFG"

ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 591;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22
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Db 557 TGAAGGTGCCCGGATCTTGT 536

RESULT 20
E10965/c
LOCUS 797 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA fragment encoding a part of GroEL protein.
ACCESSION E10965
VERSION E10965.1 GI:22028829
KEYWORDS JP 1996070873-A/1.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 797)
AUTHORS Inai,R., Inui,M., Asai,Y., Kobayashi,M. and Yugawa,H.
NEW DNA FRAGMENT
PATENT: JP 1996070873-A 1 19-MAR-1996;
MITSUBISHI CHEM CORP
OS Brevibacterium flavum
PN JP 1996070873-A/1
PD 19-MAR-1996
PF 07-SEP-1994 JP 1994213483
PI IMAI RITSUKO, INUI MASAYUKI, ASAI YOKO, KOBAYASHI MIKI, PI
YUGAWA HIDEAKI
PC C12N15/09, (C12N15/09, C12R1:13);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1. .797
FT /organism="Brevibacterium flavum" FT
FT /strain="MJ-233".
FT Location/Qualifiers
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source
1. .797
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 797;
Best Local Similarity 95.5%; Pred. No. 7.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22
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Db 748 TGAAGGTGCCCGGATCTTGT 727

RESULT 21
E41716/c
LOCUS 852 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing L-glutamic acid by fermentation.
ACCESSION E41716
VERSION E41716.1 GI:18633387
KEYWORDS JP 2001069979-A/33.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 852)
AUTHORS Fujii,M. and Imanaka,T.
TITLE Process for producing L-glutamic acid by fermentation
JOURNAL Patent: JP 2001069979-A 33 21-MAR-2001;
JAPAN TOBACCO INC, TAKDAYUKI IMANAKA
OS Corynebacterium glutamicum
PN JP 2001069979-A/33
PD 21-MAR-2001
PF 31-AUG-1999 JP 1999245121
PR
PI MIKIO FUJII, TADAYUKI IMANAKA
PC C12N15/09, C12N1/21, C12P13/14// (C12N1/21, C12R1:15), (C12P13/14,
C12R1:15),
PC C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .852
FT /organism="Corynebacterium glutamicum".
FT Location/Qualifiers
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/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
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ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 852;
Best Local Similarity 95.5%; Pred. No. 7.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22
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Db 802 TGAAGGTGCCCGGATCTTGT 781

RESULT 22
AR080019/c
LOCUS 927 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 116 from patent US 5968524.
ACCESSION AR080019
VERSION AR080019.1 GI:10006754
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 927)
AUTHORS Watson,J.D. and Tan,P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated
psoriasis
JOURNAL Patent: US 5968524-A 116 19-OCT-1999;
FEATURES
source
1. .927
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22
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Db 166 TGAAGTGCCGCGGATCTTGT 145
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RESULT 23
AR085945/c
LOCUS AR085945 927 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 116 from patent US 5985287.
ACCESSION AR085945
VERSION AR085945.1 GI:10012711
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 927)
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 5985287-A 116 16-NOV-1999;
FEATURES
source Location/Qualifiers
1..927
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGTGCCGCGGATCTTGT 145
|||||:|||||
RESULT 24
AR121711/c
LOCUS AR121711 927 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 116 from patent US 6160093.
ACCESSION AR121711
VERSION AR121711.1 GI:14105287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 927)
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6160093-A 116 12-DEC-2000;
FEATURES
source Location/Qualifiers
1..927
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGTGCCGCGGATCTTGT 145
|||||:|||||
RESULT 25
BD218120/c
LOCUS BD218120 927 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218120
VERSION BD218120.1 GI:33027890
KEYWORDS JP 2002514385-A/45.
SOURCE Mycobacterium vaccae
```

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ORGANISM Mycobacterium vaccae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 927)
AUTHORS Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for
their
JOURNAL Patent: JP 2002514385-A 45 21-MAY-2002;
COMMENT GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Mycobacterium vaccae
PN JP 2002514385-A/45
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
PC A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC C12N15/09, C12R1:32, C12N15/00, C12N5/00, (C12N15/00, C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
CC their use
FH Key Location/Qualifiers
FT source 1..927
/mol_type="genomic DNA"
/db_xref="taxon:1810"
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source Location/Qualifiers
1..927
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/db_xref="taxon:1810"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGTGCCGCGGATCTTGT 145
|||||:|||||
RESULT 26
AR213757/c
LOCUS AR213757 927 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 116 from patent US 6406704.
ACCESSION AR213757
VERSION AR213757.1 GI:23311044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 927)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6406704-A 116 18-JUN-2002;
FEATURES
source Location/Qualifiers
1..927
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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/db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
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Db 166 TGAAGGTGCCCGGATCTTGT 145

RESULT 29
LOCUS AR080046/c 985 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 161 from patent US 5968524.
ACCESSION AR080046
VERSION AR080046.1 GI:10006781
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 985)
AUTHORS Watson,J.D. and Tan,P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL Patent: US 5968524-A 161 19-OCT-1999;
FEATURES
    source
    Location/Qualifiers
    1..985
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    /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
    |||||:|||||
Db 167 TGAAGGTGCCCGGATCTTGT 146

RESULT 30
LOCUS AR085972/c 985 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 161 from patent US 5985287.
ACCESSION AR085972
VERSION AR085972.1 GI:10012738
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 985)
AUTHORS Tan,P., Skinner,M. and Prestidge,R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 161 16-NOV-1999;
FEATURES
    source
    Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
    |||||:|||||
Db 167 TGAAGGTGCCCGGATCTTGT 146

RESULT 31
LOCUS AR085972/c 927 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial infections.
ACCESSION BD008542
VERSION BD008542.1 GI:18636915
KEYWORDS JP 2001503969-A/45.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 927)
AUTHORS Tan,P., Hiyyama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and Prestidge,R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial infections
JOURNAL Patent: JP 2001503969-A 45 27-MAR-2001;
COMMENT GENESIS RESEARCH & DEVELOPMENT CO LTD
OS Unidentified
PN JP 2001503969-A/45
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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RESULT 31
LOCUS AR121738/c 985 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 161 from patent US 6160093.
ACCESSION AR121738
VERSION AR121738.1 GI:14105314
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Visser,E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6160093-A 161 12-DEC-2000;
FEATURES
source Location/Qualifiers
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 167 TGAAGTGCCRCGGATCTTGTT 146
|||||:|||||

RESULT 32
LOCUS BD218147/c 985 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218147
VERSION BD218147.1 GI:33027917
KEYWORDS JP 2002514385-A/72.
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE 1 (bases 1 to 985)
AUTHORS Tan,P., Watson,J., Visser,E.S., Skinner,M.A. and Prestid,R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for
their use
JOURNAL Patent: JP 2002514385-A 72 21-MAY-2002;
COMMENT OS Mycobacterium vaccae
PN JP 2002514385-A/72
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN,JAMES WATSON,ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
PI L PRESTIDGE
PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
A61P17/00,
PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
G01N33/68//
PC (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
their use
FH Key Location/Qualifiers
FT source 1..985
FT /organism="Mycobacterium vaccae".
FEATURES
source Location/Qualifiers
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 167 TGAAGTGCCRCGGATCTTGTT 146
|||||:|||||

RESULT 33
LOCUS AR213784/c 985 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 161 from patent US 6406704.
ACCESSION AR213784
VERSION AR213784.1 GI:23311071
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6406704-A 161 18-JUN-2002;
COMMENT NZX;
GENESIS Research and Development Corporation Limited;;
FEATURES
source Location/Qualifiers
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 167 TGAAGTGCCRCGGATCTTGTT 146
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RESULT 34
LOCUS AR366016/c 985 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 161 from patent US 6328978.
ACCESSION AR366016
VERSION AR366016.1 GI:34598269
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin
disorders
JOURNAL Patent: US 6328978-A 161 11-DEC-2001;
COMMENT NZX;
GENESIS Research & Development Corp. Ltd.; Parnell;
FEATURES
source Location/Qualifiers
/mol_type="genomic DNA"
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Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGTT 22
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Db 167 TGAAGTGCCRCGGATCTTGTT 146
|||||:|||||
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Db      167 TGAAGGTGCGCGGATCTTGTT 146
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RESULT 35
AR080017/c
LOCUS      1569 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 113 from patent US 5968524.
ACCESSION AR080017
VERSION    AR080017.1 GI:10006752
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1569)
AUTHORS   Watson,J.D. and Tan,P.L.J.
TITLE     Methods and compounds for the treatment of immunologically-mediated
psoriasis
JOURNAL   Patent: US 5968524-A 113 19-OCT-1999;
FEATURES   Location/Qualifiers
            source
            1..1569
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||:|||||:|||||
Db      808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 36
AR085943/c
LOCUS      1569 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 113 from patent US 5985287.
ACCESSION AR085943
VERSION    AR085943.1 GI:10012709
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1569)
AUTHORS   Tan,P., Skinner,M. and Prestidge,R.
TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL   Patent: US 5985287-A 113 16-NOV-1999;
FEATURES   Location/Qualifiers
            source
            1..1569
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||:|||||:|||||
Db      808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 37
AR121709/c
LOCUS      1569 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 113 from patent US 6160093.
ACCESSION AR121709
VERSION    AR121709.1 GI:14105285
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.

```

```

REFERENCE  1 (bases 1 to 1569)
AUTHORS   Visser,B.
TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL   Patent: US 6160093-A 113 12-DEC-2000;
FEATURES   Location/Qualifiers
            source
            1..1569
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||:|||||:|||||
Db      808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 38
BD218118/c
LOCUS      1569 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218118
VERSION    BD218118.1 GI:33027888
KEYWORDS   JP 2002514385-A/43.
SOURCE     Mycobacterium vaccae
ORGANISM   Mycobacterium vaccae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 1569)
AUTHORS   Tan,P., Watson,J., Visser,E.S., Skinner,M.A. and Prestid,R.L.
TITLE     Compositions derived from mycobacterium vaccae and methods for
their use
JOURNAL   Patent: JP 2002514385-A 43 21-MAY-2002;
COMMENT    GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Mycobacterium vaccae
PN JP 2002514385-A/43
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN,JAMES WATSON ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
PI L PRESTIDGE
PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
PC A61P17/00,
PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
G01N33/68//
PC (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
CC Compositions derived from mycobacterium
vacciae and methods for
CC their use
FH Key Location/Qualifiers
FT source 1..1569
FT /organism='Mycobacterium vaccae'.
FEATURES   Location/Qualifiers
            source
            1..1569
            /organism="Mycobacterium vaccae"
            /mol_type="genomic DNA"
            /db_xref="taxon:1810"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22

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source 1. .1589
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"

ORIGIN

Query Match 100.0%; Score 21.6; DB 6; Length 1589;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
DB 1533 TGAAGGTGCGCGGATCTTGT 1512

RESULT 43
LOCUS TTU90204/c 1620 bp DNA linear BCT 21-MAR-1997
DEFINITION Tsukamurella tyrosinosolvens heat shock protein 60 (hsp60) gene, complete cds.
ACCESSION U90204
VERSION U90204.1 GI:1899189
SOURCE Tsukamurella tyrosinosolvens
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.

REFERENCE 1 (bases 1 to 1620)
Zimmermann, O., Pinkenburg, O. and Koechel, H.G.
Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock protein 60
Unpublished
REFERENCE 2 (bases 1 to 1620)
Zimmermann, O., Pinkenburg, O. and Koechel, H.G.
Direct Submission
TITLE Submitted (20-FEB-1997) Med. Microbiology, University, Kreuzberg 57, Goettingen D-37075, Germany
JOURNAL Location/Qualifiers
FEATURES
source 1. .1620
/organism="Tsukamurella tyrosinosolvens"
/mol_type="genomic DNA"
/strain="IMMIB D-1411"
/db_xref="taxon:57704"
/note="aerobic, gram positive, slightly acid-alcohol fast bacilli; genus is closely related to the genera Mycobacterium, Nocardia, Rhodococcus, Gordonia, and Corynebacterium"
gene 1. .1620
/genes="hsp60"
CDS 1. .1620
/genes="hsp60"
/note="GroEL protein"
/codon_start=1
/transl_table=11
/product="heat shock protein 60"
/protein_id="AA949990.1"
/db_xref="GI:1899190"

/translation="MAKTIADFDEARRGLERGLNALADAVKVTLPKGRNVVLEKMG APTITNDGVSIAKEIELEDPEYKIGAEVLKEVAKTDDVAGDGTATTATVLAQALVREG LRNVAGANPLGKRGIEKAEVATEHLLKAEVETKQIATAGISAGDPAIGELI AEAMDVKVGEVITVEESNTFGLQLELTGEMFDFKGFISGYPATDAERQEAVIDAYI LVSQKISTVKDILPLEKVIOGKPLAIIAEDVGEALSTLIVNKIRGTFKSVAIKA PGFGRRRKMLQDMALITGGQVISEIGLSLDTAGLEVLQARQVVTXDETTVDGA GSKEQIAGRVQIRAEIESDSDYDREKIQERLAKLGGVAVIKAGATDGLKRRH IEDAVRNAAKAAVEGIVAGGSAQSGTVPDSXALEGDEATGANIVKVALDAPVKQI AVNAGLEPGVVAEKVRNSPAGTGLNAATGVYEDLLAAGINDPDKVTRSLQNAASIAA LFLTTEAVVADKPEKAGAPVPTGCGMGDMF"

ORIGIN

Query Match 100.0%; Score 21.6; DB 1; Length 1620;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 44

AF352578/c 1623 bp DNA linear BCT 13-MAR-2001
LOCUS Tsukamurella paurometabola heat shock protein 60 (hsp60) gene, complete cds.
DEFINITION AF352578
ACCESSION AF352578
VERSION AF352578.1 GI:13310800
KEYWORDS
SOURCE Tsukamurella paurometabola
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.

REFERENCE 1 (bases 1 to 1623)
Zimmermann, O.S. and Koechel, H.G.
Tsukamurella paurometabola heat shock protein 60 (hsp60) gene
Unpublished
REFERENCE 2 (bases 1 to 1623)
Zimmermann, O.S. and Koechel, H.G.
Direct Submission
TITLE Submitted (23-FEB-2001) Virology, Univ. Goettingen, Kreuzberg 57, Goettingen D-37075, Germany
JOURNAL Location/Qualifiers
FEATURES
source 1. .1623
/organism="Tsukamurella paurometabola"
/mol_type="genomic DNA"
/db_xref="taxon:2061"
gene 1. .1623
/genes="hsp60"
CDS 1. .1623
/genes="hsp60"
/codon_start=1
/transl_table=11
/product="heat shock protein 60"
/protein_id="AAK18614.1"
/db_xref="GI:13310801"

/translation="MAKTIADFDEARRGLERGLNALADAVKVTLPKGRNVVLEKMG APTITNDGVSIAKEIELEDPEYKIGAEVLKEVAKTDDVAGDGTATTATVLAQALVREG LRNVAGANPLGKRGIEKAEVATEHLLKAEVETKQIATAGISAGDPAIGELI AEAMDVKVGEVITVEESNTFGLQLELTGEMFDFKGFISGYPATDAERQEAVIDAYI LVSQKISTVKDILPLEKVIOGKPLAIIAEDVGEALSTLIVNKIRGTFKSVAIKA PGFGRRRKMLQDMALITGGQVISEIGLSLDTAGLEVLQARQVVTXDETTVDGA GSKEQIAGRVQIRAEIESDSDYDREKIQERLAKLGGVAVIKAGATDGLKRRH IEDAVRNAAKAAVEGIVAGGSAQSGTVPDSXALEGDEATGANIVKVALDAPVKQI AVNAGLEPGVVAEKVRNSPAGTGLNAATGVYEDLLAAGINDPDKVTRSLQNAASIAA LFLTTEAVVADKPEKAGAPVPTGCGMGDMF"

ORIGIN

Query Match 100.0%; Score 21.6; DB 1; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 45

A46454/c 1623 bp DNA linear PAT 07-MAR-1997
LOCUS Sequence 1 from Patent WO9525744.
DEFINITION A46454
ACCESSION A46454
VERSION A46454.1 GI:2300634
KEYWORDS
SOURCE Mycobacterium bovis
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 1623)
AUTHORS Anderton,S.M., Van,D.Z. and Van,E.W.
TITLE PEPTIDE FRAGMENTS OF MICROBIAL STRESS PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES
JOURNAL Patent: WO 9525744-A 1 28-SEP-1995;
COMMENT UNIV UTRECHT (NL)
Other publication AU 1962895 951009.
FEATURES
source Location/Qualifiers
1..1623
/organism="Mycobacterium bovis"
/mol_type="unassigned DNA"
/db_xref="taxon:1765"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787
RESULT 46
LOCUS CQ816174 1623 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 3 from Patent WO2004041304.
ACCESSION CQ816174
VERSION CQ816174.1 GI:48144533
KEYWORDS Mycobacterium tuberculosis
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1
AUTHORS Coates,A.R.
TITLE Pain relief agents
JOURNAL Patent: WO 200401304-A 3 21-MAY-2004;
Helprey Therapeutics Limited (GB)
FEATURES
source Location/Qualifiers
1..1623
/organism="Mycobacterium tuberculosis"
/mol_type="unassigned DNA"
/db_xref="taxon:1773"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787
RESULT 47
LOCUS AR266836 1623 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6495347.
ACCESSION AR266836
VERSION AR266836.1 GI:29696202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Siegel,M., Chu,N.R. and Mizzen,L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: US 6495347-A 3 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria;
CA;
REFERENCE 1 (bases 1 to 1623)
AUTHORS Siegel,M., Chu,N.R. and Mizzen,L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: WO 0104344-A 3 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
Stressgen Biotechnologies Corporation; Victoria;
CA;
FEATURES
source Location/Qualifiers
1..1623
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion sequence"
1..1623
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC28419.1"
/db_xref="GI:12710172"

FEATURES
source Location/Qualifiers
1..1623
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787
RESULT 48
LOCUS AR655543 1623 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 23 from patent US 6892139.
ACCESSION AR655543
VERSION AR655543.1 GI:67587586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Eisenberg,D., Rotstein,S.H. and Marcotte,E.M.
TITLE Determining the functions and interactions of proteins by comparative analysis
JOURNAL Patent: US 6892139-A 23 10-MAY-2005;
The Regents of the University of California; Alameda, CA
FEATURES
source Location/Qualifiers
1..1623
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787
RESULT 49
LOCUS AX073911 1623 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104344.
ACCESSION AX073911
VERSION AX073911.1 GI:12710171
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Siegel,M., Chu,N.R. and Mizzen,L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: WO 0104344-A 3 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
Stressgen Biotechnologies Corporation; Victoria;
CA;
FEATURES
source Location/Qualifiers
1..1623
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion sequence"
1..1623
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC28419.1"
/db_xref="GI:12710172"

/translation="MAKTIAYDEARRGLERGLNALADAVKVTGLGKRNVLKKGW
 APTITNDGVSIAKEIELEDPYKIGAEIVKEVAKTDDVAGDGTATTATVLAQALVREG
 LRNVAGANPLGLKRGIERAKVETTLKGAKEVETKQIAATAAISAGDSIGDLI
 LEAMDKVNGEVIITVEESNTFGLQLETEGMRFDKGYISGYFVTDPERQEAILEDPI
 LVSQKSTVKDILLPLEKVIQAGKPLLIIAEDVEGEALSTLVNKRIGTFKSVAKA
 PGFGRKAMQMLQMAILTGQVITSEEGVLTLENADISLGLKARKVVTVDKETTIVEGA
 GUTDAGRAVAQIRIENSDDYDREKLOERLAKLAGGAVIKAGAAVELEKPKH
 RIEDAVRNAKAAVEGIVAGGVTLQAAPTLDELKLEGEATGANIVKVALEAPLQ
 IAFNSGLEPGVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIA
 GLFLITTEAVVADKPEKAAAPAGDPTGGMGMDP"

ORIGIN

Query Match 100.0%; Score 21.6; DB 6; Length 1623;
 Best Local Similarity 95.5%; Pred. No. 8.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22

Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 50

AF281650/c

LOCUS

DEFINITION Mycobacterium avium heat shock protein Hsp65 gene, partial cds.

ACCESSION

AF281650

VERSION

AF281650.1

GI:9652215

KEYWORDS

Myobacterium avium

SOURCE

Myobacterium avium

ORGANISM

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

avium complex (MAC).

REFERENCE

1 (bases 1 to 1624)

Nagabhushanam, V., Praszkier, J. and Cheers, C.

Molecular and immunological characterization of Mycobacterium avium

65 kDa heat shock protein (Hsp65)

Immunol. Cell Biol. 79 (5), 454-461 (2001)

11564153

2 (bases 1 to 1624)

Nagabhushanam, V., Praszkier, J. and Cheers, C.

Direct Submission

Submitted (23-JUN-2000) Microbiology and Immunology, Melbourne

University, Royal Parade, Melbourne, Victoria 3052, Australia

Location/Qualifiers

1. .1624

/organism="Mycobacterium avium"

/mol_type="genomic DNA"

/db_xref="taxon:1764"

1. .->1624

/note="GroEL-like protein; 65 kilodalton protein"

/codon_start=1

/transl_table=11

/product="heat shock protein Hsp65"

/protein_id="AAFP1444.1"

/db_xref="GI:9652215"

/translation="MAKTIAYDEARRGLERGLNALADAVKVTGLGKRNVLKKGW

APTITNDGVSIAKEIELEDPYKIGAEIVKEVAKTDDVAGDGTATTATVLAQALVREG

LRNVAGANPLGLKRGIERAKVETTLKGAKEVETKQIAATAAISAGDSIGDLI

LEAMDKVNGEVIITVEESNTFGLQLETEGMRFDKGYISGYFVTDPERQEAILEDPI

LVSQKSTVKDILLPLEKVIQAGKPLLIIAEDVEGEALSTLVNKRIGTFKSVAKA

PGFGRKAMQMLQMAILTGQVITSEEGVLTLENADISLGLKARKVVTVDKETTIVEGA

GUTDAGRAVAQIRIENSDDYDREKLOERLAKLAGGAVIKAGAAVELEKPKH

RIEDAVRNAKAAVEGIVAGGVTLQAAPTLDELKLEGEATGANIVKVALEAPLQ

IAFNSGLEPGVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIA

GLFLITTEAVVADKPEKAAAPAGDPTGGMGMDP"

ORIGIN

Query Match 100.0%; Score 21.6; DB 1; Length 1624;
 Best Local Similarity 95.5%; Pred. No. 8.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22

Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 51

AF352577/c

LOCUS

DEFINITION

Nocardia farcinica heat shock protein 60 (hsp60) gene, complete

cds

AF352577

VERSION

AF352577.1

GI:13310798

KEYWORDS

Nocardia farcinica

ORGANISM

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Nocardia; Nocardia.

REFERENCE

1 (bases 1 to 1626)

Zimmermann, O.S. and Koechel, H.G.

Nocardia farcinica heat shock protein 60 (hsp60) gene

Unpublished

REFERENCE

2 (bases 1 to 1626)

Zimmermann, O.S. and Koechel, H.G.

Direct Submission

Submitted (23-FEB-2001) Virology, Univ. Goettingen, Kreuzberg

57, Goettingen D-37075, Germany

Location/Qualifiers

1. .1626

/organism="Nocardia farcinica"

/mol_type="genomic DNA"

/db_xref="taxon:37329"

1. .1626

/gene="hsp60"

1. .1626

/gene="hsp60"

/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AAK18613.1"

/db_xref="GI:13310799"

/translation="MAKTIAYDEARRGLERGLNLADAVKVTGLGKRNVLKKGW

APTITNDGVSIAKEIELEDPYKIGAEIVKEVAKTDDVAGDGTATTATVLAQALVREG

LRNVAGANPLGLKRGIERAKVETTLKGAKEVETKQIAATAAISAGDSIGDLI

LEAMDKVNGEVIITVEESNTFGLQLETEGMRFDKGYISGYFVTDPERQEAILEDPI

LVSQKSTVKDILLPLEKVIQAGKPLLIIAEDVEGEALSTLVNKRIGTFKSVAKA

PGFGRKAMQMLQMAILTGQVITSEEGVLTLENADISLGLKARKVVTVDKETTIVEGA

GUTDAGRAVAQIRIENSDDYDREKLOERLAKLAGGAVIKAGAAVELEKPKH

RIEDAVRNAKAAVEGIVAGGVTLQAAPTLDELKLEGEATGANIVKVALEAPLQ

IAFNSGLEPGVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIA

GLFLITTEAVVADKPEKAAAPAGDPTGGMGMDP"

ORIGIN

Query Match 100.0%; Score 21.6; DB 1; Length 1626;
 Best Local Similarity 95.5%; Pred. No. 8.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGT 22

Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 52

AR080045/c

LOCUS

DEFINITION

Sequence 159 from patent US 5968524.

ACCESSION

AR080045

VERSION

AR080045.1

GI:10006780

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 1626)

Watson, J.D. and Tan, P.L.J.

Methods and compounds for the treatment of immunologically-mediated

Db 808 TGAAGGTGCCCGGATCTTGT 787

DEFINITION

Sequence 159 from patent US 5968524.

ACCESSION

AR080045

VERSION

AR080045.1

GI:10006780

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 1626)

Watson, J.D. and Tan, P.L.J.

Methods and compounds for the treatment of immunologically-mediated

```
psoriasis
JOURNAL Patent: US 5968524-A 159 19-OCT-1999;
FEATURES Location/Qualifiers
source
1..1626
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1626;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 53
AR085971/c
LOCUS 1626 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 159 from patent US 5985287.
ACCESSION AR085971
VERSION AR085971.1 GI:10012737
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 159 16-NOV-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 54
AR121737/c
LOCUS 1626 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 159 from patent US 6160093.
ACCESSION AR121737
VERSION AR121737.1 GI:14105313
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 159 12-DEC-2000;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1626;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
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Db 808 TGAAGTGCCCGGATCTTGT 22

RESULT 55
BD218146/c
LOCUS 1626 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218146
VERSION BD218146.1 GI:33027916
KEYWORDS Mycobacterium vaccae
SOURCE Mycobacterium vaccae
ORGANISM Mycobacteriaceae; Actinobacteridae; Actinomycetales; Bacteria; Actinobacteria; Corynebacterineae; Mycobacterium.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestidge, R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for their use
JOURNAL Patent: JP 2002514385-A 71 21-MAY-2002;
COMMENT GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Mycobacterium vaccae
PN JP 2002514385-A/71
PF 21-MAY-2002
PR 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
PC A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC C12N15/09, C12R1/32, C12N15/00, C12N5/00, (C12N15/00, C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
CC their use
CC Key Location/Qualifiers
FH FT source 1..1626
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ORIGIN
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Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 56
AR213783/c
LOCUS 1626 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 159 from patent US 6406704.
ACCESSION AR213783
VERSION AR213783.1 GI:23311070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
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infections
Patent: US 6406704-A 159 18-JUN-2002;
Genesis Research and Development Corporation Limited;;
NZX;

JOURNAL
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RESULT 57
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LOCUS AR366015 1626 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 159 from patent US 6328978.
ACCESSION AR366015
VERSION AR366015.1 GI:34598268
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 159 11-DEC-2001;
Genesis Research & Development Corp. Ltd.; Parnell;
NZX;

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Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 808 TGAAGGTGCCCGGATCTTGTT 787

RESULT 58
BD165187/c
LOCUS BD165187 1644 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel polynucleotide.
ACCESSION BD165187
VERSION BD165187.1 GI:27870999
KEYWORDS JP 2002191370-A/2986.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1644)
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotide
JOURNAL Patent: JP 2002191370-A 2986 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
PN JP 2002191370-A/2986
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI, KEIKO OCHIAI,

infections
Patent: US 6406704-A 159 18-JUN-2002;
Genesis Research and Development Corporation Limited;;
NZX;

JOURNAL
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Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 823 TGAAGGTGCCCGGATCTTGTT 802

RESULT 59
AX123070/c
LOCUS AX123070 1644 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2986 from Patent EP1108790.
ACCESSION AX123070
VERSION AX123070.1 GI:14040558
KEYWORDS Corynebacterium glutamicum
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
REFERENCE 1
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 2986 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)

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Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGTT 22
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Db 823 TGAAGGTGCCCGGATCTTGTT 802

RESULT 60
E10966/c
LOCUS E10966 1647 bp DNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding GroEL protein.
ACCESSION E10966
VERSION E10966.1 GI:22028831
KEYWORDS JP 1996070873-A/2.
SOURCE Corynebacterium glutamicum

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ORGANISM
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1 (bases 1 to 1647)
AUTHORS
Imai, R., Inui, M., Asai, Y., Kobayashi, M. and Yugawa, H.
TITLE
NEW DNA FRAGMENT.
JOURNAL
Patent: JP 1996070873-A 2 19-MAR-1996;
MITSUBISHI CHEM CORP
OS Brevibacterium flavum
PN JP 1996070873-A/2
PD 19-MAR-1996
PP 07-SEP-1994 JP 1994213483
PI IMAI RITSUKO, INUI MASAYUKI, ASAI YOKO, KOBAYASHI MIKI, PI
YUGAWA HIDEAKI
PC C12N15/09, (C12N15/09, C12R1:13);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
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FT /product='GroEL protein'.
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/db_xref="taxon:1718"
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Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 823 TGAGGTGCCCGGATCTTGTT 802
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Job time : 155.853 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 16:58:33 ; Search time 12.7069 Seconds
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Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaaggtccrccggatcttgtt 22

Scoring table: IDENTITY_NUC

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	21.6	100.0	337	3	US-09-095-855-77
C 5	21.6	100.0	337	3	US-09-324-542-77
C 6	21.6	100.0	337	3	US-09-205-426-77
C 7	21.6	100.0	927	2	US-08-997-080-116
C 8	21.6	100.0	927	2	US-08-997-362-116
C 9	21.6	100.0	927	3	US-09-095-855-116
C 10	21.6	100.0	927	3	US-09-324-542-116
C 11	21.6	100.0	927	3	US-09-205-426-116
C 12	21.6	100.0	985	2	US-08-997-080-161
C 13	21.6	100.0	985	2	US-08-997-362-161
C 14	21.6	100.0	985	3	US-09-095-855-161
C 15	21.6	100.0	985	3	US-09-324-542-161
C 16	21.6	100.0	985	3	US-09-205-426-161
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C 18	21.6	100.0	1569	2	US-08-997-362-113
C 19	21.6	100.0	1569	3	US-09-095-855-113
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C 21	21.6	100.0	1569	3	US-09-205-426-113
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C 24	21.6	100.0	1623	3	US-09-712-363-23

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C 45	20	92.6	1320	3	US-09-031-606-8
C 46	20	92.6	1620	2	US-08-461-775-10
C 47	20	92.6	1620	3	US-09-031-606-10
C 48	20	92.6	2167	2	US-08-461-775-9
C 49	20	92.6	2167	3	US-09-031-606-9
C 50	20	92.6	2668	2	US-08-461-775-11
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C 56	18.4	85.2	5365	3	US-08-961-527-77
C 57	17.4	80.6	1844	3	US-10-105-729-7
C 58	17.4	80.6	2003	3	US-10-105-729-1
C 59	17	78.7	4352	3	US-09-620-312D-383
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ALIGNMENTS

RESULT 1

US-08-997-080-77/c

; Sequence 77, Application US/08997080

; Patent No. 5968524

; GENERAL INFORMATION:

; APPLICANT: WATSON, JAMES D.

; APPLICANT: TAN, PAUL L.J.

; TITLE OF INVENTION: METHODS

; CORRESPONDENCE ADDRESS: 194

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/997,080

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1007

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Sequence 11, Appl
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Sequence 1024, Ap
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Sequence 50, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 383, App
Sequence 1679, Ap

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-997-080-77

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Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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RESULT 2

US-08-997-362-77/c
Sequence 77, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-997-362-77

Query Match 100.0%; Score 21.6; DB 2; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-08-873-970-77/c
Sequence 77, Application US/08873970
Patent No. 6001361
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-873-970-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 166 TGAAGGTGCGCGGATCTTGT 145

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Sequence 77, Application US/09095855
Patent No. 6160093

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; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-09-095-855-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 5
US-09-324-542-77/c
; Sequence 77, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 6
US-09-205-426-77/c
; Sequence 77, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 7
US-08-997-080-116/c
; Sequence 116, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/997,080
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 927 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-08-997-080-116

Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGTT 22
|||
Db 166 TGAAGGTGCCCGGATCTTGTT 145

RESULT 8
US-08-997-362-116/c
/ Sequence 116, Application US/08997362
/ Patent No. 5985287
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Paul
/ APPLICANT: Hiwama, Jun
/ APPLICANT: Visser, Elizabeth
/ APPLICANT: Skinner, Margot
/ APPLICANT: Scott, Linda
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
/ TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
/ NUMBER OF SEQUENCES: 194
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Ann W. Speckman
/ STREET: 2601 Elliott Avenue, Suite 4185
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/997,362
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/705,347
/ FILING DATE: 29-AUG-1996
/ APPLICATION NUMBER: 08/873,970
/ FILING DATE: 12-JUN-1997
/ APPLICATION NUMBER: 08/997,362
/ FILING DATE: 23-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1002c3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 927 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-09-095-855-116

Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGTT 22
|||
Db 166 TGAAGGTGCCCGGATCTTGTT 145

RESULT 9
US-09-095-855-116/c
/ Sequence 116, Application US/09095855
/ Patent No. 6160093
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Paul
/ APPLICANT: Visser, Elizabeth
/ APPLICANT: Skinner, Margot
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: Compounds and Methods for
/ TREATMENT AND DIAGNOSIS OF Mycobacterial Infections
/ NUMBER OF SEQUENCES: 208
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Ann W. Speckman
/ STREET: 2601 Elliott Avenue, Suite 4185
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/095,855
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/705,347
/ FILING DATE: 29-AUG-1996
/ APPLICATION NUMBER: 08/873,970
/ FILING DATE: 12-JUN-1997
/ APPLICATION NUMBER: 08/997,362
/ FILING DATE: 23-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1002c3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 927 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-09-095-855-116
```

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 10

US-09-324-542-116/c
; Sequence 116, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; EARLIER FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-116.

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 11

US-09-205-426-116/c
; Sequence 116, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-116

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 12

US-08-997-080-161/c
; Sequence 161, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-080-161

Query Match 100.0%; Score 21.6; DB 2; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 13

US-08-997-362-161/c
; Sequence 161, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194

```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-161

Query Match 100.0%; Score 21.6; DB 2; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
Db 167 TGAAGGTGCCRCGGATCTTGTT 146

RESULT 14
US-09-855-855-161/c
; Sequence 161, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-995-855-161

Query Match 100.0%; Score 21.6; DB 3; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
Db 167 TGAAGGTGCCRCGGATCTTGTT 146

RESULT 15
US-09-324-542-161/c
; Sequence 161, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-161

Query Match 100.0%; Score 21.6; DB 3; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
Db 167 TGAAGGTGCCRCGGATCTTGTT 146

RESULT 16
US-09-205-426-161/c
; Sequence 161, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
```

; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; TYPE: DNA
; LENGTH: 985
; ORGANISM: Mycobacterium vaccae
US-09-205-426-161

Query Match 100.0%; Score 21.6; DB 3; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
Db 167 TGAAGTGCCRCGGATCTTGT 146

RESULT 17

US-08-997-080-113/c
; Sequence 113, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; CORRESPONDENCE ADDRESSES: 194
; ADDRESS: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-080-113

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 18

US-08-997-362-113/c
; Sequence 113, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESS: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-362-113

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 19

US-09-095-855-113/c

; Sequence 113, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-095-855-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGTT 22
DB 808 TGAAGTGCCCGGATCTTGTT 787

RESULT 20
US-09-324-542-113/c
; Sequence 113, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: Of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080

; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGTT 22
DB 808 TGAAGTGCCCGGATCTTGTT 787

RESULT 21
US-09-205-426-113/c
; Sequence 113, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGTT 22
DB 808 TGAAGTGCCCGGATCTTGTT 787

RESULT 22
US-09-613-303-3/c
; Sequence 3, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-09-613-303-3

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 23
US-10-267-311-3/c
; Sequence 3, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 24
US-09-712-363-23/c
; Sequence 23, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844

; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 25
US-08-997-080-159/c
; Sequence 159, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-080-159

Query Match 100.0%; Score 21.6; DB 2; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 26
US-08-997-362-159/c
; Sequence 159, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Marget
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 23-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-362-159

Query Match 100.0%; Score 21.6; DB 2; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 27
US-09-095-855-159/c
; Sequence 159, Application US/09095855

; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Marget
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 23-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-095-855-159

Query Match 100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 28
US-09-324-542-159/c
; Sequence 159, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-159

Query Match 100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||||:|||||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 29

US-09-205-426-159/c
; Sequence 159, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002e4
; CURRENT APPLICATION NUMBER: US/09/205,426
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-159.

Query Match 100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||||:|||||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 30

US-09-613-303-16/c
; Sequence 16, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-09-613-303-16

Query Match 100.0%; Score 21.6; DB 3; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||||:|||||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 31

US-10-267-311-16/c
; Sequence 16, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 21.6; DB 3; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||||:|||||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 32

US-09-613-303-28/c
; Sequence 28, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
; US-10-068-059-9

Query Match      100.0%; Score 21.6; DB 3; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1132 TGAAGTGCCRCGGATCTTGT 1111

RESULT 33
US-10-267-311-28/c
; Sequence 28, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
; US-10-267-311-28

Query Match      100.0%; Score 21.6; DB 3; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1132 TGAAGTGCCRCGGATCTTGT 1111

RESULT 34
US-10-068-059-9/c
; Sequence 9, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
; US-10-068-059-9

Query Match      100.0%; Score 21.6; DB 3; Length 2073;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1258 TGAAGTGCCRCGGATCTTGT 1237

RESULT 35
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
; US-10-068-059-7

Query Match      100.0%; Score 21.6; DB 3; Length 2130;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1315 TGAAGTGCCRCGGATCTTGT 1294

RESULT 36
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
; US-10-068-059-11
```

; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 21.6; DB 3; Length 2175;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 1360 TGAAGTGCCCGGATCTTGT 1339

RESULT 37

US-10-068-059-5/c
; Sequence 5, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 21.6; DB 3; Length 2241;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 1426 TGAAGTGCCCGGATCTTGT 1405

RESULT 38

US-09-613-303-20/c
; Sequence 20, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match 100.0%; Score 21.6; DB 3; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.9;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 868 TGAAGTGCCCGGATCTTGT 847

RESULT 39

US-10-267-311-20/c
; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match 100.0%; Score 21.6; DB 3; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.9;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 868 TGAAGTGCCCGGATCTTGT 847

RESULT 40

US-08-955-565A-3/c
; Sequence 3, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
; APPLICANT: Malkovsky, Miroslav
; APPLICANT: Wells, Andrew
; TITLE OF INVENTION: Immune Response Enhancer Therapy
; FILE REFERENCE: WARF-02625
; CURRENT APPLICATION NUMBER: US/08/955,565A
; CURRENT FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4380
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-08-955-565A-3

Query Match 100.0%; Score 21.6; DB 3; Length 4380;
Best Local Similarity 95.5%; Pred. No. 0.94;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 1059 TGAAGTGCCCGGATCTTGT 1038

```
RESULT 41
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 100.0%; Score 21.6; DB 3; Length 4403765;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
Db 530855 TGAAGTGCCGCGGATCTTGT 530834

RESULT 42
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 21.6; DB 3; Length 4411529;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
Db 529413 TGAAGTGCCGCGGATCTTGT 529392

RESULT 43
US-09-634-238-67/c
; Sequence 67, Application US/09634238
; Patent No. 6544772
```

```
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; US-09-634-238-67

Query Match 92.6%; Score 20; DB 3; Length 732;
Best Local Similarity 90.9%; Pred. No. 4.5;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
Db 229 TGAAGTGCCGCGGATCTTGT 208

RESULT 44
US-08-461-775-8/c
; Sequence 8, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION/DOCKET NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
```

;
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1320
US-08-461-775-8

Query Match 92.6%; Score 20; DB 2; Length 1320;
Best Local Similarity 90.9%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
||| ||||| ||||| |||||
DB 814 TGAACGTGCCGCGGATCTTGT 793

RESULT 45
US-09-031-606-8/c
; Sequence 8, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1320
US-09-031-606-8

Query Match 92.6%; Score 20; DB 3; Length 1320;
Best Local Similarity 90.9%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
||| ||||| ||||| |||||
DB 814 TGAACGTGCCGCGGATCTTGT 793

RESULT 46
US-08-461-775-10/c
; Sequence 10, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620
US-08-461-775-10

Query Match 92.6%; Score 20; DB 2; Length 1620;
Best Local Similarity 90.9%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
||| ||||| ||||| |||||
DB 814 TGAACGTGCCGCGGATCTTGT 793

RESULT 47
US-09-031-606-10/c
; Sequence 10, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-09-031-606-10

Query Match 92.6%; Score 20; DB 3; Length 1620;
Best Local Similarity 90.9%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
|||||:|||||

Db 814 TGAACGTGCGCGATCTTGT 793

RESULT 48
US-08-461-775-9/c
Sequence 9, Application US/08461775
Patent No. 5858773
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,775
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-461-775-9

Query Match 92.6%; Score 20; DB 2; Length 2167;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
|||||:|||||

Db 1662 TGAACGTGCGCGATCTTGT 1641

RESULT 49
US-09-031-606-9/c
Sequence 9, Application US/09031606
Patent No. 6153404
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 2167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-031-606-9

Query Match 92.6%; Score 20; DB 3; Length 2167;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

RESULT 50

US-08-461-775-11/c
; Sequence 11, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-461-775-11

Query Match 92.6%; Score 20; DB 2; Length 2668;
Best Local Similarity 90.9%; Pred. No. 5.2;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

RESULT 51

US-09-031-606-11/c
; Sequence 11, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-031-606-11

Query Match 92.6%; Score 20; DB 3; Length 2668;
Best Local Similarity 90.9%; Pred. No. 5.2;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

RESULT 52

US-09-470-191-60
; Sequence 60, Application US/09470191
; Patent No. 6465833
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods of Their Use in
; TITLE OF INVENTION: the Treatment, Prevention and Diagnosis of Tuberculosis
; FILE REFERENCE: 014058-00891005
; CURRENT APPLICATION NUMBER: US/09/470,191
; PRIOR FILING DATE: 1999-12-23
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113,952
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 706

```
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)...(706)
; OTHER INFORMATION: n = any nucleotide
US-09-470-191-60

Query Match      90.7%; Score 19.6; DB 3; Length 706;
Best Local Similarity 95.0%; Pred. No. 7;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGTGCGCGGATCTTGT 22
Db 608 AAGTGCCTCCGGAATCTTGT 627

RESULT 53
US-09-583-110-1024/c
; Sequence 1024, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1024
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1024

Query Match      85.2%; Score 18.4; DB 3; Length 1623;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 54
US-09-613-303-50/c
; Sequence 50, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1923)
US-10-267-311-50

Query Match      85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 55
US-10-267-311-50/c
; Sequence 50, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1923)
US-10-267-311-50

Query Match      85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 56
US-08-961-527-77/c
; Sequence 77, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
```

```
; LOCATION: (1)...(1923)
US-09-613-303-50

Query Match      85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
Db 808 TGAAGTTCACGAATCTTGT 787

RESULT 55
US-10-267-311-50/c
; Sequence 50, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1923)
US-10-267-311-50

Query Match      85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 56
US-08-961-527-77/c
; Sequence 77, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-77

Query Match 85.2%; Score 18.4; DB 3; Length 5365;
Best Local Similarity 86.4%; Pred. No. 33;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
Db 1085 TGAAGTTCACGATCTTGTT 1064

RESULT 57
US-10-729-7/c
; Sequence 7, Application US/10105729
; Patent No. 6911331
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Lightner, Johathan E.
; TITLE OF INVENTION: CHORISMATE BIOSYNTHESIS ENZYMES
; FILE REFERENCE: BB1159 US CIP
; CURRENT APPLICATION NUMBER: US/10/105,729
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/743,210
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Glycine max
US-10-105-729-7

Query Match 80.6%; Score 17.4; DB 3; Length 1844;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGTT 22
Db 513 GAAGGTGTCCAGGATGTTGTT 493

RESULT 58
US-10-729-1/c
; Sequence 1, Application US/10105729
; Patent No. 6911331
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Lightner, Johathan E.
; TITLE OF INVENTION: CHORISMATE BIOSYNTHESIS ENZYMES
; FILE REFERENCE: BB1159 US CIP
; CURRENT APPLICATION NUMBER: US/10/105,729
; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 09/743,210
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Zea mays
US-10-105-729-1

Query Match 80.6%; Score 17.4; DB 3; Length 2003;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGTT 22
Db 562 GAAGGTGTCCAGGATGTTGTT 542

RESULT 59
US-09-620-312D-383/c
; Sequence 383, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 383
; LENGTH: 4352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3675)
US-09-620-312D-383

Query Match 78.7%; Score 17; DB 3; Length 4352;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTG 20
Db 2943 GAAGTCCCATGGATCTTG 2925

RESULT 60

US-09-107-433-1679/c
; Sequence 1679, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1679:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...966
; SEQUENCE DESCRIPTION: SEQ ID NO: 1679:
US-09-107-433-1679

Query Match 77.8%; Score 16.8; DB 3; Length 966;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||
Db 151 TGAAGGTTCACGAATATTGT 130
|||||

Search completed: April 1, 2006, 17:06:39
Job time : 24.7069 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 21:55:10 ; Search time 44.7112 Seconds
(without alignments)
3279.340 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaagtgccrcggatctgtt 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

N_Geneseq_21.1*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	100.0	22	14	ADV99122
2	21.6	100.0	337	2	AAV34588
3	21.6	100.0	337	2	AAZ11322
4	21.6	100.0	337	6	ABL36228
5	21.6	100.0	852	4	AAH21760
6	21.6	100.0	927	2	AAV34610
7	21.6	100.0	927	2	AAZ11345
8	21.6	100.0	927	6	ABL36251
9	21.6	100.0	985	2	AAZ11372
10	21.6	100.0	985	6	ABL36278
11	21.6	100.0	985	8	ACC42533
12	21.6	100.0	1496	13	ADW23618
13	21.6	100.0	1569	2	AAV34608
14	21.6	100.0	1569	2	AAZ11343
15	21.6	100.0	1569	6	ABL36249
16	21.6	100.0	1589	4	AAH21763
17	21.6	100.0	1620	8	ACA38272
18	21.6	100.0	1620	13	ADR12623
19	21.6	100.0	1623	4	AAH51969

c 20	21.6	100.0	1623	5	AAF25002
c 21	21.6	100.0	1623	8	ACA40326
c 22	21.6	100.0	1623	8	ACA37725
c 23	21.6	100.0	1623	12	ADN11336
c 24	21.6	100.0	1626	2	AAZ11371
c 25	21.6	100.0	1626	6	ABL36277
c 26	21.6	100.0	1626	8	ACC42531
c 27	21.6	100.0	1626	9	ACC70275
c 28	21.6	100.0	1626	12	ADO51196
c 29	21.6	100.0	1626	12	ADO50828
c 30	21.6	100.0	1626	13	ADG64696
c 31	21.6	100.0	1638	8	ACA29800
c 32	21.6	100.0	1644	5	AAH67951
c 33	21.6	100.0	1647	2	AAZ14265
c 34	21.6	100.0	1701	9	AAZ57198
c 35	21.6	100.0	1752	8	ACC49833
c 36	21.6	100.0	1761	14	ADX05272
c 37	21.6	100.0	1800	10	ADK68629
c 38	21.6	100.0	1914	8	ACC49834
c 39	21.6	100.0	1920	5	AAF25012
c 40	21.6	100.0	1947	5	AAF25019
c 41	21.6	100.0	1965	13	ADW23606
c 42	21.6	100.0	1980	12	ADN00588
c 43	21.6	100.0	2016	12	ADK72374
c 44	21.6	100.0	2073	6	ABS54448
c 45	21.6	100.0	2130	6	ABS54447
c 46	21.6	100.0	2175	6	ABS54449
c 47	21.6	100.0	2241	6	ABS54446
c 48	21.6	100.0	2847	5	AAF25014
c 49	21.6	100.0	4260	1	AAH81768
c 50	21.6	100.0	4380	1	AAH80222
c 51	21.6	100.0	4380	2	AAV05708
c 52	21.6	100.0	4380	6	ABA99141
c 53	21.6	100.0	86114	6	ABX09143
c 54	21.6	100.0	110000	4	AAI99682_05
c 55	21.6	100.0	110000	4	AAI99683_05
c 56	21.6	100.0	349980	5	AAH68533
c 57	20	92.6	732	12	ADI67068
c 58	20	92.6	1320	2	AAQ22481
c 59	20	92.6	1620	2	AAQ22482
c 60	20	92.6	1626	8	ACA39632

ALIGNMENTS

RESULT 1

ADV99122
ID ADV99122 standard; DNA; 22 BP.

XX AC ADV99122;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene forward primer, STGROR2, SEQ ID 2.

XX KW Microorganism identification; microorganism detection; groEL2;

XX OS Streptomyces sp.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

```

XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
XX Claim 2; SEQ ID NO 2; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
XX Sequence 22 BP; 3 A; 4 C; 7 G; 7 T; 0 U; 1 Other;
SQ

```

Query Match 100.0%; Score 21.6; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TGAAGTGCCRCGGATCTTGTT 22
   |||||||
DB 1 TGAAGTGCCRCGGATCTTGTT 22

RESULT 2
AAV34588/c
ID AAV34588 standard; DNA; 337 BP.
XX
XX AAV34588;
XX
XX 25-AUG-1998 (first entry)
XX
XX M. vaccae GroEL-homologue clone GV-27 partial DNA sequence.
XX
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
XX CDS 1..336
XX /*tag= a
XX /product= "M. vaccae antigen GV-27 partial sequence"
XX /note= "the start and stop codons are not indicated"
XX
XX WO9808542-A2.
XX
XX 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX P-PSDB; AAW60130.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
PT detection, therapy and prevention of mycobacteria infections or as immune
PT response enhancers.
XX

```

Query Match 100.0%; Score 21.6; DB 2; Length 337;
Best Local Similarity 95.5%; Pred. No. 1.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TGAAGTGCCRCGGATCTTGTT 22
   |||||||
DB 166 TGAAGTGCCRCGGATCTTGTT 145

RESULT 3
AAZ11322/c
ID AAZ11322 standard; DNA; 337 BP.
XX
XX AAZ11322;
XX
XX 25-OCT-1999 (first entry)
XX
XX M. vaccae GroEL-homologue clone GV-27 DNA sequence.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
XX
XX WO932634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 23-DEC-1997; 97US-00997362.
XX 11-JUN-1998; 98US-00095855.
XX 17-SEP-1998; 98US-00156181.
XX 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
XX P-PSDB; AAY14876.
XX
XX Enhancing immune response to an antigen.
XX
XX Example 14; Page 175; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC

```

Query Match 100.0%; Score 21.6; DB 2; Length 337;
Best Local Similarity 95.5%; Pred. No. 1.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TGAAGTGCCRCGGATCTTGTT 22
   |||||||
DB 166 TGAAGTGCCRCGGATCTTGTT 145

RESULT 3
AAZ11322/c
ID AAZ11322 standard; DNA; 337 BP.
XX
XX AAZ11322;
XX
XX 25-OCT-1999 (first entry)
XX
XX M. vaccae GroEL-homologue clone GV-27 DNA sequence.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
XX
XX WO932634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 23-DEC-1997; 97US-00997362.
XX 11-JUN-1998; 98US-00095855.
XX 17-SEP-1998; 98US-00156181.
XX 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
XX P-PSDB; AAY14876.
XX
XX Enhancing immune response to an antigen.
XX
XX Example 14; Page 175; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC

```

CC to enhance the expression of co-stimulatory molecules on dendritic cells
 CC and monocytes, and to enhance dendritic cell maturation and function. The
 CC proteins can be expressed by standard recombinant methodology.
 CC Pharmaceutical compositions comprising the proteins or nucleic acid
 CC sequences encoding the proteins can be used for the treatment,
 CC prevention, and detection of disorders including infectious diseases,
 CC immune disorders and cancer. In particular, the compounds and methods are
 CC used for treatment of diseases of the respiratory system, such as
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
 CC sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma

SQ Sequence 337 BP; 60 A; 112 C; 108 G; 57 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 2; Length 337;
 Best Local Similarity 95.5%; Pred. No. 1.8;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
 |||||:|||||
 Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 4
 ABL36228/c
 ID ABL36228 standard; DNA; 337 BP.

XX AC ABL36228;

XX DT 08-APR-2002 (first entry)

XX DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 77.

XX KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
 KW Th2 immune response; immunomodulatory; gene; ds.

XX OS Mycobacterium vaccae.

XX PN US6328978-B1.

XX PD 11-DEC-2001.

XX PF 02-JUN-1999; 99US-00324542.

XX PR 23-DEC-1997; 97US-00997080.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Watson JD, Tan PLJ, Prestidge R;

XX WPI; 2002-138361/18.

DR P-PSDB; ABB73482.

XX Inhibiting skin inflammation associated with skin disorder e.g.

PT psoriasis, by administering composition comprising delipidated and
 PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
 PT culture filtrate.

XX Example 4; Col 95-98; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation
 CC associated with a skin disorder selected from psoriasis, atopic
 CC dermatitis and allergic contact dermatitis, which involves administering
 CC a composition containing delipidated and deglycolipidated Mycobacterium
 CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 CC treated may also include alopecia areata, and skin cancers such as basal
 CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
 CC acts by inhibiting the Th2 immune response. The present sequence is a
 CC coding sequence described in the exemplification of the invention

XX SQ Sequence 337 BP; 60 A; 112 C; 108 G; 57 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 6; Length 337;
 Best Local Similarity 95.5%; Pred. No. 1.8;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
 |||||:|||||
 Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 5
 AAH21760/c
 ID AAH21760 standard; DNA; 852 BP.

XX AC AAH21760;

XX DT 14-AUG-2001 (first entry)

XX DE Corynebacterium glutamicum chaperonin groEL nucleotide sequence SEQ:34.

XX KW Corynebacterium glutamicum; chaperone; chaperonin; CpxB; groEL;
 KW fermentation; L-glutamic acid; thermophilic microbe; ds.

XX OS Corynebacterium glutamicum.

XX PN JP2001069979-A.

XX PD 21-MAR-2001.

XX PF 31-AUG-1999; 99JP-00245121.

XX PR 31-AUG-1999; 99JP-00245121.

XX PA (NISB) JAPAN TOBACCO INC.

XX PA (BEAB-) BE ABLE KK.

XX DR WPI; 2001-321175/34.

XX PT Preparation of L-glutamic acid by fermentation.

XX FS Example 1; Page 14; 18pp; Japanese.

XX The present invention describes an L-glutamic acid-producing microbe (I)
 CC or its mutant which expresses the molecular chaperone derived from a
 CC thermophilic microbe and produces stably L-glutamic acid at a temperature
 CC near the upper limit of optimum growth or higher. (I) or its mutant
 CC transformed by a recombinant DNA containing a gene encoding the molecular
 CC chaperone derived from a thermophilic microbe and a promoter operably
 CC associated with a gene (II) comprising: (a) a fully defined 1661 base
 CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
 CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,
 CC replaced or added in AAH21757; or (ii) at least one base is deleted,
 CC replaced or added in a fully defined 519 base sequence (AAH21768), and
 CC having molecular chaperone activity in (I). Also described is a method
 CC for the preparation of L-glutamic acid by fermentation in which the
 CC transformed (I) is used and cultured at a high temperature limiting the
 CC production of L-glutamic acid with the untransformed (I). The microbe can
 CC be used for the preparation of L-glutamic acid. The present sequence
 CC represents a nucleotide sequence of the Corynebacterium glutamicum
 CC chaperonin groEL, which is used in an example from the present invention

XX SQ Sequence 852 BP; 196 A; 217 C; 258 G; 181 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 4; Length 852;
 Best Local Similarity 95.5%; Pred. No. 2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
 |||||:|||||
 Db 802 TGAAGTGCCCGGATCTTGT 781

```
RESULT 6
AAV34610/C
ID AAV34610 standard; DNA; 927 BP.
XX
AC AAV34610;
XX
XX
XX 25-AUG-1998 (first entry)
XX
DE M. vaccae antigen GV-27B encoding DNA.
XX
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX
OS Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
FH 1. .927
FT CDS /*tag= a
FT /product= "GV-27B antigen"
FT /note= "The start and stop codons are not indicated"
XX
XX WO9808542-A2.
XX
XX 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX P-PSDB; AAW60146.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
XX detection, therapy and prevention of mycobacteria infections or as immune
XX response enhancers.
XX
XX Example 6; Page 117; 153pp; English.
XX
XX This DNA encodes a Mycobacterium vaccae antigen GV-27B. The invention
XX provides M. vaccae polypeptides that comprise an immunogenic portion of a
XX soluble M. vaccae antigen, or a variant, where the antigen induces an
XX immune response in patients previously exposed to a mycobacterium. Such
XX M. vaccae polypeptides can be used in methods for enhancing non-specific
XX immune response. The methods and products can be used for the detection,
XX treatment and prevention of infectious diseases caused by mycobacteria
XX such as M. vaccae, M. avium or M. tuberculosis. The products also have
XX the ability to induce cell proliferation and cytokine production (e.g.
XX interferon-gamma and interleukin-12 production) in T cells, NK cells, B
XX cells, or macrophages. They can be used for enhancing immune responses
XX for use in vaccines or immunotherapy of infectious diseases and cancers
XX
XX Sequence 927 BP; 157 A; 317 C; 317 G; 136 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 166 TGAAGGTGCCCGGATCTTGT 145
XX
RESULT 7
AAZ11345/C
ID AAZ11345 standard; DNA; 927 BP.
XX
XX
```

```
AC AAZ11345;
XX
XX 25-OCT-1999 (first entry)
XX
DE Nucleotide sequence of M. vaccae antigen GV-27B.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
OS
XX
XX WO9932634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 11-JUN-1998; 97US-00997362.
XX 17-SEP-1998; 98US-00156181.
XX 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
XX P-PSDB; AAY14893.
XX
XX Enhancing immune response to an antigen.
XX
XX Example 14; Page 191; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
XX M. vaccae proteins. The M. vaccae proteins may be employed to activate T
XX cells and natural killer cells, to stimulate the production of cytokines,
XX to enhance the expression of co-stimulatory molecules on dendritic cells
XX and monocytes, and to enhance dendritic cell maturation and function. The
XX proteins can be expressed by standard recombinant methodology.
XX Pharmaceutical compositions comprising the proteins or nucleic acid
XX sequences encoding the proteins can be used for the treatment,
XX prevention, and detection of disorders including infectious diseases,
XX immune disorders and cancer. In particular, the compounds and methods are
XX used for treatment of diseases of the respiratory system, such as
XX mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
XX sarcoidosis and lung cancers, and disorders of the skin such as
XX psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
XX alopecia areata, and skin cancers such as basal carcinoma, squamous cell
XX carcinoma and melanoma
XX
XX Sequence 927 BP; 157 A; 317 C; 317 G; 136 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 166 TGAAGGTGCCCGGATCTTGT 145
XX
RESULT 8
ABL36251/C
ID ABL36251 standard; DNA; 927 BP.
XX
XX ABL36251;
XX
```

DT 08-APR-2002 (first entry)
DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 116.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; gene; ds.
OS Mycobacterium vaccae.
XX US6328978-B1.
XX
XX 11-DEC-2001.
XX
XX 02-JUN-1999; 99US-00324542.
XX
XX 23-DEC-1997; 97US-00997080.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Tan PLJ, Prestidge R;
XX
XX WPI: 2002-138361/18.
XX P-PSDB; ABB73499.
XX
XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
XX Example 4; Col 125-128; 116pp; English.
XX
XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present invention is a
CC coding sequence described in the exemplification of the invention
XX
SQ Sequence 927 BP; 157 A; 317 C; 317 G; 136 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 166 TGAAGGTGCGCGGATCTTGT 145
RESULT 9
AAZ11372/c
ID AAZ11372 standard; DNA; 985 BP.
XX
XX AAZ11372;
AC
XX
XX 25-OCT-1999 (first entry)
DT
DE Nucleotide sequence of M. vaccae antigen GV-27B.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
OS

PN WO9932634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
PR 23-DEC-1997; 97US-00997080.
PR 23-DEC-1997; 97US-00997362.
PR 11-JUN-1998; 98US-00095855.
PR 17-SEP-1998; 98US-00156181.
PR 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI: 1999-430163/36.
XX P-PSDB; AAY14910.
XX
XX Enhancing immune response to an antigen.
XX
XX Claim 3; Page 215; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The
CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment,
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma
XX
SQ Sequence 985 BP; 167 A; 335 C; 339 G; 144 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 2; Length 985;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 167 TGAAGGTGCGCGGATCTTGT 146
RESULT 10
ABL36278/c
ID ABL36278 standard; DNA; 985 BP.
XX
XX ABL36278;
AC
XX
XX 08-APR-2002 (first entry)
DT
XX
XX M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 161.
DE
XX
XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; gene; ds.
XX
XX Mycobacterium vaccae.
OS
XX US6328978-B1.
XX
XX 11-DEC-2001.
XX

PF 02-JUN-1999; 99US-00324542.
XX
PR 23-DEC-1997; 97US-00997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX
DR WPI; 2002-138361/18.
DR P-PSDB; ABB73516.
XX
XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
XX Example 4; Col 171-174; 116pp; English.
XX
XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC coding sequence described in the exemplification of the invention
XX
SQ Sequence 985 BP; 167 A; 335 C; 339 G; 144 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 167 TGAAGGTGCGCGGATCTTGT 146
RESULT 11
ID ACC42533/c
XX ACC42533 standard; DNA; 985 BP.
AC
AC ACC42533;
XX
DT 26-AUG-2003 (first entry)
XX
XX Mycobacterium vaccae antigen GV-27B coding sequence, SEQ ID 16.
XX
XX Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
XX antidiabetic; antipruritic; dermatological; anti-inflammatory;
XX immune response; Notch signalling pathway; autoimmune disorder;
XX Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
XX apoptotic cell death; cell proliferation; genes; ds.
XX
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
PH CDS 2..985
FT /*tag= a
FT /partial
FT /product= "Antigen GV-27B"
FT /note= "No start codon given"
XX
XX WO2003013595-A1.
XX
XX 20-FEB-2003.
XX
XX 26-JUL-2002; 2002WO-NZ000135.
PF
XX 26-JUL-2001; 2001US-0308446P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA

XX Watson JD, Tan PLJ, Abernethy N;
XX
DR WPI; 2003-239567/23.
DR P-PSDB; ABP70893.
XX
XX Methods for modulating immune responses by modulating the Notch signaling
PT and Toll-like receptor signaling pathways, and treating e.g. autoimmune
PT disorders.
XX
XX Claim 7; Page 109; 136pp; English.
XX
XX The present invention relates to methods for modulating immune responses
CC by modulating the Notch signalling and Toll-like receptor signalling
CC pathways using compositions comprising mycobacteria antigens (ACC42518-
CC ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
CC immune responses and treating e.g. autoimmune disorders (such as multiple
CC sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
CC systemic lupus erythematosus, scleroderma), allergic disease and graft
CC rejection and also disorders characterised by undesired apoptotic cell
CC death or undesired cell proliferation
XX
SQ Sequence 985 BP; 167 A; 335 C; 339 G; 144 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 8; Length 985;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 167 TGAAGGTGCGCGGATCTTGT 146
RESULT 12
ID ADW23618/c
XX ADW23618 standard; DNA; 1496 BP.
XX
AC ADW23618;
XX
DT 10-MAR-2005 (first entry)
XX
XX HSP65 DNA.
XX
XX recombinant protein; vaccine; fusion protein; HSP65; ds.
XX
XX Unidentified.
XX
XX CN1462636-A.
XX
XX 24-DEC-2003.
XX
XX 30-MAY-2002; 2002CN-00122116.
PF
XX 30-MAY-2002; 2002CN-00122116.
PR
XX (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX
XX Wang L, Sun M, Yu Y;
PI WPI; 2004-239553/23.
XX
XX Vaccine of recombinant albumen for preventing and treating infection of
PT human hepatitis C virus.
PT
XX
XX Example 1; Page 14; 54pp; Chinese.
PS
XX
XX The invention relates to a recombinant protein vaccine which is a fusion
CC protein of BCG vaccine's heat shock protein 65 and the core antigen of
CC multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
CC and nucleotide sequence for coding it, the expression carrier containing
CC nucleotide sequence, the host cell containing expression carrier, the
CC preparing process of recombinant protein vaccine, the vaccine containing
CC recombinant protein for preventing and treating hepatitis C and a method

CC for detecting the activity of specifically killing T-lymphocytes by the
CC hepatitis C induced by vaccine and its cell model are disclosed. The
CC present sequence represents a HSP65 DNA.

SQ Sequence 1496 BP; 300 A; 456 C; 523 G; 217 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 13; Length 1496;
 Best Local Similarity 95.5%; Pred. No. 2.1;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TGAAGGTG	CCRCGGATCTT	22
Db	666	TGAAGGTG	CCCGCGGATCTT	645

RESULT 13
AAV34608/c
ID AAV34608 standard; DNA; 1569 BP.

AAV34608;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27 encoding DNA.

Mycobacterium vaccae; antigen; therapy; prevention; cytokine production; M. avium; M. tuberculosis; immune response enhancer; cell proliferation; mycobacteria infection; vaccine; cancer; ss.

OS *Mycobacterium vaccae*.

	Key	Location/Qualifiers
PH	CDS	1. 1569
FT		/tag= a
FT		/product= "GV-27 an
FT		/note= "thetstop co

PN WO9808542-A2.

05-MAR-1998.

PF 28-AUG-1997; 97WO-NZ000105.

PR 29-AUG-1996; 96US-00705347.

XX
XXXX
XX
SECRET (EYES)
TOP SECRET (EYES)

XX
XX

DR P-PSDB; AAW60144.

PT Mycobacterium vaccae polypeptides - used to develop products for use in
PT detection, therapy and prevention of mycobacteria infections or as immune
PT response enhancers.

PS Example 6; Page 114; 153pp; English.

This DNA encodes a *Mycobacterium vaccae* antigen GV-27. The invention provides *M. vaccae* polypeptides that comprise an immunogenic portion of a soluble *M. vaccae* antigen, or a variant, where the antigen induces an immune response in patients previously exposed to a *Mycobacterium*. Such *M. vaccae* polypeptides can be used in methods for enhancing non-specific immune response. The methods and products can be used for the detection, treatment and prevention of infectious diseases caused by *Mycobacteria* such as *M. vaccae*, *M. avium* or *M. tuberculosis*. The products also have the ability to induce cell proliferation and cytokine production (e.g. interferon-gamma and interleukin-12 production) in T cells, NK cells, B cells, or macrophages. They can be used for enhancing immune responses for use in vaccines or immunotherapy of infectious diseases and cancers

Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;

```
. Query Match      100.0%; Score 21.6; DB 2; Length 1569;
  Best Local Similarity 95.5%; Pred. No. 2.1;
  Matches 21; Conservative 1; Mismatches 0; Indels 0;
```

QY 1 TGAAGGTCCRCGGATCTTGTT 22
|||:|||||
Db 808 TGAAGGTCCRCGGATCTTGTT 78

RESULT 14

ID AA211343 standard; DNA; 1569 BP.

AC AAZ11343;

DT 25-OCT-1999 (first entry)

DE Nucleotide sequence of *M. vaccae* antigen GV-27.

Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous cell carcinoma; melanoma; ss.

OS *Mycobacterium vaccae*.

PN WO9932634-A2.

PD 01-JUL-1999.

PF 23-DEC-1998; 98WO-NZ000189.

PR 23-DEC-1997; 97US-00996624.

PR 23-DEC-1997; 97US-00997362.

PR 17-SEP-1998; 98US-00156181.

XX
XX

XX

XX
XX

DR P-PSDB; AAY14891.

PT Enhancing immune response to an antigen.

PS Example 14; Page 188-189; 243pp; English.

The invention provides heat-killed *Mycobacterium vaccae*, or recombinant *M. vaccae* proteins. The *M. vaccae* proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology.

sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, alopecia areata, and skin cancers such as basal carcinoma, squamous cell carcinoma and melanoma.

SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 2; Length 1569;

```
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 15
ABL36249/c
ID ABL36249 standard; DNA; 1569 BP.
XX
AC ABL36249;
XX
DT 08-APR-2002 (first entry)
XX
DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 113.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipeptidic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; gene; ds.
XX
OS Mycobacterium vaccae.
XX
PN US6328978-B1.
XX
PD 11-DEC-2001.
XX
PF 02-JUN-1999; 99US-00324542.
XX
PR 23-DEC-1997; 97US-00997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX WPI; 2002-138361/18.
XX P-PSDB; ABB73497.
XX
PT Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
XX Example 4; Col 121-124; 116pp; English.
XX
PS The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present invention is a
CC coding sequence described in the exemplification of the invention
XX
SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 16
AAH21763/c
ID AAH21763 standard; DNA; 1589 BP.
XX
AC AAH21763;

Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
Db 1533 TGAAGTGCCCGGATCTTGT 1512

RESULT 17
ACA38272/c
ID ACA38272 standard; DNA; 1620 BP.
XX
AC ACA38272;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #19929.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Mycobacterium bovis.
XX
PN WO200277183-A2.

14-AUG-2001 (first entry)
Corynebacterium glutamicum chaperonin groEL nucleotide sequence SEQ.34.
Corynebacterium glutamicum; chaperone; chaperonin; CpxB; groEL;
fermentation; L-glutamic acid; thermophilic microbe; ds.
Corynebacterium glutamicum.
JP2001069979-A.
21-MAR-2001.
31-AUG-1999; 99JP-00245121.
31-AUG-1999; 99JP-00245121.
(NISB ) JAPAN TOBACCO INC.
(BEAB-) BE ABLE KK.
WPI; 2001-321175/34.
Preparation of L-glutamic acid by fermentation.
Example 1; Page 15; 18pp; Japanese.
The present invention describes an L-glutamic acid-producing microbe (I)
or its mutant which expresses the molecular chaperone derived from a
thermophilic microbe and produces stably L-glutamic acid at a temperature
near the upper limit of optimum growth or higher. (I) or its mutant
transformed by a recombinant DNA containing a gene encoding the molecular
chaperone derived from a thermophilic microbe and a promoter operably
associated with a gene (ii) comprising: (a) a fully defined 1661 base
pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
protein comprising: (i) a base sequence in which 1-20 bases are deleted,
replaced or added in AAH21757; or (ii) at least one base is deleted,
replaced or added in a fully defined 519 base sequence (AAH21768), and
having molecular chaperone activity in (I). Also described is a method
for the preparation of L-glutamic acid by fermentation in which the
transformed (I) is used and cultured at a high temperature limiting the
production of L-glutamic acid with the untransformed (I). The microbe can
be used for the preparation of L-glutamic acid. The present sequence
represents a nucleotide sequence of the Corynebacterium glutamicum
chaperonin groEL, which is used in an example from the present invention
SQ Sequence 1589 BP; 363 A; 396 C; 469 G; 361 T; 0 U; 0 Other;
```

XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Heselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU34402.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 26142; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 21.6; DB 8; Length 1620;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787
|||||:|||||

RESULT 18
ADRI2623/c
ID ADRI2623 standard; DNA; 1620 BP.
XX
XX ADRI2623;

XX DT 04-NOV-2004 (first entry)
XX DE Gene vaccine nucleic acid #41.
XX XX
XX ds; gene; antimalarial; antitubercular; tuberculostatic; anti-HIV;
KW antibacterial; haemostatic; protozoacide; antiinflammatory;
KW neuroprotective; virucide; gene vaccine; ubiquitin; antigen;
KW intracellular parasite; protozoan parasite infection; malaria;
KW tuberculosis; toxoplasmosis; trypanosomiasis; AIDS;
KW cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis;
KW Ebola hemorrhagic fever; trypanosoma; Chagas disease;
KW Japanese encephalitis; influenza; rubella; dengue virus; poliomyelitis;
KW Herpes virus; severe acute respiratory syndrome.
XX
XX Unidentified.
XX OS
XX WO2004067040-A1.
XX FN
XX 12-AUG-2004.
XX PD
XX 30-JAN-2004; 2004WO-JP000975.
XX PF
XX 31-JAN-2003; 2003JP-00023507.
XX PR
XX (KYUS-) KYUSHU TILO CO LTD.
XX PA
XX Himeno K, Iehii K;
XX PI
XX WPI; 2004-594036/57.
XX DR P-PSDB; ADRI2624.
XX
XX Gene vaccine having nucleic acids encoding ubiquitin and antigen protein
PT of intracellular parasite, useful for treating parasite infections such
PT as malaria, tuberculosis, toxoplasmosis.
XX
XX Disclosure; SEQ ID NO 90; 266pp; Japanese.
XX
XX A gene vaccine (I) comprises nucleic acid sequence encoding ubiquitin,
CC and a nucleic acid sequence encoding the antigen protein of an
CC intracellular parasite containing T-cell target sequence. (I) is useful
CC for preventing or treating the disease resulting from intracellular
CC protozoan parasite infection such as malaria, tuberculosis,
CC toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection,
CC achlamydia disease, infections caused by Rickettsia, leishmaniasis,
CC Ebola hemorrhagic fever, Trypanosoma infections, Chagas disease, Japanese
CC encephalitis, influenza, rubella and dengue viral infections,
CC poliomyelitis, Herpes virus (alpha) infections, or severe acute
CC respiratory syndrome. This sequence represent a nucleic acid used in the
CC method of the invention.
XX
XX Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 21.6; DB 13; Length 1620;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787
|||||:|||||

RESULT 19
AAH51969/c
ID AAH51969 standard; DNA; 1623 BP.
XX
XX AAH51969;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 23.
XX
XX Drug target; growth; organism viability; characterisation; ds.

```

XX OS Mycobacterium tuberculosis.
XX PN WO200135317-A1.
XX PD 17-MAY-2001.
XX PF 13-NOV-2000; 2000WO-US031152.
XX PR 12-NOV-1999; 99US-0165086P.
XX PR 12-NOV-1999; 99US-0165124P.
XX PR 01-FEB-2000; 2000US-0179531P.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Eisenberg D, Rotstein SH, Marcotte EM;
XX DR WPI; 2001-329193/34.
XX DR P-PSDB; AAG81118.
XX PT Identifying nucleotide or polypeptide sequence for use as drug target,
XX PT involves providing algorithm that analyzes a functional relationship
XX PT between nucleotide or polypeptide sequences, and comparing the sequences.
XX PS Disclosure; Page 63-64; 207pp; English.
XX CC This invention relates to a method for identifying a nucleotide or
XX CC polypeptide sequence that may be a drug target, or essential for growth
XX CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX CC tuberculosis proteins which are potential drug targets. The DNA and
XX CC protein sequences are used to illustrate the method of the invention. The
XX CC method involves providing an unknown nucleotide or polypeptide sequences,
XX CC and comparing it to a number of sequences along with at least one
XX CC algorithm capable of analysing a functional relationship between
XX CC nucleotide and polypeptide sequences. The method is useful for
XX CC characterising the function of nucleic acids and polypeptides that may be
XX CC useful as a target for a drug or essential for the growth or viability of
XX CC an organism
XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 4; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 20
AAF25002/c
ID AAF25002 standard; DNA; 1623 BP.
XX AC AAF25002;
XX DT 30-APR-2001 (first entry)
XX DE Nucleotide sequence of M. bovis BCG heat shock protein 65 (Hsp65).
XX KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
XX KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; ss.
XX OS Mycobacterium bovis.
XX PH Key Location/Qualifiers
XX FT CDS 1..1623
XX FT /*tag= a
XX FT /product= "Hsp65"
XX PN WO200104344-A2.

PD 18-JAN-2001.
XX 10-JUL-2000; 2000WO-US018828.
XX PR 08-JUL-1999; 99US-0143757P.
XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI Siegel M, Chu NR, Mizzen LA;
XX DR WPI; 2001-138361/14.
XX DR P-PSDB; AAB31606.
XX PT Screening for compounds that stimulate Th1-like responses in CD4+ T
XX PT lymphocyte cells.
XX PS Example 2; Fig 1A-B; 88pp; English.
XX CC The present sequence encodes the Mycobacterium bovis BCG heat shock
XX CC protein (Hsp) 65. Hsp65 is used in the course of the invention. The
XX CC specification describes a method of determining whether a compound
XX CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
XX CC lymphocyte cells. The method comprises contacting naive lymphocytes in
XX CC vitro with a fusion protein comprising at least a fragment of Hsp, and
XX CC then detecting the Th1-like response exhibited by the cell sample. The
XX CC proteins which may be used in the method of the invention are Hsp65,
XX CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
XX CC compounds that stimulate Th1-like responses in response to microbial
XX CC pathogens
XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 5; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 21
ACA40326/c
ID ACA40326 standard; DNA; 1623 BP.
XX AC ACA40326;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #21983.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX OS Mycobacterium tuberculosis.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX KW Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX

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DR WPI; 2003-029926/02.
DR P-PSDB; ABU36456.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 28196; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 8; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787

RESULT 22
ACA37725/c
ID ACA37725 standard; DNA; 1623 BP.
XX
AC ACA37725;
XX
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #19382.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Mycobacterium avium.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US0009107.
XX
XX

21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU33855.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 25595; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1623 BP; 304 A; 545 C; 566 G; 208 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 8; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787

RESULT 23
ADN11336/c
ID ADN11336 standard; DNA; 1623 BP.
XX
AC ADN11336;
XX
XX
DT 17-JUN-2004 (first entry)
XX
XX DE
XX Chaperonin 60.2 coding sequence.
XX

KW Analgesic; heat shock protein; pain relief; chaperonin 60.2; gene; ds.
XX Mycobacterium tuberculosis.
OS
XX
XX Key Location/Qualifiers
FH 1. .1623
FT /*tag= a
FT /product= "Chaperonin 60.2"
XX
XX GB2391477-A.
XX
XX 11-FEB-2004.
XX
XX 05-NOV-2003; 2003GB-00025782.
XX
XX 08-NOV-2002; 2002GB-00026105.
XX
XX (HELP-) HELPERBY THERAPEUTICS LTD.
XX
XX Coates ARM;
XX
XX WPI; 2004-159054/16.
DR P-PSDB; ADN11337.
XX
XX Use of heat shock polypeptide and/or encoding nucleic acid sequence, in
XX manufacture of medicament for use in relief of pain such as backache,
XX headache, or earache.
XX
XX Claim 6; Fig 2; 39pp; English.
XX
XX The present invention relates to heat shock proteins (I) and their coding
XX sequences (II), which are useful in the manufacture of a medicament for
XX use in pain relief. (I) is a chaperonin derived from Mycobacterium
XX tuberculosis (ADN11335, ADN11337 or ADN11339). (I) and (II) are useful in
XX the manufacture of a medicament used as a pain relief, where the pain is
XX at least one chosen from backache, headache, toothache, earache,
XX arthritis, gout, soft tissue trauma, ligament/tendon traumatic damage,
XX broken bones, cancer, post operative pain, menstrual pain, obstetric
XX pain, renal tract pain, visceral pain, burns, abscesses and other
XX infections. The present sequence is a coding sequence for one such
XX chaperonin.
XX
XX Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 21.6; DB 12; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787
RESULT 24
AAZ11371/c
ID AAZ11371 standard; DNA; 1626 BP.
XX
XX AAZ11371;
XX
XX 25-OCT-1999 (first entry)
XX
XX Nucleotide sequence of M. vaccae antigen GV-27.
DE
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
XX dendritic cell maturation; infectious disease; immune disorder; cancer;
XX respiratory system; mycobacterial infection; allergy; tuberculosis;
XX leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
XX dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
XX squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
OS
XX
XX W09932634-A2.
XX
XX

XX
PD 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
PR 23-DEC-1997; 97US-00997080.
PR 23-DEC-1997; 97US-00997362.
PR 11-JUN-1998; 98US-00095855.
PR 17-SEP-1998; 98US-00156181.
PR 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
DR P-PSDB; AAY14909.
XX
XX Enhancing immune response to an antigen.
XX
XX Claim 3; Page 212-213; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
XX M. vaccae proteins. The M. vaccae proteins may be employed to activate T
XX cells and natural killer cells, to stimulate the production of cytokines,
XX to enhance the expression of co-stimulatory molecules on dendritic cells
XX and monocytes, and to enhance dendritic cell maturation and function. The
XX proteins can be expressed by standard recombinant methodology.
XX Pharmaceutical compositions comprising the proteins or nucleic acid
XX sequences encoding the proteins can be used for the treatment,
XX prevention, and detection of disorders including infectious diseases,
XX immune disorders and cancer. In particular, the compounds and methods are
XX used for treatment of diseases of the respiratory system, such as
XX mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
XX sarcoidosis and lung cancer, and disorders of the skin such as
XX psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
XX alopecia areata, and skin cancers such as basal carcinoma, squamous cell
XX carcinoma and melanoma
XX
XX Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 21.6; DB 2; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787
RESULT 25
ABL36277/c
ID ABL36277 standard; DNA; 1626 BP.
XX
XX ABL36277;
XX
XX 08-APR-2002 (first entry)
XX
XX M vaccae GroEL homologue GV-27 coding sequence SEQ ID NO: 159.
DE
XX
XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
XX alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
XX antipsoriatic; dermatological; antiinflammatory; antiallergic;
XX Th2 immune response; immunomodulatory; gene; ds.
XX
XX Mycobacterium vaccae.
XX
XX US6328978-B1.
XX
XX 11-DEC-2001.
XX
XX 02-JUN-1999; 99US-00324542.
XX
XX

```
XX 23-DEC-1997; 97US-00997080.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson JD, Tan PLJ, Prestidge R;
XX WPI; 2002-138361/18.
XX P-PSDB; ABB73515.
XX Inhibiting skin inflammation associated with skin disorder e.g.
XX psoriasis, by administering composition comprising delipidated and
XX deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
XX culture filtrate.
XX Example 4; Col 167-170; 116pp; English.
XX The present invention relates to a method of inhibiting skin inflammation
XX associated with a skin disorder selected from psoriasis, atopic
XX dermatitis and allergic contact dermatitis, which involves administering
XX a composition containing delipidated and deglycolipidated Mycobacterium
XX vaccae cells or M. vaccae culture filtrate. The skin disorder to be
XX treated may also include alopecia areata, and skin cancers such as basal
XX cell carcinoma, squamous cell carcinoma and melanoma. The composition
XX acts by inhibiting the Th2 immune response. The present sequence is a
XX coding sequence described in the exemplification of the invention
XX
XX Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 21.6; DB 6; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TGAAGTGCCCGGATCTTGT 22
Db 808 TGAAGTGCCCGGATCTTGT 787
RESULT 26
ACC42531/c
ID ACC42531 standard; DNA; 1626 BP.
XX ACC42531;
XX
XX 26-AUG-2003 (first entry)
XX Mycobacterium vaccae antigen GV-27 coding sequence, SEQ ID 14.
XX Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
XX antidiabetic; antipsoriatic; dermatological; anti-inflammatory;
XX immune response; Notch signalling pathway; autoimmune disorder;
XX Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
XX apoptotic cell death; cell proliferation; gene; ds.
XX
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
XX CDS 1..1626
XX /*tag= a
XX /product= "Antigen GV-27"
XX
XX WO2003013595-A1.
XX
XX 20-FEB-2003.
XX
XX 26-JUL-2002; 2002WO-NZ000135.
XX
XX 26-JUL-2001; 2001US-0308446P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson JD, Tan PLJ, Abernethy N;
XX
```

```
DR WPI; 2003-239567/23.
DR P-PSDB; ABP70891.
XX
XX Methods for modulating immune responses by modulating the Notch signaling
XX and Toll-like receptor signaling pathways, and treating e.g. autoimmune
XX disorders.
XX Claim 7; Page 108-109; 136pp; English.
XX
XX The present invention relates to methods for modulating immune responses
XX by modulating the Notch signalling and Toll-like receptor signalling
XX pathways using compositions comprising mycobacteria antigens (ACC42518-
XX ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
XX immune responses and treating e.g. autoimmune disorders (such as multiple
XX sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
XX systemic lupus erythematosus, scleroderma), allergic disease and graft
XX rejection and also disorders characterised by undesired apoptotic cell
XX death or undesired cell proliferation
XX
XX Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 21.6; DB 8; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TGAAGTGCCCGGATCTTGT 22
Db 808 TGAAGTGCCCGGATCTTGT 787
RESULT 27
ACC70275/c
ID ACC70275 standard; DNA; 1626 BP.
XX ACC70275;
XX
XX 11-AUG-2003 (first entry)
XX
XX Nucleotide sequence of the Rhodococcus equi GroEL2 protein.
XX
XX GroEL protein; protein aggregation; protein folding; immune response;
XX antigen; pathogenic infection; gene; ss.
XX
XX Rhodococcus equi.
XX
XX Key Location/Qualifiers
XX CDS 1
XX /*tag= a
XX /product= "GroEL2"
XX
XX WO2003035676-A1.
XX
XX 01-MAY-2003.
XX
XX 25-OCT-2002; 2002WO-AU001460.
XX
XX 26-OCT-2001; 2001AU-00008523.
XX
XX (UYSA-) UNIV SOUTH AUSTRALIA.
XX (MEDV-) MEDVET SCI PTY LTD.
XX (RURA-) RURAL IND RES & DEV CORP.
XX
XX Vanniasinkam T, Barton M, Heuzenroeder MW;
XX
XX WPI; 2003-482030/45.
XX P-PSDB; ABR55530.
XX
XX New GroEL protein, useful for preparing a composition for preventing or
XX treating pathogenic infections.
XX
XX Disclosure; Fig 1; 77pp; English.
XX
XX The present sequence encodes a GroEL protein. The groEL2 gene is highly
```

CC conserved between species, and the protein facilitates the correct
CC folding of various bacterial proteins as well as prevent the aggregation
CC of denatured proteins by an ATP-dependent mechanism. The specification
CC describes a chimeric protein, consisting of a GroEL protein which has a
CC modification or analogue comprising a surface exposed exogenous amino
CC acid sequence inserted to it. The exogenous amino acid sequence is
CC configured to elicit an immune response specifically reactive to the
CC antigenic determinant. The chimeric protein is useful for preparing a
CC composition for preventing or treating pathogenic infections

XX SQ Sequence 1626 BP; 300 A; 544 C; 549 G; 233 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 9; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRGGATCTTGTT 22
|||||:|||||
Db 808 TGAAGGTGCCACGGATCTTGTT 787

RESULT 28
AD051196/c
ID AD051196 standard; DNA; 1626 BP.
XX AC AD051196;
XX DT 12-AUG-2004 (first entry)
DE Staphylococcus coelicolor cpn60 gene.
XX KW Chaperonin 60; cpn60; microbe detection; gene; ds.
XX OS Staphylococcus coelicolor.
XX FH Key Location/Qualifiers
FT primer_bind complement(244..269)
FT /*tag= a
FT primer_bind 829..854
FT /*tag= b
FT /*note= "Universal cpn60 primer binds at this location"
FT /*note= "Universal cpn60 primer binds at this location"
XX US2004101826-A1.
XX 27-MAY-2004.
XX 18-MAR-2003; 2003US-00392041.
XX 27-NOV-2002; 2002US-00306113.
XX (JONE/) JONES A M.
XX (ROBE/) ROBEY W W.
XX Jones AM, Robey WW;
XX WPI; 2004-399671/37.
XX GENBANK; AL39121.
XX Monitoring high-risk environments for presence or absence of microbes, by
XX providing a sample and detecting presence or absence of cpn60 markers in
XX the sample, which indicates the presence of microbes.
XX Disclosure; SEQ ID NO 3; 30pp; English.
XX The invention relates to methods for monitoring high-risk environments
XX for the presence or absence of microbes by detecting the presence or
XX absence of chaperonin 60 (cpn60) marker in the sample. The method is
XX useful for monitoring the presence of one or more microbes such as
XX bacteria, protozoan microbe, fungi and rickettsiae microbe in high-risk
XX environment such as butcher shop, grocery store, restaurant, cafeteria,
XX convenience store, entertainment facility, school and medical
XX environment. The present sequence is Staphylococcus coelicolor cpn60

CC gene. This sequence is used to illustrate the method of the invention.
XX SQ Sequence 1626 BP; 303 A; 585 C; 532 G; 206 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 12; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRGGATCTTGTT 22
|||||:|||||
Db 814 TGAAGGTGCCGGATCTTGTT 793

RESULT 29
AD050828/c
ID AD050828 standard; DNA; 1626 BP.
XX AC AD050828;
XX DT 12-AUG-2004 (first entry)
DE S. coelicolor chaperonin protein 60, cpn60, gene.
XX KW Chaperonin protein 60; cpn60; ds; gene; GroEL; HSP60; heat shock protein;
XX food poisoning; animal processing operation; microbial load;
XX enteric bacteria; food-born illness.
XX OS Staphylococcus coelicolor.
XX PN US2004101917-A1.
XX PD 27-MAY-2004.
XX PF 21-MAR-2003; 2003US-00394763.
XX 27-NOV-2002; 2002US-00306113.
XX (ROBE/) ROBEY W W.
XX (JONE/) JONES A M.
XX Robey WW, Jones AM;
XX WPI; 2004-459891/43.
XX Management of an animal e.g. chicken processing operation comprises
XX determining microbial load of each biological sample from animal and
XX scheduling processing of the animals based on the microbial load.
XX Disclosure; SEQ ID NO 3; 21pp; English.
XX The invention relates to managing an animal processing operation
XX involving determining the microbial load, e.g. total number of enteric
XX bacteria of each biological sample, from animals and scheduling
XX processing of animals based on the microbial load. Scheduling comprises
XX ranking the animals from lowest to highest microbial load and integrating
XX the ranking with factors selected from number and weight of animals to be
XX processed, time of delivery etc. Also included are a system for
XX scheduling animals for processing and a computer readable storage medium
XX having instruction stored for causing a programmable processor to rank
XX animals from lowest to highest microbial load. The biological samples are
XX gastrointestinal tract sample (e.g. mucus, mucosal tissue and/or faeces)
XX or periodontal samples (e.g. blood, urine, saliva, sputum or semen). The
XX microbes are bacteria, protozoa or fungi. Scheduling comprises ranking
XX animals from lowest microbial load to highest microbial load and
XX integrating ranking with one or more factors selected from the group
XX consisting of number of animals to be processed, weight targets of
XX animals, proximity of animals to animal processing facility, and time of
XX delivery of animals to animal processing facility. The method further
XX comprises determining the microbial profile of each said biological
XX sample and scheduling processing of the plurality of animals based at
XX least in part on microbial load and microbial profile. Determining the
XX microbial profile comprises histological analysis, immunological
XX analysis, genetic fingerprinting, ribosomal genotyping, or cpn60

CC genotyping. The method can be used for any farmed animal that will be
CC subjected to mass processing. Effectively reduces human food-borne illness
CC i.e. food poisoning. Scheduling of animals minimises contamination during
CC the processing. The present sequence is an enteric bacteria cpn60
CC (Chaperonin protein 60 also known as Hsp60 and GroEL) gene used in the
CC method of the invention to genotype/identify enteric bacteria.

XX Sequence 1626 BP; 303 A; 585 C; 532 G; 206 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 21.6; DB 12; Length 1626;

Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22

DB 814 TGAAGTGCCCGGATCTTGT 793

RESULT 30

ADS64696/c

ID ADS64696 standard; DNA; 1626 BP.

XX AC

ADS64696;

XX DT 16-DEC-2004 (first entry)

XX DE

Streptomyces coelicolor cpn60 gene.

XX KW

GroEL; cpn60; hsp60; microbe detection; gene; da.

XX OS

Streptomyces coelicolor.

XX FH

Key Location/Qualifiers

FT primer_bind complement(244..269)

FT /tag= a

FT primer_bind /note= "Universal cpn60 primer binds at this location"

FT 829..854

FT /tag= b

FT primer_bind /note= "Universal cpn60 primer binds at this location"

XX PN

US2004185446-A1.

XX PD

23-SEP-2004.

XX PF

18-MAR-2003; 2003US-00392387.

XX PR

18-MAR-2003; 2003US-00392387.

XX PA

(JONES/) JONES A M.

PA (ROBE/) ROBEY W W.

PA (HEMM/) HEMMINGSEN S.

PA (HILL/) HILL J.

PA (KES/) VAN KESSEL A.

XX PI

Jones AM, Robey WW, Hemmingesen S, Hill J, Van Kessel A;

XX WPI

2004-676187/66.

DR GENBANK; AL939121.

XX PT

Quantifying microbial species in a biological sample, comprises
PT subjecting the sample to amplification in the presence of cpn60 primers
PT and quantifying the amplified product, which correlates with the amount
PT of microbial species.

XX PS

Disclosure; SEQ ID NO 3; 28pp; English.

XX CC

The invention relates to cpn60 (also known as hsp60 or GroEL) nucleic
CC acid-based methods for quantifying microbial species in a biological
CC sample. The method comprises subjecting the sample to amplification in
CC the presence of cpn60 primers and quantifying the amplified product,
CC which correlates with the amount of microbial species. The method is
CC useful for quantifying the amount of one or more microbial species in a
CC biological or non-biological sample. The present sequence is the

CC Streptomyces coelicolor cpn60 gene.

XX SQ Sequence 1626 BP; 303 A; 585 C; 532 G; 206 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 13; Length 1626;

Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22

DB 814 TGAAGTGCCCGGATCTTGT 793

RESULT 31

ACA29800/c

ID ACA29800 standard; DNA; 1638 BP.

XX AC

ACA29800;

XX DT 19-JUN-2003 (first entry)

XX DE

Prokaryotic essential gene #11457.

XX KW

Antisense; ds; prokaryotic essential gene; cell proliferation;

XX KW

drug design; gene.

XX OS

Corynebacterium diphtheriae.

XX PN

WO200277183-A2.

XX PD

03-OCT-2002.

XX PF

21-MAR-2002; 2002WO-US009107.

XX PR

21-MAR-2001; 2001US-00815242.

XX PR

06-SEP-2001; 2001US-00948993.

XX PR

25-OCT-2001; 2001US-0342923P.

XX PR

08-FEB-2002; 2002US-00072851.

XX PR

06-MAR-2002; 2002US-0362699P.

XX PA

(ELIT-) ELITRA PHARM INC.

XX PI

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI

2003-029926/02.

XX P-PSDB; ABU25930.

XX PS

New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 17670; 1766pp; English.

XX CC

The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences

XX SQ Sequence 1638 BP; 353 A; 418 C; 497 G; 370 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 8; Length 1638;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 823 TGAAGTGCCCGGATCTTGT 802

RESULT 32

AAH67951/c
ID AAH67951 standard; DNA; 1644 BP.

XX AC AAH67951;

XX DT 26-SEP-2001 (first entry)

XX DE C glutamicum coding sequence fragment SEQ ID NO: 2986.

XX KW Corynebacterium; amino acid synthesis; vitamin; saccharide;

XX KW organic acid synthesis; ds.

XX OS Corynebacterium glutamicum.

XX PN EP1108790-A2.

XX PD 20-JUN-2001.

XX PF 18-DEC-2000; 2000EP-00127688.

XX PR 16-DEC-1999; 99JP-00377484.

XX PR 07-APR-2000; 2000JP-00159162.

XX PR 03-AUG-2000; 2000JP-00280988.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX XX WPI; 2001-376931/40.

XX DR P-PSDB; AAG92732.

XX PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.

XX PS Claim 8; SEQ ID NO 2986; 246pp + Sequence Listing; English.

XX CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of corynebacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Corynebacterium, and identifying a homologue of a gene derived from
CC corynebacterium. Corynebacterium bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office

XX SQ Sequence 1644 BP; 346 A; 454 C; 500 G; 344 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 5; Length 1644;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 823 TGAAGTGCCCGGATCTTGT 802

RESULT 33

AAT14265/c

ID AAT14265 standard; DNA; 1647 BP.

XX AC AAT14265;

XX DT 16-OCT-2003 (revised)

XX DT 16-SEP-1996 (first entry)

XX DE Brevibacterium flavum MJ-233 GroEL gene.

XX KW GroEL; coryneform bacteria; recombinant; chaperonin; protein; folding;
XX KW ds.

XX OS Brevibacterium flavum; MJ-233.

XX FH Key Location/Qualifiers

XX FT CDS 1..1650

XX FT /*tag= a

XX FT /product= "GroEL_protein"

XX PN JP08070873-A.

XX PD 19-MAR-1996.

XX PF 07-SEP-1994; 94JP-00213483.

XX PR 07-SEP-1994; 94JP-00213483.

XX PA (MITU) MITSUBISHI CHEM CORP.

XX XX WPI; 1996-203153/21.

XX DR P-PSDB; AAR94368.

XX PT DNA fragment contg. gene encoding GroEL protein - derived from Coryneform
PT bacteria, used for recombinant prodn. of GroEL protein and in genetic
PT engineering of bacteria.

XX PS Claim 5; Page 8-10; 11pp; Japanese.

XX CC AAT14265 is the GroEL gene derived from the coryneform bacterium,
CC Brevibacterium flavum strain MJ-233. The gene may be used for the
CC recombinant prodn. of the GroEL protein. The GroEL protein is a
CC chaperonin protein, the coryneform equivalent of hsp60, which ensures
CC that other cellular proteins are folded correctly. Fragments of the GroEL
CC gene are useful for genetic engineering of bacteria to increase activity,
CC extend life and increase the formation and secretion of an objective
CC protein. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 1647 BP; 349 A; 458 C; 497 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 2; Length 1647;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 823 TGAAGTGCCCGGATCTTGT 802

```

RESULT 34
AAD57198/c
ID AAD57198 standard; DNA; 1701 BP.
XX
XX AAD57198;
AC
XX
DT 06-NOV-2003 (first entry)
XX
DE Mycobacterium avium subspecies paratuberculosis protein gene #11.
XX
KW Immunogenic fragment; vaccine; Map infection; wild-type infection;
KW antibacterial; gene; ds.
XX
OS Mycobacterium avium.
XX
FH Key Location/Qualifiers
FT CDS 76..1701
FT /*tag= a
FT /product= "Protein"
XX
PN WO2003058248-A2.
XX
XX 17-JUL-2003.
XX
XX 13-JAN-2003; 2003WO-NL000020.
XX
XX 11-JAN-2002; 2002EP-00075089.
XX
XX (IDLE-) ID-LELYSTAD INST DIERHOUDERIJ EN DIERGEZ.
XX
XX Willemssen PTJ, Westerveen SF, Bakker D, Van Zijderveld FG;
XX Thole JER;
XX
XX WPI: 2003-598398/56.
XX P-PSDB; AAE37881.
XX
PT Novel Mycobacterium avium subspecies paratuberculosis protein, useful as
PT vaccine for combating the bacterial infection, and for diagnosing the
PT infection.
XX
XX Disclosure; Page 84-86; 88pp; English.
XX
XX The invention relates to Mycobacterium avium subspecies paratuberculosis
XX protein or an immunogenic fragment of the protein. The invention is
XX useful in the manufacture of a vaccine for combating Map infection. The
XX nucleic acids, the proteins and antibodies are also useful in
XX diagnostics. The vaccines are also suitable as marker vaccines, in that
XX it allows discrimination of vaccinated and field-infected mammals on the
XX basis of characteristic antibody panel induced by wild-type infection.
XX The present sequence is Mycobacterium avium subspecies paratuberculosis
XX protein gene
XX
XX Sequence 1701 BP; 318 A; 569 C; 591 G; 223 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 9; Length 1701;
XX Best Local Similarity 95.5%; Pred. No. 2.1;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 TGAAGGTGCCCGGATCTTGT 22
DB 883 TGAAGGTGCCCGGATCTTGT 862
XX
RESULT 35
ACC49833/c
ID ACC49833 standard; DNA; 1752 BP.
XX
XX ACC49833;
AC
XX
DT 27-JUN-2003 (first entry)
XX
DE Human recombinant protein vaccine gene.
XX
XX Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
XX antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..1752
XX /*tag= a
XX
XX CNI362263-A.
XX
XX 07-AUG-2002.
XX
XX 15-NOV-2001; 2001CN-00134935.
XX
XX 04-JAN-2001; 2001CN-00100380.
XX (BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
XX
XX Wang L, Li D, Yu Y;
XX
XX WPI: 2003-230415/23.
XX P-PSDB; ABR40246.
XX
XX Recombinant protein vaccine for preventing and treating human prostate
XX cancer.
XX
XX Claim 7; Page 15-19; 35pp; Chinese.
XX
XX The invention relates to a novel recombinant protein vaccine, a fusion
XX protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of
XX human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The
XX vaccine of the invention is useful for treating and preventing carcinoma
XX of prostate. The invention also discloses the genes encoding the
XX recombinant protein vaccines. The present sequence is used in the
XX exemplification of the invention
XX
XX Sequence 1752 BP; 356 A; 535 C; 595 G; 266 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 8; Length 1752;
XX Best Local Similarity 95.5%; Pred. No. 2.1;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 TGAAGGTGCCCGGATCTTGT 22
DB 808 TGAAGGTGCCCGGATCTTGT 787
XX
RESULT 36
ADX05272/c
ID ADX05272 standard; DNA; 1761 BP.
XX
XX ADX05272;
AC
XX
DT 21-APR-2005 (first entry)
XX
DE HSP65-MUC1-ME fusion protein coding sequence, SEQ ID 1.
XX
XX Fusion protein; Cytostatic; Gene Therapy; heat shock protein 65; HSP65;
XX mucin; MUC1; carcinoma; gene; ds.
XX
XX Mycobacterium bovis BCG.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..1761
XX /*tag= a
XX /product= "HSP65-MUC1-ME fusion protein"
XX
XX US2005031649-A1.

```

```

XX PD 10-FEB-2005.
XX XX
XX PF 06-AUG-2003; 2003US-00635211.
XX XX
XX PR 06-AUG-2003; 2003US-00635211.
XX XX
XX PA (YUYV/) YU Y.
XX PA (LIHH/) LI H.
XX PA (WANG/) WANG L.
XX XX
XX PI Yu Y, Li H, Wang L;
XX XX
XX DR WPI; 2005-131970/14.
XX DR P-PSDB; ADX05273.
XX XX
XX PT New recombinant fusion protein comprises Bacillus Calmette Guerin (BCG)
XX PT heat shock protein 65 and 1-5 copies of an epitope of MUC1, useful for
XX PT treating or preventing human MUC1 expressing carcinomas.
XX XX
XX PS Claim 31; SEQ ID NO 1; 19pp; English.
XX XX
XX CC The present invention relates to a novel recombinant fusion protein
XX CC (HSP65-MUC1-ME, ADX05273) which comprises Bacillus Calmette Guerin (BCG)
XX CC heat shock protein 65 (HSP65) and an epitope of mucin protein MUC1 (MUC1-
XX CC ME). The BCG HSP65 is located at the amino terminal portion of the fusion
XX CC protein and the epitope of MUC1 is located at the carboxy terminal
XX CC portion of the fusion protein. The MUC1 epitope can generate MUC1
XX CC specific cytotoxic T lymphocytes. The recombinant fusion protein is
XX CC useful for treating or preventing human carcinomas, preferably MUC1
XX CC expressing carcinomas. The present sequence is the coding sequence for
XX CC the fusion protein of the invention.
XX XX
XX SQ Sequence 1761 BP; 338 A; 543 C; 608 G; 272 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 21.6; DB 14; Length 1761;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 37
ADK68629/c
ID ADK68629 standard; cDNA; 1800 BP.
XX AC
XX AC ADK68629;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE HSP65-MUC1 antigen CTL epitope related cDNA #1.
XX XX
XX KW Human breast cancer; Mycobacterium bovis; heat shock protein 65; BCG;
XX KW HSP65; cytotoxic T lymphocyte; CTL; MUC1; HSP65-MUC1 antigen CTL epitope;
XX KW gene; ss.
XX XX
XX OS Unidentified.
XX XX
XX PN CN1368384-A.
XX XX
XX PD 11-SEP-2002.
XX XX
XX XX 08-FEB-2001; 2001CN-00102614.
XX XX
XX PF 08-FEB-2001; 2001CN-00102614.
XX XX
XX PA (DIWE-) DIWEIHUAYU BIO TECHNOLOGY CO LTD BEIJING.
XX XX
XX PI Yu Y, Li H;
XX XX
XX DR WPI; 2003-854662/80.
XX XX

DR P-PSDB; ADK68630.
XX PT Genetically engineered vaccine of MUC-1 antigen for human breast cancer.
XX XX
XX PS Claim 1; SEQ ID NO 1; 14pp; Chinese.
XX XX
XX CC The invention relates to a method of preparation of a genetically
XX CC engineered vaccine for preventing and treating human breast cancer. The
XX CC method comprises fusing the coding gene of the Mycobacterium bovis heat
XX CC shock protein 65 (BCG HSP65) with the cytotoxic T lymphocyte (CTL)
XX CC epitope gene of MUC1 (antigen cell expressed by human breast cancer
XX CC cells) and the HSP65-MUC1 antigen CTL epitope is expressed in Escherichia
XX CC coli cells. This sequence represents DNA used in the method of the
XX CC invention.
XX XX
XX SQ Sequence 1800 BP; 347 A; 561 C; 616 G; 276 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 21.6; DB 10; Length 1800;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 38
ACC49834/c
ID ACC49834 standard; DNA; 1914 BP.
XX AC
XX AC ACC49834;
XX XX
XX DT 27-JUN-2003 (first entry)
XX XX
XX DE Human recombinant protein vaccine gene.
XX XX
XX KW Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
XX KW antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FH Key
XX FT CDS
XX FT 1..1914
XX FT /*tag= a
XX XX
XX PN CN1362263-A.
XX XX
XX PD 07-AUG-2002.
XX XX
XX PF 15-NOV-2001; 2001CN-00134935.
XX XX
XX PR 04-JAN-2001; 2001CN-00100380.
XX XX
XX PR (BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
XX PA Wang L, Li D, Yu Y;
XX PI
XX XX
XX DR WPI; 2003-230415/23.
XX DR P-PSDB; ABR40247.
XX XX
XX PT Recombinant protein vaccine for preventing and treating human prostate
XX PT cancer.
XX XX
XX PS Claim 7; Page 23-26; 35pp; Chinese.
XX XX
XX CC The invention relates to a novel recombinant protein vaccine, a fusion
XX CC protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of
XX CC human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The
XX CC vaccine of the invention is useful for treating and preventing carcinoma
XX CC of prostate. The invention also discloses the genes encoding the
XX CC recombinant protein vaccines. The present sequence is used in the
XX CC exemplification of the invention

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XX SQ Sequence 1914 BP; 397 A; 576 C; 633 G; 308 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 8; Length 1914;
 Best Local Similarity 95.5%; Pred. No. 2.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
 DB 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 39
 AAF25012/C
 ID AAF25012 standard; DNA; 1920 BP.
 AC AAF25012;
 XX 30-APR-2001 (first entry)
 DE Nucleotide sequence of Hsp65-E7 fusion protein.
 KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein; ss.
 XX Synthetic.
 OS Mycobacterium bovis.
 OS Human papillomavirus.
 XX Key Location/Qualifiers
 FT 1..1920
 FT /*tag= a
 FT /product= "Hsp65-E7 fusion protein"
 XX WO200104344-A2.
 PD 18-JAN-2001.
 PF 10-JUL-2000; 2000WO-US018828.
 PR 08-JUL-1999; 99US-0143757P.
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 PI Siegel M, Chu NR, Mizzen LA;
 DR WPI: 2001-138361/14.
 DR P-PSDB; AAB31609.
 XX Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
 PS Example 5; Fig 4A-B; 88pp; English.
 CC The present sequence encodes a fusion protein comprising a Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens

SQ Sequence 1920 BP; 415 A; 551 C; 638 G; 316 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 5; Length 1920;
 Best Local Similarity 95.5%; Pred. No. 2.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
 DB 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 40
 AAF25019/C
 ID AAF25019 standard; DNA; 1947 BP.
 AC AAF25019;
 XX 30-APR-2001 (first entry)
 DE Nucleotide sequence of Hsp65-E7 fusion protein.
 KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein; ss.
 XX Synthetic.
 OS Mycobacterium bovis.
 OS Human papillomavirus.
 XX Key Location/Qualifiers
 FT 1..1947
 FT /*tag= a
 FT /product= "Hsp65-E7 fusion protein"
 XX WO200104344-A2.
 PD 18-JAN-2001.
 PF 10-JUL-2000; 2000WO-US018828.
 PR 08-JUL-1999; 99US-0143757P.
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 PI Siegel M, Chu NR, Mizzen LA;
 DR WPI: 2001-138361/14.
 DR P-PSDB; AAB31614.
 XX Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
 PS Example 11; Fig 10A-B; 88pp; English.
 CC The present sequence encodes a fusion protein comprising a Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens

SQ Sequence 1947 BP; 417 A; 557 C; 653 G; 320 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 5; Length 1947;
 Best Local Similarity 95.5%; Pred. No. 2.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
 DB 1132 TGAAGGTGCCCGGATCTTGT 1111

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RESULT 41
ADW23606/c
ID ADW23606 standard; DNA; 1965 BP.
XX AC ADW23606;
XX DT 10-MAR-2005 (first entry)
XX DE Hepatitis C virus related DNA SEQ ID NO 6.
XX KW recombinant protein; vaccine; fusion protein; hepatitis C; ds; gene.
XX OS Synthetic.
XX PN CN1462636-A.
XX PD 24-DEC-2003.
XX PF 30-MAY-2002; 2002CN-00122116.
XX PR 30-MAY-2002; 2002CN-00122116.
XX PA (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX PI Wang L, Sun M, Yu Y;
XX DR WPI; 2004-239553/23.
XX DR P-PSDB; ADW23607.
XX PT Vaccine of recombinant albumen for preventing and treating infection of
XX PT human hepatitis C virus.
XX PS Claim 9; SEQ ID NO 6; 54pp; Chinese.
XX CC The invention relates to a recombinant protein vaccine which is a fusion
CC protein of BCG vaccine's heat shock protein 65 and the core antigen of
CC multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
CC and nucleotide sequence for coding it, the expression carrier containing
CC nucleotide sequence, the host cell containing expression carrier, the
CC preparing process of recombinant protein vaccine, the vaccine containing
CC recombinant protein for preventing and treating hepatitis C and a method
CC for detecting the activity of specifically killing T-lymphocytes by the
CC hepatitis C induced by vaccine and its cell model are disclosed. The
CC present sequence represents a hepatitis C virus related DNA.
XX SQ Sequence 1965 BP; 405 A; 593 C; 658 G; 309 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 13; Length 1965;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 42
ADN00588/c
ID ADN00588 standard; DNA; 1980 BP.
XX AC ADN00588;
XX DT 17-JUN-2004 (first entry)
XX DE BCG vaccine HSP65-MOMP fusion protein coding sequence, SEQ ID 3.
XX KW Antibacterial; gynaecological; protein vaccine;
XX KW BCG vaccine heat shock protein 65; major outer membrane protein; MOMP;
XX KW Chlamydia infection; urogenital infection; gene; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX Key 1.2016
XX CDS /*tag= a
XX /product= "BCG-HER2 fusion protein"

Query Match 100.0%; Score 21.6; DB 12; Length 1980;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 43
ADK72374/c
ID ADK72374 standard; DNA; 2016 BP.
XX AC ADK72374;
XX DT 06-MAY-2004 (first entry)
XX DE BCG-HER-2 fusion gene construct for breast cancer vaccine treatment.
XX KW vaccine; fusion protein; BCG; heat-shock protein 65; HSP65; HER-2;
XX KW antigen; breast cancer; gene; ds.
XX OS Homo sapiens.
XX OS Bacillus sp.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX CDS 1.2016
XX /*tag= a
XX /product= "BCG-HER2 fusion protein"
XX CN1410127-A.
XX PD 16-APR-2003.
XX PF 10-OCT-2001; 2001CN-00136347.
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XX 10-OCT-2001; 2001CN-00136347.
XX (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX Wang L, Wang X, Yu Y;
XX WPI; 2004-000146/01.
XX P-PSDB; ADK72375.
XX Tuberculosis vaccine heat reversal protein 65 and multi-epitope HER-2
XX antigen fusion protein recombinant protein vaccine.
XX Claim 6; SEQ ID NO 5; 30pp; Chinese.
XX The invention relates to a novel recombinant protein vaccine which is a
XX fusion protein prepared from the BCG vaccine heat-shock protein 65 and
XX multi-epitope HER-2 antigen and can be used for effectively preventing
XX and treating breast cancer. The gene for coding the recombinant protein
XX vaccine is also disclosed. This sequence represents the coding sequence
XX for the BCG-HER2 fusion protein used in the vaccine of the invention.
XX
XX Sequence 2016 BP; 417 A; 603 C; 658 G; 338 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 12; Length 2016;
XX Best Local Similarity 95.5%; Pred. No. 2.2;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 44
ABS54448/c
ID ABS54448 standard; DNA; 2073 BP.
XX
AC ABS54448;
XX
DT 07-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX
DE BCG Hsp65/mutant HBV core antigen, HepCorT(151/97F)Hsp65, DNA.
XX
KW HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
KW Hsp65; immune response; non-cytotoxic DNA virus; vaccine; morbidity;
KW mortality; infection; gene therapy; hepatitis; cirrhosis;
KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
KW antiinflammatory; BCG; chimera; mutant.
XX
OS Hepatitis B virus.
OS Mycobacterium bovis.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..2073
XX /*tag= a
XX /product= "HepCorT(151/97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2001; 2001US-0266733P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizzen L, Liu H, Siegel M;
XX WPI; 2002-706903/76.
XX

P-PSDB; ABG70777.
Novel isolated fusion protein useful for treating hepatitis B virus
infection in a subject, comprises a stress protein or its portion, and a
hepatitis B virus core antigen.
Example 1; Fig 9; 58pp; English.
The invention discloses an isolated fusion protein, and the
polynucleotide encoding it, that comprises a stress protein (e.g.
Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
when administered to an individual, induces or enhances an immune
response against the HBV core antigen. HBV is a non-cytotoxic DNA virus
against which a vaccine has been developed. However, due to the morbidity
and mortality arising from chronic HBV infection occurring over a period
of decades, the impact of vaccinations will not be apparent for some time
yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
therapy and as a pharmaceutical composition for inducing or enhancing an
immune response against an HBV core antigen in a subject for treating an
HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
The sequence presented is the DNA encoding the truncated hepatitis B
virus core antigen fused to the N-terminus of the M. bovis variant
Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65,
HepCorT(151/97F)Hsp65. The core antigen the DNA encodes has been
truncated to include residues 1 to 151 and has had an amino acid changed
from the wild-type sequence. (Updated on 07-AUG-2003 to correct OS
field.)
XX
XX Sequence 2073 BP; 433 A; 595 C; 665 G; 380 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 6; Length 2073;
XX Best Local Similarity 95.5%; Pred. No. 2.2;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 1258 TGAAGGTGCGCGGATCTTGT 1237

RESULT 45
ABS54447/c
ID ABS54447 standard; DNA; 2130 BP.
XX
AC ABS54447;
XX
DT 07-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX
DE BCG Hsp65/mutant HBV core antigen, hisHepCorT(149/87S97F)Hsp65, DNA.
XX
KW HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
KW Hsp65; immune response; non-cytotoxic DNA virus; vaccine; morbidity;
KW mortality; infection; gene therapy; hepatitis; cirrhosis;
KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
KW antiinflammatory; BCG; chimera; mutant.
XX
OS Hepatitis B virus.
OS Mycobacterium bovis.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..2130
XX /*tag= a
XX /product= "HisHepCorT(149/87S97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2002; 2002WO-US003460.
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PR 05-FEB-2001; 2001US-0266733P.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PA Mizzen L, Liu H, Siegel M;
XX WPI; 2002-706903/76.
DR P-PSDB; ABG70776.
XX Novel isolated fusion protein useful for treating hepatitis B virus
PT infection in a subject, comprises a stress protein or its portion, and a
PT hepatitis B virus core antigen.
XX Example 1; Fig 7; 58pp; English.
XX The invention discloses an isolated fusion protein, and the
CC polynucleotide encoding it, that comprises a stress protein (e.g.
CC Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
CC hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
CC when administered to an individual, induces or enhances an immune
CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus
CC against which a vaccine has been developed. However, due to the morbidity
CC and mortality arising from chronic HBV infection occurring over a period
CC of decades, the impact of vaccinations will not be apparent for some time
CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
CC therapy and as a pharmaceutical composition for inducing or enhancing an
CC immune response against an HBV core antigen in a subject for treating an
CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
CC The sequence presented is the DNA encoding the truncated hepatitis B
CC virus core antigen fused to the N-terminus of the M. bovis variant
CC Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65.
CC hisHepCorT(149/87S97P)Hsp65. The core antigen the DNA encodes has been
CC truncated to include residues 1 to 149, had an N-terminal histidine tag
CC added, had two amino acids changed from the wild-type sequence and there
CC has been an additional residue added between the HBV core protein and the
CC Hsp65 protein. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 2130 BP; 444 A; 616 C; 681 G; 389 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 2130;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCGCGGATCTTGT 22
Db 1315 TGAAGGTGCCGCGGATCTTGT 1294
RESULT 46
ABS54449/C
ID ABS54449 standard; DNA; 2175 BP.
XX
AC ABS54449;
XX
XX 07-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX BCG Hsp65/mutant HBV core antigen, HepCor(97P)Hsp65, DNA.
DE
XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
KW Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity;
KW mortality; infection; gene therapy; hepatitis; cirrhosis;
KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
KW antiinflammatory; BCG; chimera; mutant.
XX
XX Hepatitis B virus.
OS Mycobacterium bovis.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 1. .2175
FT CDS /*tag= a
FT
```

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FT XX WO200262959-A2.
XX PN /product= "HepCor(97P)Hsp65"
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX PF
XX 05-FEB-2001; 2001US-0266733P.
XX PR
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PA
XX Mizzen L, Liu H, Siegel M;
XX WPI; 2002-706903/76.
XX DR P-PSDB; ABG70778.
XX
XX Novel isolated fusion protein useful for treating hepatitis B virus
PT infection in a subject, comprises a stress protein or its portion, and a
PT hepatitis B virus core antigen.
XX Example 1; Fig 11; 58pp; English.
XX The invention discloses an isolated fusion protein, and the
CC polynucleotide encoding it, that comprises a stress protein (e.g.
CC Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
CC hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
CC when administered to an individual, induces or enhances an immune
CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus
CC against which a vaccine has been developed. However, due to the morbidity
CC and mortality arising from chronic HBV infection occurring over a period
CC of decades, the impact of vaccinations will not be apparent for some time
CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
CC therapy and as a pharmaceutical composition for inducing or enhancing an
CC immune response against an HBV core antigen in a subject for treating an
CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
CC The sequence presented is the DNA encoding the hepatitis B virus core
CC antigen fused to the N-terminus of the M. bovis variant Bacille-Calmette-
CC Guerin (BCG) heat shock protein (Hsp) 65, HepCor(97P)Hsp65. The core
CC antigen the DNA encodes has had an amino acid changed from the wild-type
CC sequence. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 2175 BP; 459 A; 628 C; 691 G; 397 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 2175;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCGCGGATCTTGT 22
Db 1360 TGAAGGTGCCGCGGATCTTGT 1339
RESULT 47
ABS54446/C
ID ABS54446 standard; DNA; 2241 BP.
XX
AC ABS54446;
XX
XX 07-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX His tagged BCG Hsp65/mutant HBV core antigen, hisHepCor(97P)Hsp65, DNA.
DE
XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
KW Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity;
KW mortality; infection; gene therapy; hepatitis; cirrhosis;
KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
KW antiinflammatory; BCG; chimera; mutant.
XX
XX Hepatitis B virus.
OS Mycobacterium bovis.
OS Synthetic.
```

OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..2241
FT /tag= a
FT /product= "HisHepCor (97F)Hsp65"
XX
PN WO200262959-A2.
XX
PD 15-AUG-2002.
XX
PP 05-FEB-2002; 2002WO-US003460.
XX
PR 05-FEB-2001; 2001US-0266733P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Mizzen L, Liu H, Siegel M;
XX
XX WPI; 2002-706903/76.
DR P-PSDB; ABG70775.
XX
PT Novel isolated fusion protein useful for treating hepatitis B virus
PT infection in a subject, comprises a stress protein or its portion, and a
PT hepatitis B virus core antigen.
XX
PS Example 1; Fig 5; 58pp; English.
XX
CC The invention discloses an isolated fusion protein, and the
CC polynucleotide encoding it, that comprises a stress protein (e.g.
CC Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
CC hepatitis B virus (HBV) core antigen (HBc), where the fusion protein,
CC when administered to an individual, induces or enhances an immune
CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus
CC against which a vaccine has been developed. However, due to the morbidity
CC and mortality arising from chronic HBV infection occurring over a period
CC of decades, the impact of vaccinations will not be apparent for some time
CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
CC therapy and as a pharmaceutical composition for inducing or enhancing an
CC immune response against an HBV core antigen in a subject for treating an
CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
CC The sequence presented is the DNA encoding the full length hepatitis B
CC virus core antigen fused to the N-terminus of the M. bovis variant
CC Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65,
CC hisHepCor(97F)Hsp65. The core antigen the DNA encodes has had an N-
CC terminal histidine tag added and had an amino acid changed from the wild-
CC type sequence. Two additional residues have also been added between the
CC HBV core protein and the Hsp65 protein. (Updated on 07-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 2241 BP; 474 A; 650 C; 709 G; 408 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 2241;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
DB 1426 TGAAGGTGCCCGGATCTTGT 1405
RESULT 48
AAP25014/c
ID AAP25014 standard; DNA; 2847 BP.
XX
AC AAP25014;
XX
XX 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of Hsp65-ovalbumin fusion protein.
XX
XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

KW ovalbumin; ss.
XX
XX Synthetic.
OS Mycobacterium bovis.
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..2847
FT /tag= a
FT /product= "Hsp65-ovalbumin fusion protein"
XX
PN WO200104344-A2.
XX
PD 18-JAN-2001.
XX
PP 10-JUL-2000; 2000WO-US018828.
XX
PR 08-JUL-1999; 99US-0143757P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mizzen LA;
XX
XX WPI; 2001-138361/14.
DR P-PSDB; AAB31611.
XX
PT Screening for compounds that stimulate Th1-like responses in CD4+ T
PT lymphocyte cells.
XX
PS Example 8; Fig 7A-B; 89pp; English.
XX
CC The present sequence encodes a fusion protein comprising a Mycobacterium
CC bovis heat shock protein (Hsp) 65 fused at its C terminal to an ovalbumin
CC protein. The fusion protein is used in the method of the invention. The
CC specification describes a method of determining whether a compound
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
CC lymphocyte cells. The method comprises contacting naive lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
XX
SQ Sequence 2847 BP; 678 A; 761 C; 863 G; 545 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 5; Length 2847;
Best Local Similarity 95.5%; Pred. No. 2.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
DB 868 TGAAGGTGCCCGGATCTTGT 847
RESULT 49
AAN81768/c
ID AAN81768 standard; DNA; 4260 BP.
XX
AC AAN81768;
XX
XX 25-MAR-2003 (revised)
DT 29-DEC-1990 (first entry)
XX
XX Sequence encoding Mycobacterium tuberculosis 540 and 517 AA residue
DE proteins.
XX
XX Diagnosis; assay; M.bovis; vaccine; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
FH 252..1874
FT CDS

```

FT FT /*tag= a
FT FT /label= 540 AA protein
FT FT /note= "AAP81351"
CDS complement (3948. .2395)
FT FT /*tag= b
FT FT /label= 517 AA protein
FT FT /note= "AAP81868"
XX
FN WO8806591-A.
XX
XX 07-SEP-1988.
XX
XX 25-FEB-1988; 88WO-US000598.
XX
XX 26-FEB-1987; 87US-00019529.
XX 24-FEB-1988; 88US-00159667.
XX
XX (SCRI ) SCRIPPS CLINIC & RE.
XX
XX Shinnick T, Houghten R;
XX
XX WPI; 1988-271136/38.
XX P-PSDB; AAP81351, AAP81868.
XX
XX Recombinant mycobacterial peptide(s) - used in assays for diagnosis of
XX infection, for producing vaccines and for producing antibodies.
XX
XX Disclosure; Fig 2a-2d; 117pp; English.
XX
XX An isolated DNA molecule that consists essentially of the nucleotide
XX sequence that corresponds to the sequence represented by position 3950 to
XX about 2390 and from position 3948 through position 2398 of AAN81768 is
XX claimed. Also claimed is a peptide sequence that consists of a 5-40 AA
XX residue sequence that corresponds to a sequence of the 540 AA residue
XX protein (AAP81351) or the 517 AA residue protein (AAP81868) coded for by
XX the DNA sequence. The proteins can be used for determining previous
XX immunological exposure of a mammal to M.tuberculosis or M.bovis and for
XX producing a vaccine. (Updated on 25-MAR-2003 to correct PR field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 4260 BP; 733 A; 1332 C; 1481 G; 714 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 1; Length 4260;
Best Local Similarity 95.5%; Pred. No. 2.4;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCRCGGATCTTGT 22
DB 1059 TGAAGGTGCCRCGGATCTTGT 1038
RESULT 50
AAN80222/c
ID AAN80222 standard; DNA; 4380 BP.
XX
XX AAN80222;
XX
XX 25-MAR-2003 (revised)
DT 19-MAR-1991 (first entry)
XX
XX Sequence of Mycobacterium tuberculosis DNA contg. gene encoding 65
DE protein.
XX
XX Antigen; vaccine; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
XX CDS 192..1874
FT /*tag= a
FT CDS complement (2398. .4101)
FT /*tag= b
XX

```

```

PN WO8805823-A.
XX
XX 11-AUG-1988.
XX
XX 01-FEB-1988; 88WO-US000281.
XX
XX 02-FEB-1987; 87US-00010007.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Husson RN, Young RA, Nick TM;
XX
XX WPI; 1988-235175/33.
XX P-PSDB; AAP80215, AAP80216.
XX
XX Genes encoding Mycobacterium tuberculosis protein antigens - useful for
XX developing reagents for diagnosis, prevention and treatment of
XX tuberculosis.
XX
XX Claim 12; Fig 8; 82pp; English.
XX
XX The gene was isolated by probing a lambda gt11 expression library of
XX M.tuberculosis DNA with monoclonal antibodies directed against
XX M.tuberculosis-specific antigens. The 19kD, 71kD and the 65kD proteins
XX and genes are claimed, and so is a vaccine comprising DNA encoding
XX M.tuberculosis protein in a recombinant vaccine vector. AAP80216 is
XX encoded on the complementary strand. (Updated on 25-MAR-2003 to correct
XX PA field.)
XX
XX SQ Sequence 4380 BP; 757 A; 1373 C; 1512 G; 738 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 1; Length 4380;
Best Local Similarity 95.5%; Pred. No. 2.4;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCRCGGATCTTGT 22
DB 1059 TGAAGGTGCCRCGGATCTTGT 1038
RESULT 51
AAV05708/c
ID AAV05708 standard; DNA; 4380 BP.
XX
XX AAV05708;
XX
XX 22-JUN-1998 (first entry)
XX
XX Mycobacterium tuberculosis 65 kDa heat shock protein gene.
XX
XX Heat shock protein; Mt Hsp65; autoimmune disease; immunotherapy;
XX gene therapy; rheumatoid arthritis; multiple sclerosis; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
XX CDS 252..1874
FT /*tag= a
FT /product= "65 kDa heat shock protein"
XX
XX WO9746253-A2.
XX
XX 11-DEC-1997.
XX
XX 03-JUN-1997; 97WO-US0009427.
XX
XX 03-JUN-1996; 96US-0019100P.
XX
XX 03-JUN-1997; 97US-00019100.
XX
XX (AURA-) AURAGEN INC.
XX
XX Haynes JR, Prayaga SK, Ramshaw IA;
XX

```

DR WPI; 1998-041892/04.
 XX P-PSDB; AAW44702.
 PT Treatment of auto-immune diseases - by administering auto-antigen-coated
 XX particles or auto-antigen-encoding nucleic acid construct.
 PS Example 2; Page 55-59; 72pp; English.
 XX This DNA sequence encodes the 65 kDa heat shock protein (see AAW44702),
 CC designated Mt Hsp65, of Mycobacterium tuberculosis. This protein cross-
 CC reacts with a component of articular cartilage, human Hsp60, that is up-
 CC regulated in the joints of arthritic patients. A claimed method for
 CC treating or preventing an autoimmune disease in a mammal comprises: (a)
 CC providing a particle coated with an antigen against which an immune
 CC response is mounted in the autoimmune disease; (b) delivering the
 CC particle into the recipient cell of the mammal; and (c) repeating step
 CC (b) until either a reduction in a cytotoxic immune response or a
 CC desensitizing immune response is induced in the mammal. Alternatively,
 CC step (a) comprises providing a nucleic acid construct comprising a coding
 CC sequence for the antigen, operably linked to control elements such that
 CC the coding sequence can be transcribed and translated in a recipient
 CC cell, and delivering the construct to the recipient cell using a gene
 CC gun. The antigen of step (a) is selected from collagen, Mt Hsp65, myelin
 CC basic protein, myelin oligodendrocyte glycoprotein, proteolipid protein,
 CC and epitopes thereof. These antigens mitigate cytotoxic responses and
 CC elicit antigen desensitisation. The method is used especially for
 CC treating rheumatoid arthritis or multiple sclerosis. It represents a
 CC novel use for the known Mt Hsp65 gene
 XX
 SQ Sequence 4380 BP; 757 A; 1371 C; 1514 G; 738 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 2; Length 4380;
 Best Local Similarity 95.5%; Pred. No. 2.4;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAAGTGCCCGGATCTTGT 22
 DB 1059 TGAAGTGCCCGGATCTTGT 1038
 RESULT 52
 ABA99141/c
 ID ABA99141 standard; DNA; 4380 BP.
 AC ABA99141;
 XX
 DT 23-MAY-2002 (first entry)
 DE hsp65 encoding sequence.
 XX
 KW hsp65; heat shock protein; cytostatic; antibacterial; antiparasitic;
 XX MHC class I; ds.
 OS Mycobacterium tuberculosis.
 XX
 PN US6331388-B1.
 XX
 PD 18-DEC-2001.
 XX
 PF 17-OCT-1997; 97US-00955565.
 XX
 PR 17-OCT-1997; 97US-00955565.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Malkovsky M, Wells AD;
 XX
 DR WPI; 2002-138381/18.
 XX
 PT Increasing expression of an MHC class I molecule in a cell, useful in
 PT increasing antigen presentation and enhancing immune recognition of cells
 PT infected with pathogens, by expressing a heat shock protein introduced by
 PT a vector.

XX Example 5; Fig 9; 89pp; English.
 PS This invention relates to increasing expression of an MHC class I
 CC molecule in a target cell, infected with a pathogen that is processed by
 CC the MHC class I endogenous pathway. The method of expressing a HSP is
 CC achieved by the introduction of an expressed vector encoding HSP to
 CC produce a transfected cell with increased expression of at least one MHC
 CC class I molecule. The method is cytostatic, antibacterial and
 CC antiparasitic. The method can be used to increase expression of an MHC
 CC class I molecule in a target cell and to increase presentation of an
 CC antigen on a cell surface by an MHC class I molecule. The method can
 CC enhance the immunogenicity of the endogenous antigen in vivo, by
 CC enhancing the generation of antibodies to an otherwise poorly immunogenic
 CC antigen or cell. The method can be used in the immunotherapy of cancer
 CC and pathogen infections, and for enhancing or reducing radiation
 CC resistance of cells. The expression of the heat shock protein in a cell
 CC enhances the presentation of endogenous antigens by MHC class I molecules
 CC onto the cell surface in vitro, and can enhance the immunogenicity of the
 CC endogenous antigen in vivo, by enhancing the generation of antibodies to
 CC an otherwise poorly immunogenic antigen or cell. This sequence represents
 CC hsp65 encoding sequence
 XX
 SQ Sequence 4380 BP; 757 A; 1372 C; 1513 G; 738 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 6; Length 4380;
 Best Local Similarity 95.5%; Pred. No. 2.4;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAAGTGCCCGGATCTTGT 22
 DB 1059 TGAAGTGCCCGGATCTTGT 1038
 RESULT 53
 ABA99143/c
 ID ABA99143 standard; DNA; 86114 BP.
 XX
 AC ABA99143;
 XX
 DT 08-APR-2003 (first entry)
 DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV265.
 XX
 KW Mycobacteriosis; survival; virulence; protective antigen; vaccine;
 XX Mycobacterial disease; tuberculosis; leprosy; ds; cosmid.
 OS Mycobacterium tuberculosis.
 XX
 PN WO200274903-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-IB001973.
 XX
 PR 22-FEB-2001; 2001US-0270123P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Cole S;
 XX
 DR WPI; 2002-759885/82.
 XX
 PT Identifying and selecting genes for survival or virulence of mycobacteria
 PT by a comparative genomic analysis of the sequences of Mycobacterium
 PT tuberculosis and M. leprae.
 XX
 PS Disclosure; Fig 7; 874pp; English.
 XX
 CC This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a

CC polynucleotide sequence that is highly conserved in both genomes with no
CC counterparts in other bacterial genomic sequences and that corresponds to
CC an essential gene for the survival or virulence of mycobacterium species.
CC The method of the invention is useful for detecting M. tuberculosis or M.
CC leprae infection. The method reduces the number of potential new targets
CC and protective antigens for new drugs and vaccine compositions to treat
CC and prevent mycobacterial diseases, particularly tuberculosis and
CC leprosy. The present sequence represents a Mycobacterial cosmid DNA
CC sequence used in the method of the invention

XX

SQ Sequence 86114 BP; 14693 A; 27103 C; 28984 G; 15334 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 6; Length 86114;
Best Local Similarity 95.5%; Pred. No. 3.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
Db 16012 TGAAGGTGCGCGGATCTTGTT 15991

RESULT 54

AAI99682_05/c
Continuation (6 of 45) of AAI99682 from base 500001 (Mycobacterium tuberculosis strain H
WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682

WP	Fragment Name	Begin	End
WP	AAI99682_00	1	110000
WP	AAI99682_01	100001	210000
WP	AAI99682_02	200001	310000
WP	AAI99682_03	300001	410000
WP	AAI99682_04	400001	510000
WP	AAI99682_05	500001	610000
WP	AAI99682_06	600001	710000
WP	AAI99682_07	700001	810000
WP	AAI99682_08	800001	910000
WP	AAI99682_09	900001	1010000
WP	AAI99682_10	1100001	1210000
WP	AAI99682_11	1200001	1310000
WP	AAI99682_12	1300001	1410000
WP	AAI99682_13	1400001	1510000
WP	AAI99682_14	1500001	1610000
WP	AAI99682_15	1600001	1710000
WP	AAI99682_16	1700001	1810000
WP	AAI99682_17	1800001	1910000
WP	AAI99682_18	1900001	2010000
WP	AAI99682_19	2000001	2100000
WP	AAI99682_20	2100001	2210000
WP	AAI99682_21	2200001	2310000
WP	AAI99682_22	2300001	2410000
WP	AAI99682_23	2400001	2510000
WP	AAI99682_24	2500001	2610000
WP	AAI99682_25	2600001	2710000
WP	AAI99682_26	2700001	2810000
WP	AAI99682_27	2800001	2910000
WP	AAI99682_28	2900001	3010000
WP	AAI99682_29	3000001	3100000
WP	AAI99682_30	3100001	3210000
WP	AAI99682_31	3200001	3310000
WP	AAI99682_32	3300001	3410000
WP	AAI99682_33	3400001	3510000
WP	AAI99682_34	3500001	3610000
WP	AAI99682_35	3600001	3710000
WP	AAI99682_36	3700001	3810000
WP	AAI99682_37	3800001	3910000
WP	AAI99682_38	3900001	4010000
WP	AAI99682_39	4000001	4100000
WP	AAI99682_40	4100001	4210000
WP	AAI99682_41	4200001	4310000
WP	AAI99682_42	4300001	4410000
WP	AAI99682_43	4400001	4411529

Query Match 100.0%; Score 21.6; DB 4; Length 110000;

Best Local Similarity 95.5%; Pred. No. 3.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
Db 29413 TGAAGGTGCGCGGATCTTGTT 29392

RESULT 55

AAI99683_05/c
Continuation (6 of 44) of AAI99683 from base 500001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession Aai99683

WP	Fragment Name	Begin	End
WP	AAI99683_00	1	110000
WP	AAI99683_01	100001	210000
WP	AAI99683_02	200001	310000
WP	AAI99683_03	300001	410000
WP	AAI99683_04	400001	510000
WP	AAI99683_05	500001	610000
WP	AAI99683_06	600001	710000
WP	AAI99683_07	700001	810000
WP	AAI99683_08	800001	910000
WP	AAI99683_09	900001	1010000
WP	AAI99683_10	1000001	1110000
WP	AAI99683_11	1100001	1210000
WP	AAI99683_12	1200001	1310000
WP	AAI99683_13	1300001	1410000
WP	AAI99683_14	1400001	1510000
WP	AAI99683_15	1500001	1610000
WP	AAI99683_16	1600001	1710000
WP	AAI99683_17	1700001	1810000
WP	AAI99683_18	1800001	1910000
WP	AAI99683_19	1900001	2010000
WP	AAI99683_20	2000001	2110000
WP	AAI99683_21	2100001	2210000
WP	AAI99683_22	2200001	2310000
WP	AAI99683_23	2300001	2410000
WP	AAI99683_24	2400001	2510000
WP	AAI99683_25	2500001	2610000
WP	AAI99683_26	2600001	2710000
WP	AAI99683_27	2700001	2810000
WP	AAI99683_28	2800001	2910000
WP	AAI99683_29	2900001	3010000
WP	AAI99683_30	3000001	3110000
WP	AAI99683_31	3100001	3210000
WP	AAI99683_32	3200001	3310000
WP	AAI99683_33	3300001	3410000
WP	AAI99683_34	3400001	3510000
WP	AAI99683_35	3500001	3610000
WP	AAI99683_36	3600001	3710000
WP	AAI99683_37	3700001	3810000
WP	AAI99683_38	3800001	3910000
WP	AAI99683_39	3900001	4010000
WP	AAI99683_40	4000001	4110000
WP	AAI99683_41	4100001	4210000
WP	AAI99683_42	4200001	4310000
WP	AAI99683_43	4300001	4403765

Query Match 100.0%; Score 21.6; DB 4; Length 110000;

Best Local Similarity 95.5%; Pred. No. 3.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
Db 30855 TGAAGGTGCGCGGATCTTGTT 30834

RESULT 56

AAH68533
ID AAH68533 standard; DNA; 349980 BP.
XX
AC AAH68533;
XX

DT 26-SEP-2001 (first entry)
XX C glutamicum coding sequence fragment SEQ ID NO: 7068.
DE
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
KW
XX Corynebacterium glutamicum.
OS
XX BP1108790-A2.
PN
XX 20-JUN-2001.
PD
XX 18-DEC-2000; 2000BP-00127688.
PF
XX 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
PI
XX WPI; 2001-376931/40.
DR
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
PT
XX Disclosure; SEQ ID NO 7068; 245pp + Sequence Listing; English.
PS
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification. But was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 5; Length 349980;
Best Local Similarity 95.5%; Pred. NO. 3.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCTCCGATCTTGT 22
Db 189718 TGAAGTGCCTCCGATCTTGT 189739
RESULT 57
ADI67068/c
ID ADI67068 standard; DNA; 732 BP.
XX
AC ADI67068;
XX
DT 24-FEB-2005 (revised)
DT 22-APR-2004 (first entry)
XX
DE Novel Lactobacillus rhamnosus polynucleotide sequence #63.
XX
KW Lactic acid bacteria; vaccine; bacterial infection; microbe;
KW milk-derived product; food product; food additive;
KW nutritional supplement; bioactive substance; probiotic supplement;
KW flavour; aroma; texture; nutritional value; food; microorganism;
KW antibacterial; gene; ds.
XX

OS Lactobacillus rhamnosus; strain HN001.
XX
PN US2004009490-A1.
XX
PD 15-JAN-2004.
XX
PF 03-OCT-2002; 2002US-00264213.
XX
PR 09-AUG-1999; 99US-0147852P.
PR 09-AUG-1999; 99US-0147853P.
PR 01-SEP-1999; 99US-0152031P.
PR 01-SEP-1999; 99US-0152032P.
PR 08-AUG-2000; 2000US-00634238.
PR 02-OCT-2001; 2001US-00971536.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Glenn M, Havukkala IJ, Lubbers M, Dekker J;
PI
XX WPI; 2004-090459/09.
PI P-PSDB; ADI67193.
DR
XX New polynucleotide from Lactobacillus rhamnosus HN001 strain, useful for
PT preparing a vaccine against bacterial infections or for modifying the
PT flavor, aroma or nutritional benefits of a bioactive or probiotic
PT supplement product.
XX
PS Claim 1; SEQ ID NO 63; 54pp; English.
XX
CC The present invention relates to the isolation of novel lactic acid
CC bacteria (Lactobacillus rhamnosus strain HN001) polynucleotide sequences,
CC and the proteins encoded by them. Also disclosed are oligonucleotide
CC probes and primers, and genetic constructs comprising the polynucleotide
CC sequences of the invention. The polynucleotide sequences are useful for
CC preparing a vaccine against bacterial infections or for improving the
CC properties of microbes used in the manufacture of milk-derived products,
CC food products, food additives, nutritional supplements, bioactive
CC substances or probiotic supplements, and for modifying the flavour,
CC aroma, texture and/or nutritional value of foods. They are also useful
CC for identifying microorganisms having a trait associated with the
CC polynucleotide. The present sequence represents a novel L. rhamnosus
CC polynucleotide sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification. The complete
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov.
XX
SQ Sequence 732 BP; 187 A; 159 C; 205 G; 181 T; 0 U; 0 Other;
Query Match 92.6%; Score 20; DB 12; Length 732;
Best Local Similarity 90.9%; Pred. NO. 12;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAAGTGCCTCCGATCTTGT 22
Db 229 TGAAGTGCCTCCGATCTTGT 208
RESULT 58
AAQ22481/c
ID AAQ22481 standard; DNA; 1320 BP.
XX
AC AAQ22481;
XX
DT 29-JUL-1992 (first entry)
XX
DE groEL-1 gene partial sequence.
XX
KW Heat shock protein; HSP18; ss.
KW
OS Streptomyces albus.
XX
FH Key Location/Qualifiers
FT CDS 1..510

```
PT FT      /*tag= a
PT PT      /note= "groEL-1 gene encoding HSP18"
XX
XX WO9204452-A.
XX PN
XX PD
XX PD      19-MAR-1992.
XX
XX PF      03-SEP-1991; 91WO-FR000701.
XX
XX PR      10-SEP-1990; 90FR-00011186.
XX
XX PA      (INSP ) INST PASTEUR.
XX
XX PI      Mazodier P, Guglielmi G;
XX
XX DR      WPI; 1992-114358/14.
XX DR      P-PSDB; AAR22362.
XX
XX PT      Recombinant DNA contg. heat inducible promoter and heterologous gene -
XX PT      also vectors, transformed cells and new heat shock proteins of
XX PT      Streptococcus albus.
XX
XX PS      Claim 18; Fig 6; 50pp; French.
XX
XX CC      This is a partial sequence of the groEL-1 gene which codes for the 18 kDa
XX CC      heat shock protein HSP18. The gene actually codes for a 56 kDa protein
XX CC      but this is subjected to post translation modification to give the 18
XX CC      kDa HSP18 protein, the partial sequence given here is missing the last
XX CC      300 nucleotides encoding the C-terminal of the 56 kDa protein. See also
XX CC      AAQ22477-Q22486
XX
XX SQ      Sequence 1320 BP; 237 A; 469 C; 444 G; 170 T; 0 U; 0 Other;

Query Match      92.6%; Score 20; DB 2; Length 1320;
Best Local Similarity 90.9%; Pred. No. 13;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TGAAGTGCRCGGATCTTGT 22
DB      814 TGAACGTGCGCGGATCTTGT 793

RESULT 59
AAQ22482/C
ID      AAQ22482 standard; DNA; 1620 BP.
XX
XX AC      AAQ22482;
XX
XX DT      29-JUL-1992 (first entry)
XX
XX DE      groEL-1 gene coding region.
XX
XX KW      Heat shock protein; HSP18; ss.
XX
XX OS      Streptomyces albus.
XX
XX FH      Key      Location/Qualifiers
XX CDS      1..510
XX FT      /*tag= a
XX PT      /note= "groEL-1 gene encoding HSP18"
XX
XX PN      WO9204452-A.
XX
XX PD      19-MAR-1992.
XX
XX PF      03-SEP-1991; 91WO-FR000701.
XX
XX PR      10-SEP-1990; 90FR-00011186.
XX
XX PA      (INSP ) INST PASTEUR.
XX
XX PI      Mazodier P, Guglielmi G;

DR      WPI; 1992-114358/14.
DR      P-PSDB; AAR22363.
XX
XX PT      Recombinant DNA contg. heat inducible promoter and heterologous gene -
XX PT      also vectors, transformed cells and new heat shock proteins of
XX PT      Streptococcus albus.
XX
XX PS      Claim 18; Fig 8; 50pp; French.
XX
XX CC      The sequence is that of the coding region of the groEL-1 gene which codes
XX CC      for the 18 kDa heat shock protein HSP18. The gene actually codes for a 56
XX CC      kDa protein but this is subjected to post translation modification to
XX CC      give the 18 kDa HSP18 protein. See also AAQ22477-Q22486
XX
XX SQ      Sequence 1620 BP; 287 A; 590 C; 539 G; 204 T; 0 U; 0 Other;

Query Match      92.6%; Score 20; DB 2; Length 1620;
Best Local Similarity 90.9%; Pred. No. 13;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TGAAGTGCRCGGATCTTGT 22
DB      814 TGAACGTGCGCGGATCTTGT 793

RESULT 60
ACA39632/C
ID      ACA39632 standard; DNA; 1626 BP.
XX
XX AC      ACA39632;
XX
XX DT      19-JUN-2003 (first entry)
XX
XX DE      Prokaryotic essential gene #21289.
XX
XX KW      Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW      drug design; gene.
XX
XX OS      Mycobacterium leprae.
XX
XX PN      WO200277183-A2.
XX
XX PD      03-OCT-2002.
XX
XX PF      21-MAR-2002; 2002WO-US009107.
XX
XX PR      21-MAR-2001; 2001US-00815242.
XX PR      06-SEP-2001; 2001US-00948993.
XX PR      25-OCT-2001; 2001US-0342923P.
XX PR      08-FEB-2002; 2002US-00072851.
XX PR      06-MAR-2002; 2002US-0362699P.
XX
XX PA      (ELIT-) ELITRA PHARM INC.
XX
XX PI      Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI      Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX DR      WPI; 2003-029926/02.
XX DR      P-PSDB; ABU35762.
XX
XX PT      New antisense nucleic acids, useful for identifying proteins or screening
XX PT      for homologous nucleic acids required for cellular proliferation to
XX PT      isolate candidate molecules for rational drug discovery programs.
XX
XX PS      Claim 14; SEQ ID NO 27502; 1766pp; English.
XX
XX CC      The invention relates to an isolated nucleic acid comprising any one of
XX CC      the 6213 antisense sequences given in the specification where expression
XX CC      of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC      (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC      encoding a polypeptide whose expression is inhibited by the antisense
XX CC      nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC      polypeptide or its fragment whose expression is inhibited by the
```

CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 1626 BP; 352 A; 450 C; 540 G; 284 T; 0 U; 0 Other;

Query Match 92.6%; Score 20; DB 8; Length 1626;
 Best Local Similarity 90.9%; Pred. No. 13;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
 ||| |||||:|||||||
 Db 808 TGAAGTGCCACGGATCTTGTT 787

Search completed: April 1, 2006, 22:21:38
 Job time : 46.7112 secs

THIS PAGE BLANK (USP) 6,

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:06:31 ; Search time 303.022 Seconds
(without alignments)
3396.840 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaagtgccrccggtattgtt 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	88.0	163	1	AW113955
C 2	19	88.0	232	1	AW111034
C 3	19	88.0	341	5	EX632408
C 4	19	88.0	459	1	AW111035
C 5	19	88.0	616	1	AI303526
C 6	19	88.0	629	2	BG081027
C 7	19	88.0	858	7	CV070443
C 8	18.8	87.0	393	3	BP637291
C 9	18.8	87.0	403	3	BP596595
C 10	18.8	87.0	409	3	BP793678
C 11	18.8	87.0	425	3	BP605386
C 12	18.8	87.0	432	1	AV533334
C 13	18.8	87.0	432	1	AV562602
C 14	18.8	87.0	433	3	BP589232
C 15	18.8	87.0	434	3	BP606850
C 16	18.8	87.0	439	3	BP593318
C 17	18.8	87.0	441	3	BP604921
C 18	18.8	87.0	518	1	AV563537
C 19	18.8	87.0	524	1	AV563538
C 20	18.8	87.0	552	1	AI999651
C 21	18.8	87.0	3509	4	CNS0ADWK
C 22	18.4	85.2	303	8	DN316919

C 23	18.4	85.2	673	1	AJ808396
C 24	18.4	85.2	859	8	DR731656
C 25	18.4	85.2	889	7	CK154849
C 26	18.4	85.2	893	5	BU601986
C 27	18.4	85.2	893	7	CK152837
C 28	18	83.3	281	7	CR458933
C 29	18	83.3	335	1	AA875097
C 30	18	83.3	570	1	AA061605
C 31	18	83.3	582	3	BP294923
C 32	18	83.3	1349	1	AW27610
C 33	17.6	81.5	559	10	CL174879
C 34	17.4	80.6	179	2	BP705257
C 35	17.4	80.6	218	8	DR705480
C 36	17.4	80.6	243	8	CX223617
C 37	17.4	80.6	280	3	BJ280260
C 38	17.4	80.6	285	5	BQ752687
C 39	17.4	80.6	360	1	AJ474162
C 40	17.4	80.6	374	8	DR793683
C 41	17.4	80.6	386	6	CF646223
C 42	17.4	80.6	391	2	BI098781
C 43	17.4	80.6	397	2	BI098170
C 44	17.4	80.6	404	6	CF646224
C 45	17.4	80.6	417	2	BI098323
C 46	17.4	80.6	426	9	AQ406201
C 47	17.4	80.6	432	2	BI074698
C 48	17.4	80.6	437	1	AW666066
C 49	17.4	80.6	438	2	BF325403
C 50	17.4	80.6	447	3	BQ133585
C 51	17.4	80.6	462	6	CB541407
C 52	17.4	80.6	464	2	BG050084
C 53	17.4	80.6	474	2	BG104062
C 54	17.4	80.6	480	10	CG785031
C 55	17.4	80.6	481	10	CW368267
C 56	17.4	80.6	487	2	BG267138
C 57	17.4	80.6	487	6	CA181673
C 58	17.4	80.6	489	2	BG550996
C 59	17.4	80.6	499	6	CA182253
C 60	17.4	80.6	504	1	AA763342

ALIGNMENTS

RESULT 1

LOCUS AW113955/c 163 bp mRNA linear EST 31-JAN-2000
DEFINITION MC6373 mouse liver, vehicle control Mus musculus cDNA clone MC6373
3' similar to X86561 Rat gene for alpha-fibrinogen, mRNA sequence.
ACCESSION AW113955
VERSION AW113955.1 GI:6826668
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 163)
AUTHORS Thomas, R.S., Rank, D.R., Penn, S.G., Zastrow, G.M., Jovanovich, S. and
Bradfield, C.A.

TITLE Mcardle Laboratory/Molecular Dynamics Dioxin EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Bradfield CA
McArdle Laboratory for Cancer Research
University of Wisconsin
1400 University Ave., Madison, WI 53706, USA
Tel: 608 262 2034
Fax: 608 262 2824

Email: bradfield@oncology.wisc.edu
This clone was sequenced as part of a project to develop a database
on gene expression changes following exposure to various
environmental toxicants. The database can be accessed at
http://mcardle.oncology.wisc.edu/bradfield/. Treatment- dioxane
vehicle (400 ul/kg). Animals sacrificed- 48 hrs post-injection.

Seq primer: dt(23)v (anchored polyT).

FEATURES

source
1. 163
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MC6373"
/sex="male"
/lab_host="JM109"
/clone_lib="mouse liver, vehicle control"

NotI; Site 2: EcoRI; Vector: pGEM11zf (Promega); Site 1:
NotI; Site 2: EcoRI; First strand cDNA was primed with a
NotI-polyT primer
[5'-AAGTGAAGATTCGCGCGCAGGAATTTTTTTTTTTT-3']
Double-stranded cDNA was ligated with EcoRI adapters
(Pharmacia), digested with NotI, and ligated into the
EcoRI/NotI sites of the pGEM11zf vector. The library was
NOT normalized.

ORIGIN

Query Match 88.0%; Score 19; DB 1; Length 163;
Best Local Similarity 90.5%; Pred. No. 3.1e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||:|||||
Db 134 TGAAGGTGTCAGGATCTTGT 114

RESULT 2

AW111034/c 232 bp mRNA linear EST 31-JAN-2000
LOCUS
DEFINITION
MW725 mouse liver, dioxin treated Mus musculus cDNA clone MT725 3'
similar to X86561 Rat gene for alpha-fibrinogen, mRNA sequence.

AW111034

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW111034.1 GI:6823747
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 232)

Thomas, R.S., Rank, D.R., Penn, S.G., Zaestrow, G.M., Jovanovich, S. and
Bradfield, C.A.
McArdle Laboratory/Molecular Dynamics Dioxin EST Project
Unpublished (1999)
Contact: Bradfield CA

McArdle Laboratory for Cancer Research

University of Wisconsin

1400 University Ave., Madison, WI 53706, USA

Tel: 608 262 2024

Fax: 608 262 2824

Email: bradfield@oncology.wisc.edu

This clone was sequenced as part of a project to develop a database
on gene expression changes following exposure to various
environmental toxicants. The database can be accessed at
http://mcarchive.oncology.wisc.edu/bradfield/. Treatment- Dioxin (10
ug/kg, ip) in a dioxane vehicle. Animals sacrificed- 48 hrs
post-injection.

Seq primer: SP6

FEATURES

source
1. 232
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MT725"
/sex="male"
/lab_host="JM109"
/clone_lib="mouse liver, dioxin treated"
/note="Organ: liver; Vector: pGEM11zf (Promega); Site 1:

NotI; Site 2: EcoRI; First strand cDNA was primed with a
NotI-polyT primer
[5'-AAGTGAAGATTCGCGCGCAGGAATTTTTTTTTTTT-3']
Double-stranded cDNA was ligated with EcoRI adapters
(Pharmacia), digested with NotI, and ligated into the
EcoRI/NotI sites of the pGEM11zf vector. The library was
NOT normalized.

ORIGIN

Query Match 88.0%; Score 19; DB 1; Length 232;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||:|||||
Db 122 TGAAGGTGTCAGGATCTTGT 102

RESULT 3

BX632408/c 341 bp mRNA linear EST 12-AUG-2003
LOCUS
DEFINITION
BX632408 pBluescript Lion Mus musculus cDNA clone LIONp462C03455
3', mRNA sequence.

BX632408

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BX632408.1 GI:33612283
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 341)

REFERENCE

AUTHORS

Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schluster, T.,
Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.

TITLE

JOURNAL

COMMENT

Mouse ArrayTAG cDNA (LION)
Unpublished (2003)
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONp462C03455.
RZPDLIB;
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=4
62 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.

FEATURES

source

1. 341
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONp462C03455"
/lab_host="DH10B"
/clone_lib="pBluescript Lion"

ORIGIN

Query Match 88.0%; Score 19; DB 5; Length 341;
Best Local Similarity 90.5%; Pred. No. 3.3e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||:|||||
Db 139 TGAAGGTGTCAGGATCTTGT 119

RESULT 4

AW111035/c
 LOCUS MT8449 mouse liver, dioxin treated Mus musculus cDNA clone MT8449
 DEFINITION 3' similar to X86561 Rat gene for alpha-fibrinogen, mRNA sequence.
 ACCESSION AW111035
 VERSION AW111035.1 GI:6823748
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 459)
 AUTHORS Thomas, R.S., Rank, D.R., Penn, S.G., Zastrow, G.M., Jovanovich, S. and
 Bradfield, C.A.
 TITLE McArdle Laboratory/Molecular Dynamics Dioxin EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Bradfield CA
 McArdle Laboratory for Cancer Research
 University of Wisconsin
 1400 University Ave., Madison, WI 53706, USA
 Tel: 608 262 2024
 Fax: 608 262 2824
 Email: bradfield@oncology.wisc.edu
 This clone was sequenced as part of a project to develop a database
 on gene expression changes following exposure to various
 environmental toxicants. The database can be accessed at
 http://mcarchive.oncology.wisc.edu/bradfield/. Treatment- Dioxin (10
 ug/kg, ip) in a dioxane vehicle. Animals sacrificed- 48 hrs
 post-injection.
 Seq primer: dT(23)V (anchored polyT primer).
 Location/Qualifiers
 1..459
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MT8449"
 /sex="male"
 /lab_host="JM109"
 /clone_lib="mouse liver, dioxin treated"
 /note="Organ: liver; Vector: pGEM11zf (Promega); Site 1:
 NotI; Site 2: EcoRI; First strand cDNA was primed with a
 NotI-polyT primer
 [5'-AAGTGGAGATTCGCGCCGAGAAATTTTCTTTTCTTTT-3'].
 Double-stranded cDNA was ligated with EcoRI adapters
 (Pharmacia), digested with NotI, and ligated into the
 EcoRI/NotI sites of the pGEM11zf vector. The library was
 NOT normalized."

FEATURES

source
 1..459
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MT8449"
 /sex="male"
 /lab_host="JM109"
 /clone_lib="mouse liver, dioxin treated"
 /note="Organ: liver; Vector: pGEM11zf (Promega); Site 1:
 NotI; Site 2: EcoRI; First strand cDNA was primed with a
 NotI-polyT primer
 [5'-AAGTGGAGATTCGCGCCGAGAAATTTTCTTTTCTTTT-3'].
 Double-stranded cDNA was ligated with EcoRI adapters
 (Pharmacia), digested with NotI, and ligated into the
 EcoRI/NotI sites of the pGEM11zf vector. The library was
 NOT normalized."

ORIGIN

Query Match 88.0%; Score 19; DB 1; Length 459;
 Best Local Similarity 90.5%; Pred.No. 3.4e+02;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 21
 ||||| |
 Db 101 TGAAGTGTCACGGATCTTGT 81
 ||||| |

RESULT 5

AI303526/c
 LOCUS ui80f03.x1 Sugano mouse liver mlia Mus musculus cDNA clone
 DEFINITION IMAGE:1888733 3', similar to gb:M64982_cde2 FIBRINOGEN ALPHA CHAIN
 PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION AI303526
 VERSION AI303526.1 GI:3987276
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE

AUTHORS

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 616)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HHMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:973057
 Seq primer: custom primer used
 High quality sequence stop: 487.
 Location/Qualifiers
 1..616
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1888733"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
 (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTCCTTTTCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTCTAAAGCTCGG and 3' end
 primer CGACCTGCTCGACGACA."

FEATURES

source
 1..616
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1888733"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
 (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTCCTTTTCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTCTAAAGCTCGG and 3' end
 primer CGACCTGCTCGACGACA."

ORIGIN

Query Match 88.0%; Score 19; DB 1; Length 616;
 Best Local Similarity 90.5%; Pred.No. 3.5e+02;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 21
 ||||| |
 Db 150 TGAAGTGTCACGGATCTTGT 130
 ||||| |

RESULT 6

BG081027/c
 LOCUS H3060C06-5 NTA Mouse 15K Clone Set Mus musculus cDNA clone
 DEFINITION H3060C06 5', mRNA sequence.
 ACCESSION BG081027
 VERSION BG081027.2 GI:40015264
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 629)
 AUTHORS Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X.,
 Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H.,
 Wood, W.H. III, Becker, K.G. and Ko, M.S.H.

TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

PUBLISHED 10922068

COMMENT On Jan 26, 2001 this sequence version replaced gi:12563595. Other ESTs: H3060C06-3

Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cda@gaun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3060 Row: C Column: 06
Seq primer: -21M13 Reverse
High quality sequence stop: 629
POLYA=No.

FEATURES source
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/mol_type="mRNA"
/strain="C57BL/6J"
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/dev_stage="Clones arrayed from a variety of cDNA libraries"
/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN
Query Match 88.0%; Score 19; DB 2; Length 629;
Best Local Similarity 90.5%; Pred. No. 3.5e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||||:|||||||
Db 51 TGAAGGTGCGCGGATCTTGT 31

RESULT 7
LOCUS CV070443/c 858 bp mRNA linear EST 24-AUG-2004
DEFINITION WPAEhux1516F2.002_430126.H1_012.abl Preamplified custom cDNA library in pCMVaport6.1 (ResGen, Invitrogen Inc.) Emiliana huxleyi cDNA, mRNA sequence.

ACCESSION CV070443
VERSION CV070443.1 GI:51533607
KEYWORDS EST.
SOURCE Emiliana huxleyi
ORGANISM Emiliana huxleyi
REFERENCE 1 (bases 1 to 858) Eukaryota; Haptophyceae; Isochrysidales; Emiliana.

AUTHORS Wahlund, T.W., Zhang, X. and Read, B.A.
TITLE Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying Cultures of Emiliana huxleyi

JOURNAL Micropaleontology (2004) In press

COMMENT Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
Email: bread@csu.san.edu.

FEATURES source
1. 858 Location/Qualifiers
/organism="Emiliana huxleyi"
/mol_type="mRNA"
/strain="1516"
/db_xref="taxon:2903"
/dev_stage="Late log growth phase"
/clone_lib="Preamplified custom cDNA library in pCMVaport6.1 (ResGen, Invitrogen Inc.)"
/note="Emiliana huxleyi grown in Artificial Seawater (Guillard's F/2 media)."

ORIGIN
Query Match 88.0%; Score 19; DB 7; Length 858;
Best Local Similarity 90.5%; Pred. No. 3.6e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||||:|||||||
Db 364 TGAAGGTGCGCGGATCTTGT 344

RESULT 8
LOCUS BP637291 393 bp mRNA linear EST 27-JUN-2004
DEFINITION BP637291 RAFL19 Arabidopsis thaliana cDNA clone RAFL19-05-B20 3', mRNA sequence.

ACCESSION BP637291
VERSION BP637291.1 GI:49288543
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)

ORIGIN Arabidopsis thaliana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 393)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)

TITLE Motoaki Seki
JOURNAL Plant Functional Genomics Research Group
PUBLISHED RIKEN Genomic Sciences Center
COMMENT 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekic@rcc.riken.go.jp
reversed clone; Please visit our web site
(<http://pfweb.gsc.riken.go.jp/>) for further details.

FEATURES source
1. 393 Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL19-05-B20"
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/lab_host="DH10B"
/clone_lib="RAFL19"
/note="Site 1: BamHI; Site 2: SalI; Subtraction Library"

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Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
Db 356 TGAAGGTCTCGGATCTTGTT 377

RESULT 9
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DEFINITION BP596595 RAPL15 Arabidopsis thaliana cDNA clone RAFL15-36-A01 3',
mRNA sequence.
ACCESSION BP596595
VERSION BP596595.1 GI:49164063
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 403)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
PUBMED
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.

FEATURES
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1..403
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
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/clone_lib="RAFL15"
/note="Site 1: BamHI; Site 2: SalI"

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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
Db 377 TGAAGGTCTCGGATCTTGTT 398

RESULT 11
BP605386
LOCUS BP605386 425 bp mRNA linear EST 25-JUN-2004
DEFINITION BP605386 RAPL16 Arabidopsis thaliana cDNA clone RAFL16-66-K06 3',
mRNA sequence.
ACCESSION BP605386
VERSION BP605386.1 GI:49252899
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 425)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
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Science 296 (5565), 141-145 (2002)
11910074
PUBMED
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.

TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
Unpublished (2005)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002). This clone is in a
modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and
http://large.gsc.riken.jp) for further details.
reversed clone.
Location/Qualifiers
1..409
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
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/clone="RAFL07-57-E07"
/dev_stage="rosette plants"
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/clone_lib="RAFL7"
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cold-treated (1, 2, 5, 10, 24 hr)"

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Query Match      87.0%; Score 18.8; DB 3; Length 409;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
Db 377 TGAAGGTCTCGGATCTTGTT 398

RESULT 11
BP605386
LOCUS BP605386 425 bp mRNA linear EST 25-JUN-2004
DEFINITION BP605386 RAPL16 Arabidopsis thaliana cDNA clone RAFL16-66-K06 3',
mRNA sequence.
ACCESSION BP605386
VERSION BP605386.1 GI:49252899
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 425)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
PUBMED
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.

TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
Unpublished (2005)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
reversed clone; Please visit
(http://pfgweb.gsc.riken.go.jp/) for further details.

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FEATURES
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  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
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Db 382 TGAAGGTCTCTCGATCTTGT 403

RESULT 12
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LOCUS
DEFINITION
  AV533334 Arabidopsis thaliana flower buds Columbia Arabidopsis
  thaliana cDNA clone FB059h07F 3', mRNA sequence.
ACCESSION
  AV533334
VERSION
  AV533334.1 GI:8693617
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  REFERENCE
    1 (bases 1 to 432)
  AUTHORS
    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE
    A large scale analysis of cDNA in Arabidopsis thaliana: Generation
    of 12, 028 non-redundant expressed sequence tags from normalized and
    size-selected cDNA libraries
  JOURNAL
    DNA Res. 7 (3), 175-180 (2000)
  PUBMED
    10907847
  COMMENT
    Contact: Erika Asamizu
    The First Laboratory for Plant Gene Research
    Kazusa DNA Research Institute
    Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
    Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

FEATURES
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QY 1 TGAAGGTGCGCGATCTTGT 22
    ||||| ||||| ||||| |||||
Db 357 TGAAGTCTCTCGATCTTGT 378

RESULT 14
BP589232
LOCUS
DEFINITION
  BP589232 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-49-B10 3',
  mRNA sequence.
ACCESSION
  BP589232
VERSION
  BP589232.1 GI:49156700
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  REFERENCE
    1 (bases 1 to 433)
  AUTHORS
    Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
    Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
    Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
    Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
  TITLE
    Functional annotation of a full-length Arabidopsis cDNA collection
  JOURNAL
    Science 296 (5565), 141-145 (2002)
  PUBMED
    11910074
  COMMENT
    Contact: Motoaki Seki
    Plant Functional Genomics Research Group
    RIKEN Genomic Sciences Center
    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
    Tel: 81-298-36-4359
    Fax: 81-298-36-9060
    Email: msekita@tc.riken.go.jp
    reversed clone; Please visit our web site
    (http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
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    1..433
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QY 1 TGAAGGTGCGCGATCTTGT 22
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Db 357 TGAAGTCTCTCGATCTTGT 378

RESULT 13
AV562602
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DEFINITION
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  thaliana cDNA clone SQ172g05F 3', mRNA sequence.
ACCESSION
  AV562602

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
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/lab_host="DH10B"
/clone_lib="RAFL15"
/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 433;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGTT 22
||||| ||||| ||||| ||||| |||||
Db 358 TGAAGGTTCTCGGATCTTGTT 379

RESULT 15
BP606850
LOCUS BP606850 434 bp mRNA linear EST 25-JUN-2004
DEFINITION BP606850 RAPL16 Arabidopsis thaliana cDNA clone RAFL16-72-107 3',
mRNA sequence.
ACCESSION BP606850
VERSION BP606850
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
1 (bases 1 to 434)
Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
Nakajima,M., Enju,A., Akiyama,K., Ono,Y., Muramatsu,M.,
Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
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Science 296 (5565), 141-145 (2002)
11910074
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekietc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
source
location/Qualifiers
1..434
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/clone_lib="RAFL15"
/notes="Site_1: BamHI; Site_2: SalI"

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Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGTT 22
||||| ||||| ||||| ||||| |||||
Db 360 TGAAGTTCCTCGGATCTTGTT 381

RESULT 17
BP604921
LOCUS BP604921 441 bp mRNA linear EST 25-JUN-2004
DEFINITION BP604921 RAPL16 Arabidopsis thaliana cDNA clone RAFL16-64-N16 3',
mRNA sequence.
ACCESSION BP604921
VERSION BP604921
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
1 (bases 1 to 441)
Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
Nakajima,M., Enju,A., Akiyama,K., Ono,Y., Muramatsu,M.,
Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359

/organism="Arabidopsis thaliana"
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/clone="RAFL15-21-K07"
/tissue_type="mixture of silique and flower"
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/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 434;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGTT 22
||||| ||||| ||||| ||||| |||||
Db 358 TGAAGGTTCTCGGATCTTGTT 379

RESULT 16
BP593318
LOCUS BP593318 439 bp mRNA linear EST 23-JUN-2004
DEFINITION BP593318 RAPL15 Arabidopsis thaliana cDNA clone RAFL15-21-K07 3',
mRNA sequence.
ACCESSION BP593318
VERSION BP593318
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
1 (bases 1 to 439)
Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
Nakajima,M., Enju,A., Akiyama,K., Ono,Y., Muramatsu,M.,
Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359

```

```

Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
source
1. .441
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL16-64-N16"
/lab host="DH10B"
/clone_lib="RAFL16"
/note="Site_1: BamHI; Site_2: SalI; dark-grown"

ORIGIN
Query Match 87.0%; Score 18.8; DB 3; Length 441;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGCGATCTTGT 22
||||| ||| ||||| |||||
Db 354 TGAAGTTCCTCGGATCTTGT 375

RESULT 18
AV563537 518 bp mRNA linear EST 23-FEB-2004
LOCUS
DEFINITION
AV563537 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ189b02F 3', mRNA sequence.
ACCESSION
AV563537
VERSION
AV563537.1 GI:8734963
KEYWORDS
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
REFERENCE
1 (bases 1 to 518)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
JOURNAL
PUBMED
10907847
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. .518
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SQ189b03F"
/tissue type="green siliques"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 87.0%; Score 18.8; DB 1; Length 524;
Best Local Similarity 90.9%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGCGATCTTGT 22
||||| ||| ||||| |||||
Db 384 TGAAGTTCCTCGGATCTTGT 405

RESULT 20
AV563537 552 bp mRNA linear EST 08-SEP-1999
LOCUS
DEFINITION
AV563537 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis
thaliana cDNA clone 701556873, mRNA sequence.
ACCESSION
AV563537
VERSION
AV563537.1 GI:5846556
KEYWORDS
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 552)
Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
Nobriga,A., Murrey,L., Turner,C., Krikorian,S., Elder,L. and
Hanson,D.
Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733

TITLE
JOURNAL
COMMENT

```

```

Fax: 314-427-3324
Email: servicegenomesystems.com.
FEATURES
source
  1. .552
    /organism="Arabidopsis thaliana"
    /mol_type="mRNA"
    /ecotype="Col-0"
    /db_xref="taxon:3702"
    /clone="701556873"
    /tissue_type="rosette"
    /dev_stage="4 - 7 weeks"
    /clone_lib="A. thaliana, Columbia Col-0, rosette-3"
    /note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA
    library was derived from untreated rosette tissue from
    Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
    Plants were grown in 1:1:1 peat moss/vermiculite/perlite
    soil at 22 deg. C +/- 3 deg. C under constant light, and
    watered with fertilizer. cDNA synthesis was initiated
    using a NotI-oligo(dT) primer. Double-stranded cDNA was
    blunt-ended, ligated to SalI adaptors, digested with NotI,
    size-selected, and cloned into the NotI and SalI sites of
    the pSPORT vector."
ORIGIN
Query Match      87.0%; Score 18.8; DB 1; Length 552;
Best Local Similarity 90.9%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 329 TGAAGTTCCTCGGATCTTGT 350

RESULT 21
CNS0ADWK/c
LOCUS
DEFINITION
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLT9192D05 of Adult vegetative tissue of strain col-0 of
Arabidopsis thaliana (thale cress).
ACCESSION
BX814924
VERSION
1 GI:42474528
KEYWORDS
HTC; GSIT cDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 3509)
Castelli,V., Aury,J.M., Jallou,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 3509)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
_length

http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.
FEATURES
source
  Location/Qualifiers
  1. .3509
    /organism="Arabidopsis thaliana"
    /mol_type="mRNA"
    /db_xref="taxon:3702"
    /clone="GSLT9192D05"
    /tissue_type="Adult vegetative tissue"
    /ecotype="Col-0"
    /plasmid="pCMVSPORT_6"
    /gene="Atlg72180"
  gene
  1. .3509
  /gene="Atlg72180"
ORIGIN
Query Match      87.0%; Score 18.8; DB 4; Length 3509;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 3176 TGAAGTTCCTCGGATCTTGT 3155

RESULT 22
DN316919
LOCUS
DEFINITION
LIB3171-007-PI-K1-C3 LIB3171 Canis familiaris cDNA clone
CLN1349011, mRNA sequence.
ACCESSION
DN316919
VERSION
DN316919.1 GI:60478174
KEYWORDS
EST.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 303)
Staten,N.R.
AUTHORS
Direct Submission (Staten,N.R.)
JOURNAL
Unpublished (2005)
COMMENT
Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
Location/Qualifiers
1. .303
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN1349011"
/tissue_type="pancreas"
/lab_host="DH10B"
/clone_lib="LIB3171"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
female"
FEATURES
source
  Location/Qualifiers
  1. .3509
    /organism="Arabidopsis thaliana"
    /mol_type="mRNA"
    /db_xref="taxon:3702"
    /clone="GSLT9192D05"
    /tissue_type="Adult vegetative tissue"
    /ecotype="Col-0"
    /plasmid="pCMVSPORT_6"
    /gene="Atlg72180"
  gene
  1. .3509
  /gene="Atlg72180"
ORIGIN
Query Match      85.2%; Score 18.4; DB 8; Length 303;
Best Local Similarity 86.4%; Pred. No. 6.4e+02;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 263 TGAAGTTCCTCGGATCTTGT 284

RESULT 23
AJ808396/c
LOCUS
DEFINITION
AJ808396 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.6.09.h23, mRNA sequence.
ACCESSION
AJ808396
VERSION
AJ808396.1 GI:51123724

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KEYWORDS
SOURCE
ORGANISM
Antirrhinum majus (snapdragon)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Plantaginales; Antirrhineae;
Antirrhinum.
REFERENCE
1 (bases 1 to 673)
AUTHORS
Bay, M., Stuber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
Saedler, H. and Zachgo, S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
Location/Qualifiers
1..673
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018.6.09.b23"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
ORIGIN
Query Match 85.2%; Score 18.4; DB 1; Length 673;
Best Local Similarity 86.4%; Pred. No. 6.8e+02;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TGAAGTGCCRCGGATCTTGT 22
||||| :||:|||||
Db 93 TGAAGGAGCCACGATCTTGT 72
||||| :||:|||||
RESULT 24
DR731656 859 bp mRNA linear EST 18-JUL-2005
LOCUS FGAS077576 Triticum aestivum FGAS: Talt2 Triticum aestivum cDNA,
DEFINITION mRNA sequence.
ACCESSION DR731656.1 GI:70958035
VERSION DR731656
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 859)
AUTHORS Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, P.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [109,609].
Plate: Talt258 row: P column: 09.
FEATURES
source
Location/Qualifiers
1..889
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Talt2"
/clone_host="DH5 alpha"
/notes="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
Clt1406 cold hardened at 2 C for 1 day (24 H) (tester) and
subtracted against genotype Norstar cold hardened at 2 C
for 21 days and 49 days (equal amount of cDNA pooled
together before subtraction, driver). Nitro-pyrole
anchored oligo-dT priming and non-directional cloning."

```


Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 281)
 Henrich, J., Hermanns, J., Kranz, H., Loebert, R., Schlueter, T., Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Rat ArrayTAG cDNA

Unpublished (2004)

Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD: LIONp463A10178.

RZPDLIB;

Rat ArrayTAG cDNA

http://www.rzpd.de/cgi-

bin/products/showlib.pl.cgi?response?libNo=463 Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

RP: CAGGAACAGCTATGAC.

Location/Qualifiers

1. .281

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="LIONp463A10178"

/lab_host="DH10B"

/clone_lib="Rat pBluescript Lion"

ORIGIN

Query Match 83.3%; Score 18; DB 7; Length 281;
 Best Local Similarity 90.0%; Pred. No. 9.8e+02;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

ORIGIN

QY 2 GAAGGTGCGCGGATCTTGT 21
 ||||| :|||||||
 Db 136 GAAGGTGTCGGGATCTTGT 117

RESULT 29

AA875097/c

LOCUS

DEFINITION

AA875097 335 bp mRNA linear EST 04-JUL-1999
 UI-R-E0-cf-g-09-0-UI.61 UI-R-E0 Rattus norvegicus cDNA clone
 UI-R-E0-cf-g-09-0-UI.3' similar to gi|790485|emb|X86561|RNLFIB Rat
 gene for alpha-fibrinogen, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AA875097.1 GI:4230978
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE

AUTHORS

TITLE

Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL

PUBLISHED

COMMENT

Genome Res. 6 (9), 791-806 (1996)
 8889548
 On Mar 20, 1998 this sequence version replaced gi:2980045.
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: benton-soares@uiowa.edu

The sequence tag present in the cDNA between the NotI site and the

FEATURES

source

Location/Qualifiers
 1. .335
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-E0-cf-g-09-0-UI"
 /dev_stage="embryonic"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-E0"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: NotI; Site 2: EcoRI; This library
 consists of a mixture of individually tagged normalized
 libraries constructed from 8, 12 and 18-day embryo. The
 tag is a string of 3-5 nucleotides present between the
 Not I site and the oligo-dT track which allows
 identification of the library of origin of a clone within
 the mixture."

ORIGIN

Query Match 83.3%; Score 18; DB 1; Length 335;
 Best Local Similarity 90.0%; Pred. No. 1e+03;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGTGCRCGCGATCTTGT 21
 ||||| :|||||||

Db 149 GAAGGTGTCGCGATCTTGT 130

RESULT 30

AA061605

LOCUS

DEFINITION

AA061605 570 bp mRNA linear EST 03-FEB-1997
 ml33e10.r1 Stratagene mouse testis (#937308) Mus musculus cDNA
 clone IMAGE:513834 5' similar to gb:X07862 Human mRNA for protamine
 2 (HUMAN); gb:X14004 Mouse protamine 2 mRNA (MOUSE);, mRNA
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AA061605.1 GI:1555405
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 570)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE

JOURNAL

COMMENT

The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:307682

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 241.

Location/Qualifiers

FEATURES

```

source
1. .570
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:513834"
/sex="males"
/tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse testis (#937308)"
/notes="Organ: testis; Vector: pBluecript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Oligo dr. Average insert size: 1.0 Kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match      83.3%; Score 18; DB 1; Length 570;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 543 AAGGGCCACGGATCTTGT 562

RESULT 31
BP294923/c
LOCUS
DEFINITION
BP294923 Sugano cDNA library, macrophage Homo sapiens cDNA clone
MPB06013, mRNA sequence.
ACCESSION
BP294923
VERSION
BP294923.1 GI:52223883
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 582)
Suzuki,Y., Yanashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1. .582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MPB06013"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

ORIGIN
Query Match      83.3%; Score 18; DB 3; Length 582;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTG 20
|||||:|||||
Db 353 TGAAGTGCACGGATCTTG 334

RESULT 32
AW727610
LOCUS
DEFINITION
AW727610 Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0015C14, mRNA sequence.
ACCESSION
AW727610
VERSION
AW727610.1 GI:7625168
KEYWORDS
EST.
SOURCE
Gossypium arboreum
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 1349)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1349.
Location/Qualifiers
1. .1349
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0015C14"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match      83.3%; Score 18; DB 1; Length 1349;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGTGCGCGGATCTTGT 21
|||||:|||||
Db 199 GAAGTACCACGGATCTTGT 218

RESULT 33
CL174879
LOCUS
DEFINITION
CL174879 Sorghum bicolor genomic clone 10891971, genomic survey
sequence.
ACCESSION
CL174879
VERSION
CL174879.1 GI:40687394
KEYWORDS
GSS.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 559)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and
Martensen,R.A.
Sorghum genome sequencing by methylation filtration
PLoS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA

```

```

LOCUS
DEFINITION
AW727610 1349 bp mRNA linear EST 08-MAR-2001
GA_Ea0015C14 Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0015C14, mRNA sequence.
ACCESSION
AW727610
VERSION
AW727610.1 GI:7625168
KEYWORDS
EST.
SOURCE
Gossypium arboreum
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 1349)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1349.
Location/Qualifiers
1. .1349
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0015C14"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match      83.3%; Score 18; DB 1; Length 1349;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGTGCGCGGATCTTGT 21
|||||:|||||
Db 199 GAAGTACCACGGATCTTGT 218

RESULT 33
CL174879
LOCUS
DEFINITION
CL174879 Sorghum bicolor genomic clone 10891971, genomic survey
sequence.
ACCESSION
CL174879
VERSION
CL174879.1 GI:40687394
KEYWORDS
GSS.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 559)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and
Martensen,R.A.
Sorghum genome sequencing by methylation filtration
PLoS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA

```

Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 379 row: O column: 03
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 559.

FEATURES

source

1. .559
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultiivar="ATx623"
/db_xref="taxon:4558"
/clone_lib="Sorghum methylation-filtered library (LibID: 104)"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."

ORIGIN

Query Match 81.5%; Score 17.6; DB 10; Length 559;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGTGCCRCGGATCTTGT 22
|||||:|||||
DB 375 GGTGCCACGGATCTTGT 392

RESULT 34

BF705257/c

LOCUS BF705257 179 bp mRNA linear EST 29-DEC-2000
DEFINITION RHIZ2_2_G01.b1_A003 Rhizome2 (RHIZ2) Sorghum propinquum cDNA, mRNA sequence.

ACCESSION BF705257

VERSION BF705257

KEYWORDS EST.

SOURCE Sorghum propinquum

ORGANISM Sorghum propinquum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 179)

AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.

TITLE An EST database from Sorghum: Sorghum propinquum rhizomes

JOURNAL Unpublished (2000)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Seq primer: JEN REV

High quality sequence stop: 141

POLYA=No.

FEATURES

source

1. .179
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/notes="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 179;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 127 GAAGTGTCACGGATCTTGT 107

RESULT 35

DR705480

LOCUS DR705480

DEFINITION Asn_05659 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus niger cDNA clone Asn_05659, mRNA sequence.

ACCESSION DR705480

VERSION DR705480

KEYWORDS EST.

SOURCE Aspergillus niger

ORGANISM Aspergillus niger

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. 1 (bases 1 to 218)

REFERENCE Tsang, A., Storms, R. and Bulter, G.

AUTHORS Expressed sequence tags from Aspergillus niger cDNA library

TITLE Unpublished (2005)

JOURNAL Contact: Tsang A

COMMENT Centre for Structural and Functional Genomics

Concordia University

7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada

Tel: 514 848 2424 3405

Fax: 514 848 4504

Email: tsang@vax2.concordia.ca

POLYA=No.

FEATURES

source

1. .218
/organism="Aspergillus niger"
/mol_type="mRNA"
/strain="N402"
/db_xref="taxon:5061"
/clone="Asn_05659"
/dev_stage="mycelial growth"
/lab_host="E. coli"
/clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
/note="Vector: pBluescript KS+; Site 1: XhoI; Site 2: EcoRI; Complementary DNA was synthesized with ZAP kit (Stratagene) using poly(A)+RNA isolated from Aspergillus niger cultured under different carbon sources (glucose, maltose, xylose, lactose, sorbitol, xylan, and bran). Synthesis was primed with oligo(dT)/XhoI primer. EcoRI adaptors were ligated to the blunt-ended, double-stranded cDNA. The EcoRI-XhoI-digested cDNA was ligated with EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."

ORIGIN

Query Match 80.6%; Score 17.4; DB 8; Length 218;
Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 21
|||||:|||||
DB 52 TGAAGGTACCACGGATCTTGT 72

RESULT 36

CX223617/c

LOCUS CX223617/c

DEFINITION MNS42007 Mouse Neurosphere Normalized cDNA library Mus musculus cDNA 5', mRNA sequence.

ACCESSION CX223617

VERSION CX223617

KEYWORDS EST.

```

SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 243)
AUTHORS
Williams, C., Wirtz, V., Lundberg, J. and Friese, J.
TITLE
Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL
Unpublished (2005)
COMMENT
Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
AlbaNova University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13REV.

FEATURES
source
Location/Qualifiers
1..243
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA
library was constructed in pCMVSPORT6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen"

ORIGIN
Query Match 80.6%; Score 17.4; DB 8; Length 243;
Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 21
Db 159 TGAAGTGTCTGGATCTTGT 139

RESULT 37
BJ280260/c
LOCUS
BJ280260 Y. Ogiwara unpublished cDNA library, Wh_r Triticum
DEFINITION
aestivum cDNA clone whr7e14 5', mRNA sequence.
ACCESSION
BJ280260
VERSION
BJ280260.1 GI:23144418
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 280)
AUTHORS
Ogiwara, Y. and Murai, K.
TITLE
Expressed genes in Triticum aestivum
JOURNAL
Unpublished (2002)
COMMENT
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
Location/Qualifiers
1..280
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"

```

```

/db_xref="taxon:4565"
/clone="whr7e14"
/tissue_type="root"
/dev_stage="Feekes" scale 1"
/clone_lib="Y. Ogiwara unpublished cDNA library, Wh_r"

ORIGIN
Query Match 80.6%; Score 17.4; DB 3; Length 280;
Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
Db 101 GAAGGTGTCCCGATGTGT 81

RESULT 38
BQ752687/c
LOCUS
BQ752687 Wheat salt-stressed root cDNA library Triticum
DEFINITION
aestivum cDNA clone WHE4118_A02_A04, mRNA sequence.
ACCESSION
BQ752687
VERSION
BQ752687.1 GI:21930469
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 285)
AUTHORS
Anderson, O.D., Akhunov, E., Chao, S., Crossman, C., Deal, K.,
Dvorak, J., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
TITLE
The structure and function of the expressed portion of the wheat
genomes - Salt-stressed root cDNA library
JOURNAL
Unpublished (2002)
COMMENT
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES
source
Location/Qualifiers
1..285
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4118_A02_A04"
/tissue_type="Roots"
/dev_stage="Full tillering"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Hydroponic
plants grown to full tillering stage were treated with 150
mM NaCl for either 12 hours or 7 days. Root tissues of the
plants subjected to both types of treatment were collected
separately at University of California, Davis (E. Akhunov
and K. Deal in J. Dvorak's Lab). Total RNA was prepared
separately from the two samples (12h and 7day treatments),
and equal amount of RNA was then pooled. PolyA RNA was
purified from the pooled RNA, a cDNA library was made, and
the cDNA clones were in vivo excised to give pluescript
SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak)
at the University of California, Davis. Colony plating,
plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."

ORIGIN

```

Query Match 80.6%; Score 17.4; DB 5; Length 285;
 Best Local Similarity 85.7%; Pred. No. 1.9e+03;
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCGCGGATCTTGT 22
 ||||| : |||||
 Db 203 GAAGGTGTCACGGATGTTGT 183

RESULT 39
 AJ474162/c 360 bp mRNA linear EST 24-MAY-2002
 LOCUS AJ474162 S00008 Hordeum vulgare cDNA clone S0000800247F08F1, mRNA
 DEFINITION sequence.

ACCESSION AJ474162
 VERSION AJ474162.1 GI:21190118
 KEYWORDS EST.
 SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 360)
 Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.
 TITLE Barley EST's
 JOURNAL Unpublished (2002)
 COMMENT Contact: Schulman AH
 Institute of Biotechnology
 University of Helsinki
 P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
 Finland.

FEATURES
 source
 1..360 Location/Qualifiers
 /organism="Hordeum vulgare"
 /mol_type="mRNA"
 /db_xref="taxon:4513"
 /clone="S0000800247F08F1"
 /tissue_type="Callus"
 /clone_lib="S00008"
 /note="Callus K19"

ORIGIN
 Query Match 80.6%; Score 17.4; DB 1; Length 360;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCGCGGATCTTGT 22
 ||||| : |||||
 Db 62 GAAGGTGTCGCGGATGTTGT 42

RESULT 40
 DR793683/c 374 bp mRNA linear EST 27-JUL-2005
 LOCUS DR793683
 DEFINITION ZM_BFB001A24.f_ZM_BFB Zea mays cDNA 3', mRNA sequence.

ACCESSION DR793683
 VERSION DR793683.1 GI:71314135
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 374)
 Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
 TITLE Maize Full-length cDNA Project
 JOURNAL Unpublished (2005)
 COMMENT Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585

Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu
 Plate: 0014 Row: A Column: 24.

FEATURES

source
 1..374 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="mixed (silks, husks, ears, pollen, shoot
 tips, leaf, root tips, whole seed, embryo)"
 /dev_stage="varies by tissue"
 /lab_host="DH10B T1 phage resistant"
 /clone_lib="ZM_BFB"
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
 NotI; Maize Full length cDNA library (3530 library)
 created by invitrogen from multiple tissues; Organ: silks,
 husks, ears, pollen, shoot tips, leaf, root tips, whole
 seed, embryo. This is a Gateway compatible vector,
 permitting clone movement to new vector backbones for
 expression in diverse host cells using recombination
 rather than restriction enzymes. poly(A)+ mRNA was
 prepared by invitrogen, and equimolar amounts of RNA from
 each of the 12 tissue samples were mixed together for
 selection of mRNA with a 5' cap. After synthesis of cDNA,
 a normalization step was conducted against the mixture of
 RNA sources. Tissues prepared: 1. just emerging silks; 2.
 inner husks from ears of sample #1; 3. 20 day aleurone; 4.
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
 15 day old seedlings; all leaves with an expanded or
 partially expanded sheath were removed; 8. mature leaf
 tissue; 9. 0.5 cm long root tips from 15 day old
 seedlings; 10. 10 day whole seed; 11. 12 day endosperm and
 embryo; 12. 17 day endosperm and embryo. All of the
 sequenced clones in Maize Full-length cDNA Project will be
 archived at the University of Arizona. Clones, high
 density filters and amplified library can be ordered from
 the University of Arizona
 (http://www.genome.arizona.edu/orders/)."

ORIGIN

Query Match 80.6%; Score 17.4; DB 8; Length 374;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCGCGGATCTTGT 22
 ||||| : |||||
 Db 307 GAAGGTGTCACGGATGTTGT 287

RESULT 41
 CF646223 386 bp mRNA linear EST 02-OCT-2003
 LOCUS CF646223
 DEFINITION 3530.1.111.1_C03.x.1 3530 - Full length cDNA library created by
 invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION CF646223
 VERSION CF646223.1 GI:37417141
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 386)
 Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3530.1.111.1 row: C column: 03.

FEATURES

source

Location/Qualifiers

1. .386
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="PH108"
 /clone_lib="3530 - Full length cDNA library created by
 Invitrogen from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
 Project contracted with Invitrogen to produce a
 normalized, full length library in a pSPORT vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZmDB in the EST library description tables. poly(A)+
 mRNA was prepared by Invitrogen, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 dap aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
 12 dap endosperm and embryo; 12. 17 dap endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 Unigene clones from the Maize Gene Discovery EST
 sequencing projects. Clones can be ordered through the
 ZmDB web site or directly from the University of Arizona
 (<http://www.genome.arizona.edu/orders/>). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

ORIGIN

Query Match 80.6%; Score 17.4; DB 6; Length 386;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAAGTGCCRCGGATCTGTT 22
 ||||| : |||||
 Db 100 GAAGGTGTCACGGATGTTT 120

RESULT 42

BI098781/c

LOCUS

DEFINITION IPI 33_B04.b1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
 mRNA sequence.

ACCESSION

BI098781

VERSION

EST.

KEYWORDS

Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 391)

AUTHORS

Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and

TITLE
 JOURNAL
 COMMENT

Pratt,L.H.
 An EST database from Sorghum: developing preanthesis pannicles
 Unpublished (2001)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
 below three quality 16. The threshold for high quality sequence is
 20. Three-prime sequences, which are obtained with PolyTwix or T7
 sequencing primer, are presented as the reverse complement.

Seq primer: JEN REV

High quality sequence stop: 239

POLYA=No.

FEATURES
 source

Location/Qualifiers

1. .391

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="BTx623"

/db_xref="taxon:4558"

/clone_lib="Immature pannicle 1 (IP1)"

/note="Organ: Developing preanthesis pannicles; Vector:

pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;

Site 2: EcoRI; The library was made from poly-A RNA in the

cloning vector lambda Zap II. Clones to be sequenced were

prepared by mass excision."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 391;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAAGTGCCRCGGATCTGTT 22

||||| : |||||

Db 58 GAAGGTGTCACGGATATTGTT 38

RESULT 43

BI098170/c

LOCUS

DEFINITION IPI 29_A02.b1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
 mRNA sequence.

ACCESSION

BI098170

VERSION

EST.

KEYWORDS

Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 397)

AUTHORS

Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and
 Pratt,L.H.

An EST database from Sorghum: developing preanthesis pannicles

Unpublished (2001)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below three quality 16. The threshold for high quality sequence is

20. Three-prime sequences, which are obtained with PolyTwix or T7

sequencing primer, are presented as the reverse complement.

Seq primer: JEN REV

High quality sequence stop: 389

POLYA=No.

FEATURES

Location/Qualifiers

```

source
1. .397
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IPI)"
/notes="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Query Match      80.6%; Score 17.4; DB 2; Length 397;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGTCRCGGATCTTGT 22
||||| 1:|||||
Db 330 GAAGGTGTCRCGGATCTTGT 310

RESULT 44
CF646224/c
LOCUS CF646224 404 bp mRNA linear EST 02-OCT-2003
DEFINITION 3530.1.111.1.C03.Y.1.3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION CF646224
VERSION CF646224.1 GI:37417143
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 404)
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530.1.111.1 row: C column: 03.

FEATURES
source
1. .404
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/notes="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSport vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the

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mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. Immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
vegetative shoot tips from 15 day old seedlings; all
leaves with an expanded or partially expanded sheath
were removed; 8. mature leaf tissue; 9. 0.5 cm long root
tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
12 dap endosperm and embryo; 12. 17 dap endosperm and
embryo. All of the sequenced clones in project 3530 will
be archived at the University of Arizona along with the
Unigene clones from the Maize Gene Discovery EST
sequencing projects. Clones can be ordered through the
ZmDB web site or directly from the University of Arizona
(http://www.genome.arizona.edu/orders/). High density
filters containing over 18,000 clones can also be ordered
from the University of Arizona."

ORIGIN
Query Match      80.6%; Score 17.4; DB 6; Length 404;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGTCRCGGATCTTGT 22
||||| 1:|||||
Db 305 GAAGGTGTCRCGGATCTTGT 285

RESULT 45
BI098323/c
LOCUS BI098323 417 bp mRNA linear EST 26-JUN-2001
DEFINITION IPI_31_A02.b1_A002 Immature pannicle 1 (IPI) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BI098323
VERSION BI098323.1 GI:14569905
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 417)
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and
Pratt, L.H.
An EST database from Sorghum: developing preanthesis pannicles
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTMix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 402
POLYA=No.

FEATURES
source
1. .417
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IPI)"
/notes="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

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ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 417;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCCGGATCTTGT 22
 |||||:|||||
 Db 330 GAAGGTGCCCGGATCTTGT 310

RESULT 46

AQ406201
 LOCUS
 DEFINITION HS_5047_B2_F08_SP68 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=623 Col=16 Row=L, genomic survey sequence.

ACCESSION AQ406201
 VERSION AQ406201.1 GI:4411566

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 426)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764

JOURNAL

PUBMED

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu

Plate: 623 row: L column: 16

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 426.

FEATURES

source

1..426
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=623 Col=16 Row=L"
 /sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 80.6%; Score 17.4; DB 9; Length 426;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGTCGCGGATCTTGT 21
 |||||:|||||

Db 77 TGAAGTGTCGCGGATCTTGT 97

RESULT 47

BI074698/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

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QY

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QY

Db

QY

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QY

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QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 2036 Std Error: 0.00
High quality sequence stop: 421.

FEATURES

source

1. .437
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Supernod"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-3806"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
/clone_lib="Gm-cl028"
/notes="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicum, strain USDA110 prior to harvest. Stratagene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGACTGCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

ORIGIN

Query Match 80.6%; Score 17.4; DB 1; Length 437;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAAGGTGCCRCGGATCTTGT 22

|||||1:|||||

Db 363 GAAGGTGCACGGATCTTGT 343

RESULT 49

BF325403/c

LOCUS

438 bp mRNA linear EST 13-JUL-2004

DEFINITION

su21c08.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl066-2056 5' similar to TR:024052 024052
3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE PRECURSOR ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 438)

REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corveill,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

TITLE

JOURNAL

COMMENT

Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1931 Std Error: 0.00
High quality sequence stop: 421.

FEATURES

source

1. .438
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2056"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week old seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 438;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAAGGTGCCRCGGATCTTGT 22

|||||1:|||||

Db 342 GAAGGTGCACGGATCTTGT 322

RESULT 50

```

BQ133585/c
LOCUS       BQ133585               447 bp     mRNA      linear      EST 05-JUL-2004
DEFINITION  3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE PRECURSOR ;,
            Gm-c1052-3943 5' similar to TR:024052 024052
            mRNA sequence.
ACCESSION   BQ133585
VERSION     BQ133585.1  GI:20207496
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 447)
AUTHORS    Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvett,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Stebbins,M., Theising,B., Allen,M.,
            Bowers,J., Person,B., Swallier,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
            Public Soybean EST Project
            Unpublished (1999)
            Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES    Location/Qualifiers
             1..447
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Harosoy"
                /db_xref="taxon:3847"
                /clone="SOYBEAN CLONE ID: Gm-c1052-3943"
                /tissue_type="whole seedlings of greenhouse grown plants"
                /dev_stage="1 week old"
                /lab_host="DH10B"
                /clone_lib="Gm-c1052"
                /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                XhoI; The Harosoy NIL was constructed and seed was
                provided by Dr. J. Specht, University of Nebraska
                (Shoemaker and Specht, 1995). The cDNA library was
                constructed from mRNA isolated from whole seedlings of 1
                week old greenhouse grown plants. Complementary DNA was
                synthesized from mRNA using a primer consisting of a
                poly(dT) sequence with a XhoI restriction site and a 3'
                anchor. EcoRI adapters were ligated to the blunt-ended
                cDNA fragments followed by XhoI digestion. The cDNA
                fragments were directionally cloned into the EcoRI-XhoI
                restriction site of the pBluescript vector. The ligated
                cDNA fragments were transformed into DH10B host cells
                (GibcoBRL). The library was constructed in cooperation
                with Dr. Paul Keim's laboratory at Northern Arizona
                University."
ORIGIN
Query Match      80.6%; Score 17.4; DB 3; Length 447;
Best Local Similarity 85.7%; Pred. NO. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2  GAAGGTGCGCGGATCTGTT 22
        ||||| : |||||
DB      380 GAAGGTGTCACGGATGTTGTT 360

```

RESULT 51
CB541407/c

LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS

SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

FEATURES
source

ORIGIN

Query Match
Best Local Similarity
Matches 18; Conservative

80.6%; Score 17.4; DB 6; Length 462;
85.7%; Pred. No. 2e+03;
1; Mismatches 2; Indels 0; Gaps 0;

CB541407
PVPFSE2033C10.9 Common bean seedling EST Library - PVPFSE2
Phaseolus vulgaris cDNA clone PVPFSE2033C10 5', mRNA sequence.

CB541407
EST.
CB541407.1 GI:59935970

Phaseolus vulgaris
Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.

1 (bases 1 to 462)
Melotto,M., Monteiro-Vitorello,C.B., Bruschi,A.G. and
Camargo,L.E.A.

Comparative bioinformatic analysis of genes expressed in common
bean (Phaseolus vulgaris L.) seedlings
Genome 48 (3), 562-570 (2005)

Contact: Maeli Melotto
Laboratory of Molecular Genetics, Dept. of Plant Pathology
ESALQ - University of Sao Paulo

Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4124
Fax: 55 19 3434 3839

Email: melotto@msu.edu
PCR Primers
BACKWARD: M13 reverse

High quality sequence stop: 461.
Location/Qualifiers
1..462

/organism="Phaseolus vulgaris"
/mol_type="mRNA"
/cultivar="SEL 1308"

/db_xref="taxon:3885"
/clone="PVPFSE2033C10"
/tissue_type="shoot"

/dev_stage="10 days after seed germination"
/lab_host="E. coli DH10B"

/clone_lib="Common bean seedling EST Library - PVPFSE2"
/note="Vector: pSPORT 1; Site 1: Not I; Site 2: Sal I;
mRNA from bean tissue was extracted with the FastTrack 2.0

kit (Invitrogen) and mRNA sample quality was checked in
1.2% formaldehyde-agarose gel. cDNA was synthesized and
cloned into either pCMV Sport 6 or the pSPORT 1 vector

with the SuperScript Plasmid System with Gateway
Technology kit (Gibco BRL) as indicated by the
manufacturer. Recombinant colonies were cultured in

96-well plates and maintained in liquid LB medium with
ampicillin (100ug/ml) and 8% glycerol at -80°C. Plasmid
miniprep was conducted in 96-well plates using standard

procedure and sequencing of the cDNA was performed in
96-well PCR plates using the Big Dye Terminator Cycle
Sequencing Ready Reaction Kit (Applied Biosystems). Clones

were sequenced from the 5' end using either M13 Reverse or
the T7 primer. PCR file consisted of 25 cycles of 10 sec.
at 96°C, 5 sec. at 50°C, and 4 min. at 60°C. After PCR

product precipitation, large-scale automated sequencing
was carried out in a capillary system (3700 ABI Sequencer,
Applied Biosystems). Raw data from sequencing was

validated in a series of automated routine analyses
including Phred/CRP3/Consed programs and Perl scripts
created by our team. Reads that did not have at least 300

bases with Phred quality of 20 were not included in the
analysis."


```

/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/notes="Vector: pGT0Lxf"

ORIGIN
Query Match      80.6%; Score 17.4; DB 10; Length 480;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 21
||||| : |||||
Db 390 TGAAGGTGCTGCGAATCTTGT 370

RESULT 55
CW368267/c
LOCUS
DEFINITION
fabb001f042c11f0 Sorghum methylation filtered library (LibID: 104)
Sorghum bicolor genomic clone fabb001f042c11, genomic survey
sequence.
ACCESSION
CW368267
VERSION
CW368267.1 GI:55086711
KEYWORDS
GSS
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 481)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Hogleman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
Plos Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 5979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fbb001f042 row: c column: 11
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 481.
Location/Qualifiers
1..481
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match      80.6%; Score 17.4; DB 10; Length 481;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 21
||||| : |||||
Db 59 TGAAGGTTCACGAATCTTGT 39

/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/notes="Vector: pGT0Lxf"

ORIGIN
Query Match      80.6%; Score 17.4; DB 10; Length 480;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 21
||||| : |||||
Db 390 TGAAGGTGCTGCGAATCTTGT 370

RESULT 56
CW367138/c
LOCUS
DEFINITION
1000111H09.x3 1000 - Unigene 1 from Maize Genome Project Zea mays
cDNA, mRNA sequence.
ACCESSION
BG267138
VERSION
BG267138.1 GI:12970747
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 487)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1000111 row: H column: 09.
Location/Qualifiers
1..487
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="dbEST:605050H10.x1"
/db_xref="taxon:4577"
/clone_lib="1000 - Unigene 1 from Maize Genome Project"
/notes="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets were
also selected."

ORIGIN
Query Match      80.6%; Score 17.4; DB 2; Length 487;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCRCGGATCTTGT 22
||||| : |||||
Db 39 GAAGGTGTCACGAATCTTGT 19

RESULT 57
CA181673/c
LOCUS
DEFINITION
SCBFST3135C05.g ST3 Saccharum officinarum cDNA clone SCBFST3135C05
5', mRNA sequence.
ACCESSION
CA181673
VERSION
CA181673.1 GI:35116676
KEYWORDS
EST.
SOURCE
Saccharum officinarum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE
1 (bases 1 to 487)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica

```

Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccen.ufv.br
Plate: 135 row: C column: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers

FEATURES

source
1. .487
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCBFST3135C05"
/lab_host="DH10B"
/clone_lib="ST3"

/notes="Organ: Fourth apical internodes of adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 80.6%; Score 17.4; DB 6; Length 487;

Best Local Similarity 85.7%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 2;

QY 2 GAAGGTGCCRCGGATCTTGT 22
||||| :|||||
Db 52 GAAGGTGCCRCGGATCTTGT 32

RESULT 58

BG550996/c

LOCUS

DEFINITION

BG550996 489 bp mRNA linear EST 22-JUL-2004
ead31h01.y1 Gm-cl074 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl074-1898 5' similar to TR.Q42921 Q42921
3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE ; mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 489)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCam, R., Waterston, R. and Wilson, R.

TITLE

JOURNAL

COMMENT

Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 400.

FEATURES

source

1. .489
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl074-1898"
/tissue type="seedlings induced for HR (hypersensitive
response)"

/dev stage="9-11 day old"

/lab_host="DH10B"

/clone_lib="Gm-cl074"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from 9-11 day old seedlings that were induced for HR
(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
and 53 hrs after inoculation and their mRNA pooled equally
for cDNA construction. The library was prepared using the
Stratagene pBluescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with an XhoI restriction
site. EcoRI adaptors were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA insert is
protected from XhoI digestion via methylation during first
strand synthesis. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into E.coli ElectroMax DH10B host cells. Plant
care, inoculations, and library construction were
performed by Steve Clough (Lila Vodkin lab, University of
Illinois)."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 489;

Best Local Similarity 85.7%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 2;

QY 2 GAAGGTGCCRCGGATCTTGT 22
||||| :|||||
Db 30 GAAGGTGCCRCGGATCTTGT 10

RESULT 59

LOCUS

DEFINITION

CA182253 499 bp mRNA linear EST 24-SEP-2003
SCBGST3109D03.g S73 Saccharum officinarum cDNA clone SCBGST3109D03
5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 499)
Vettore, A.L., da Silva, P.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bccccenter.fcav.unesp.br>
 Plate: 109 row: D column: 03
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers
 1. .499
 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCBGST3109D03"
 /lab_host="DH10B"
 /clone_lib="ST3"
 /note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 80.6%; Score 17.4; DB 6; Length 499;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 ||||| : |||||
 Db 119 GAAGTGTCGCGGATGTTGT 99

RESULT 60

AA763342
 LOCUS
 DEFINITION
 IMAGE:1247520 5' similar to TR:Q12845 Q12845 HYPOTHETICAL PROTEIN
 ; mRNA sequence.
 AA763342
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 504)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:661208
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 495.
 Location/Qualifiers
 1. .504

FEATURES

source

/organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1247520"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /clone_lib="Soares mammary gland NLMG"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
 ORIGIN
 Query Match 80.6%; Score 17.4; DB 1; Length 504;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TGAAGTGCCRCGGATCTTGT 21
 ||||| : |||||
 Db 8 TGAAGTGTCGCGGATCTTGT 28

Search completed: April 2, 2006, 00:09:46
 Job time : 308.022 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:17:36 ; Search time 59.2198 Seconds
(without alignments)
3072.051 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaagtgccrcggatctgtt 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : Published Applications NA_Main:*
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	100.0	22	8	US-10-824-527-2
2	21.6	100.0	337	3	US-09-880-505-77
3	21.6	100.0	337	5	US-10-051-643-77
4	21.6	100.0	927	3	US-09-880-505-116
5	21.6	100.0	927	5	US-10-051-643-116
6	21.6	100.0	985	3	US-09-880-505-161
7	21.6	100.0	985	5	US-10-051-643-161
8	21.6	100.0	985	6	US-10-205-979-16
9	21.6	100.0	1569	3	US-09-880-505-113
10	21.6	100.0	1569	5	US-10-051-643-113
11	21.6	100.0	1620	7	US-10-282-122A-26142
12	21.6	100.0	1623	3	US-09-712-363-23
13	21.6	100.0	1623	5	US-10-267-311-3
14	21.6	100.0	1623	6	US-10-156-761-3915
15	21.6	100.0	1623	7	US-10-282-122A-25595
16	21.6	100.0	1623	9	US-10-282-122A-28196
17	21.6	100.0	1623	3	US-09-880-505-159
18	21.6	100.0	1626	5	US-10-051-643-159
19	21.6	100.0	1626	6	US-10-205-979-14
20	21.6	100.0	1626	7	US-10-392-041-3
21	21.6	100.0	1626	8	US-10-394-763-3
22	21.6	100.0	1626	8	US-10-392-387-3
23	21.6	100.0	1626	8	US-10-392-387-3

C 24	21.6	100.0	1626	9	US-10-491-300-1	Sequence 1, Appl
C 25	21.6	100.0	1638	7	US-10-282-122A-17670	Sequence 17670, A
C 26	21.6	100.0	1644	3	US-09-738-626-2986	Sequence 2986, App
C 27	21.6	100.0	1701	9	US-10-501-127A-21	Sequence 21, Appl
C 28	21.6	100.0	1761	8	US-10-635-211-1	Sequence 1, Appl
C 29	21.6	100.0	1920	5	US-10-267-311-16	Sequence 16, Appl
C 30	21.6	100.0	1920	5	US-10-679-956-16	Sequence 16, Appl
C 31	21.6	100.0	1947	5	US-10-267-311-28	Sequence 28, Appl
C 32	21.6	100.0	1947	5	US-10-679-956-28	Sequence 28, Appl
C 33	21.6	100.0	2073	5	US-10-068-059-9	Sequence 9, Appl
C 34	21.6	100.0	2073	9	US-10-941-049-9	Sequence 9, Appl
C 35	21.6	100.0	2130	5	US-10-068-059-7	Sequence 7, Appl
C 36	21.6	100.0	2130	9	US-10-941-049-7	Sequence 7, Appl
C 37	21.6	100.0	2175	5	US-10-068-059-11	Sequence 11, Appl
C 38	21.6	100.0	2175	9	US-10-941-049-11	Sequence 11, Appl
C 39	21.6	100.0	2241	5	US-10-068-059-5	Sequence 5, Appl
C 40	21.6	100.0	2241	9	US-10-941-049-5	Sequence 5, Appl
C 41	21.6	100.0	2847	5	US-10-267-311-20	Sequence 20, Appl
C 42	21.6	100.0	2847	9	US-10-679-956-20	Sequence 20, Appl
C 43	21.6	100.0	86114	6	US-10-080-170-648	Sequence 648, App
C 44	21.6	100.0	86114	7	US-10-080-170-648	Sequence 648, App
C 45	21.6	100.0	86114	8	US-10-468-356-648	Sequence 648, App
C 46	21.6	100.0	3309400	3	US-09-738-626-1	Sequence 1, Appl
C 47	21.6	100.0	9025608	6	US-10-156-761-1	Sequence 1, Appl
C 48	20	92.6	732	6	US-10-264-213-63	Sequence 63, Appl
C 49	20	92.6	1626	6	US-10-156-761-4976	Sequence 4976, Ap
C 50	20	92.6	1626	7	US-10-282-122A-27502	Sequence 27502, A
C 51	20	92.6	1728	6	US-10-369-493-32009	Sequence 32009, A
C 52	20	92.6	2256646	7	US-10-470-565-1	Sequence 1, Appl
C 53	20	92.6	9025608	6	US-10-156-761-1	Sequence 1, Appl
C 54	19.6	90.7	20	8	US-10-500-586-56	Sequence 56, Appl
C 55	18.4	85.2	552	8	US-10-857-542-18	Sequence 18, Appl
C 56	18.4	85.2	552	8	US-10-857-542-27	Sequence 27, Appl
C 57	18.4	85.2	552	8	US-10-857-542-35	Sequence 35, Appl
C 58	18.4	85.2	552	8	US-10-857-542-38	Sequence 38, Appl
C 59	18.4	85.2	552	8	US-10-857-542-39	Sequence 39, Appl
C 60	18.4	85.2	552	8	US-10-857-542-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-10-824-527-2
; Sequence 2, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823 0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer

US-10-824-527-2

Query Match 100.0%; Score 21.6; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||

RESULT 2

US-09-880-505-77/c
; Sequence 77, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.6; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 3

US-10-051-643-77/c
; Sequence 77, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-77

Query Match 100.0%; Score 21.6; DB 5; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.6; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 4

US-09-880-505-116/c
; Sequence 116, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-116

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 5

US-10-051-643-116/c
; Sequence 116, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-116

Query Match 100.0%; Score 21.6; DB 5; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

```
RESULT 6
US-09-880-505-161/c
; Sequence 161, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-161

Query Match      100.0%; Score 21.6; DB 3; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 7
US-10-051-643-161/c
; Sequence 161, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-161

Query Match      100.0%; Score 21.6; DB 5; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 8
US-10-205-979-16/c
; Sequence 16, Application US/10205979
; Publication No. US20030147861A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-205-979-16

Query Match      100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 9
US-09-880-505-113/c
; Sequence 113, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-113

Query Match      100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 10
US-10-051-643-113/c
; Sequence 113, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
```

; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-113

Query Match 100.0%; Score 21.6; DB 5; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 11
US-10-282-122A-26142/c
; Sequence 26142, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26142
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-26142

Query Match 100.0%; Score 21.6; DB 7; Length 1620;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 12
US-09-712-363-23/c
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 13
US-10-267-311-3/c
; Sequence 3, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08

; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 1623
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 100.0%; Score 21.6; DB 5; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 14
US-10-156-761-3915/c
; Sequence 3915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3915
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
US-10-156-761-3915

Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 15
US-10-282-122A-25595/c
; Sequence 25595, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25595
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25595

Query Match 100.0%; Score 21.6; DB 7; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 16
US-10-282-122A-28196/c
; Sequence 28196, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

```
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28196
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28196

Query Match      100.0%; Score 21.6; DB 7; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 17
US-10-679-956-3/c
; Sequence 3, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-679-956-3

Query Match      100.0%; Score 21.6; DB 9; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 18
US-09-880-505-159/c
```

```
; Sequence 159, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-159

Query Match      100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 19
US-10-051-643-159/c
; Sequence 159, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-159

Query Match      100.0%; Score 21.6; DB 5; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 20
US-10-205-979-14/c
; Sequence 14, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
```

; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-205-979-14

Query Match 100.0%; Score 21.6; DB 6; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 21
US-10-392-041-3/c
; Sequence 3, Application US/10392041
; Publication No. US20040101826A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Alison M.
; APPLICANT: Robey, W. Wade
; TITLE OF INVENTION: Monitoring High-Risk Environments
; FILE REFERENCE: 12794/010001
; CURRENT APPLICATION NUMBER: US/10/392,041
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 10/306,113
; PRIOR FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Staphylococcus coelicolor
US-10-392-041-3

Query Match 100.0%; Score 21.6; DB 7; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 814 TGAAGGTGCGCGGATCTTGT 793

RESULT 22
US-10-394-763-3/c
; Sequence 3, Application US/10394763
; Publication No. US20040101917A1
; GENERAL INFORMATION:
; APPLICANT: Robey, W. Wade
; APPLICANT: Jones, Alison M.
; TITLE OF INVENTION: Methods for Managing Animal Processing
; FILE REFERENCE: 12794/012001
; CURRENT APPLICATION NUMBER: US/10/394,763
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 10/306,113
; PRIOR FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1626

; TYPE: DNA
; ORGANISM: Staphylococcus coelicolor
US-10-394-763-3

Query Match 100.0%; Score 21.6; DB 7; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
|||||:|||||
Db 814 TGAAGTGCGCGGATCTTGT 793

RESULT 23
US-10-392-387-3/c
; Sequence 3, Application US/10392387
; Publication No. US20040185446A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Alison M.
; APPLICANT: Robey, W. Wade
; APPLICANT: Hemmingsen, Sean
; APPLICANT: Hill, Janet
; APPLICANT: Van Kessel, Andrew
; TITLE OF INVENTION: Cpns60 targets for Quantification of
; FILE REFERENCE: 16671-009001
; CURRENT APPLICATION NUMBER: US/10/392,387
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-392-387-3

Query Match 100.0%; Score 21.6; DB 8; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22
|||||:|||||
Db 814 TGAAGTGCGCGGATCTTGT 793

RESULT 24
US-10-491-300-1/c
; Sequence 1, Application US/10491300
; Publication No. US20050063984A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTH AUSTRALIA
; APPLICANT: MEDVET SCIENCE PTY LTD
; APPLICANT: RURAL INDUSTRIES RESEARCH AND DEVELOPMENT CORPORATION
; TITLE OF INVENTION: GroEL Chimeric Protein and Vaccine
; FILE REFERENCE: A20-061
; CURRENT APPLICATION NUMBER: US/10/491,300
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rhodococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
; OTHER INFORMATION: groEL gene
US-10-491-300-1

Query Match 100.0%; Score 21.6; DB 9; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGT 22

Db 808 TGAAGGTGCCACGGAATCTTGT 787
|||||:|||||:|||||:|||||

RESULT 25

US-10-282-122A-17670/c
; Sequence 17670, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Cheryl
; APPLICANT: Malone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17670

; LENGTH: 1638

; TYPE: DNA

; ORGANISM: Corynebacterium diptheriae

US-10-282-122A-17670

Query Match 100.0%; Score 21.6; DB 7; Length 1638;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCACGGAATCTTGT 22
|||||:|||||:|||||:|||||
Db 823 TGAAGGTGCCACGGAATCTTGT 802

RESULT 26

US-09-738-626-2986/c
; Sequence 2986, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2986
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-2986

Query Match 100.0%; Score 21.6; DB 3; Length 1644;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCACGGAATCTTGT 22
|||||:|||||:|||||:|||||
Db 823 TGAAGGTGCCACGGAATCTTGT 802

RESULT 27

US-10-501-127A-21/c
; Sequence 21, Application US/10501127A
; Publication No. US20050232937A1
; GENERAL INFORMATION:
; APPLICANT: ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid.
; TITLE OF INVENTION: Paramycobacterial diagnostics and vaccines
; FILE REFERENCE: 2002-032-US
; CURRENT APPLICATION NUMBER: US/10/501,127A
; CURRENT FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: mycobacterium avium paratuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1701)
US-10-501-127A-21

Query Match 100.0%; Score 21.6; DB 9; Length 1701;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCACGGAATCTTGT 22
|||||:|||||:|||||:|||||
Db 883 TGAAGGTGCCACGGAATCTTGT 862

RESULT 28

US-10-635-211-1/c
; Sequence 1, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein
; FILE REFERENCE: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
; NAME/KEY: CDS
; LOCATION: (1)..(1761)
US-10-635-211-1

Query Match 100.0%; Score 21.6; DB 8; Length 1761;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 29

US-10-267-311-16/c
; Sequence 16, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)....(1917)
US-10-267-311-16

Query Match 100.0%; Score 21.6; DB 5; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 30

US-10-679-956-16/c
; Sequence 16, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303

; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)....(1917)
US-10-679-956-16

Query Match 100.0%; Score 21.6; DB 9; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 31

US-10-267-311-28/c
; Sequence 28, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)....(1944)
US-10-267-311-28

Query Match 100.0%; Score 21.6; DB 5; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 1132 TGAAGTGCCRCGGATCTTGT 1111

RESULT 32

US-10-679-956-28/c
; Sequence 28, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001

```
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match          100.0%; Score 21.6; DB 9; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1132 TGAAGTGCCGCGGATCTTGT 1111

RESULT 33
US-10-068-059-9/c
; Sequence 9, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match          100.0%; Score 21.6; DB 5; Length 2073;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1258 TGAAGTGCCGCGGATCTTGT 1237

RESULT 34
US-10-941-049-9/c
; Sequence 9, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
```

; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-7

Query Match 100.0%; Score 21.6; DB 9; Length 2130;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1315 TGAAGTGCCRCGGATCTTGT 1294

RESULT 37
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 21.6; DB 5; Length 2175;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1360 TGAAGTGCCRCGGATCTTGT 1339

RESULT 38
US-10-941-049-11/c
; Sequence 11, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14

; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-11

Query Match 100.0%; Score 21.6; DB 9; Length 2175;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1360 TGAAGTGCCRCGGATCTTGT 1339

RESULT 39
US-10-068-059-5/c
; Sequence 5, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 21.6; DB 5; Length 2241;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1426 TGAAGTGCCRCGGATCTTGT 1405

RESULT 40
US-10-941-049-5/c
; Sequence 5, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059

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; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-5

Query Match      100.0%; Score 21.6; DB 9; Length 2241;
Best Local Similarity 95.5%; Pred. No. 0.72;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGCGATCTTGT 22
    |||||:|||||
Db 1426 TGAAGTGCRCGCGATCTTGT 1405

RESULT 41
US-10-267-311-20/c
; Sequence 20, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
; OTHER INFORMATION: fusion sequence
US-10-679-956-20/c

Query Match      100.0%; Score 21.6; DB 9; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.72;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGCGATCTTGT 22
    |||||:|||||
Db 868 TGAAGTGCRCGCGATCTTGT 847

RESULT 42
US-10-679-956-20/c
; Sequence 20, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; SEQ ID NO 5
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
; OTHER INFORMATION: fusion sequence
US-10-679-956-20/c

Query Match      100.0%; Score 21.6; DB 5; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.72;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGCGATCTTGT 22
    |||||:|||||
Db 868 TGAAGTGCRCGCGATCTTGT 847

RESULT 43
US-10-080-170-648/c
; Sequence 648, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: fusion sequence
US-10-080-170-648

Query Match      100.0%; Score 21.6; DB 6; Length 86114;
Best Local Similarity 95.5%; Pred. No. 0.97;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGCGATCTTGT 22
    |||||:|||||
Db 16012 TGAAGTGCRCGCGATCTTGT 15991

RESULT 44
US-10-080-170-648/c
; Sequence 648, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; CURRENT APPLICATION NUMBER: US/10/679,956

```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-648

Query Match      100.0%; Score 21.6; DB 7; Length 86114;
Best Local Similarity 95.5%; Pred. No. 0.97;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 16012 TGAAGGTGCCRCGGATCTTGT 15991

RESULT 45
US-10-468-356-648/c
; Sequence 648, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468,356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-468-356-648

Query Match      100.0%; Score 21.6; DB 8; Length 86114;
Best Local Similarity 95.5%; Pred. No. 0.97;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 16012 TGAAGGTGCCRCGGATCTTGT 15991

RESULT 46
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
```

```
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      100.0%; Score 21.6; DB 3; Length 3309400;
Best Local Similarity 95.5%; Pred. No. 1.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 2889718 TGAAGGTGCCRCGGATCTTGT 2889739

RESULT 47
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      100.0%; Score 21.6; DB 6; Length 9025608;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 4855012 TGAAGGTGCCRCGGATCTTGT 4855033

RESULT 48
US-10-264-213-63/c
; Sequence 63, Application US/10264213
; Publication No. US20040009490A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Lubbers, Mark William
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043c
; CURRENT APPLICATION NUMBER: US/10/264,213
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 253
```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-10-264-213-63

Query Match 92.6%; Score 20; DB 6; Length 732;
Best Local Similarity 90.9%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||
Db 229 TGAAGGTGCCACGAATCTTGT 208

RESULT 49
US-10-156-761-4976/c
; Sequence 4976, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4976
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1626)
US-10-156-761-4976

Query Match 92.6%; Score 20; DB 6; Length 1626;
Best Local Similarity 90.9%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||
Db 814 TGAAGGTGCCCGCATCTTGT 793

RESULT 50
US-10-282-122A-27502/c
; Sequence 27502, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27502
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-282-122A-27502

Query Match 92.6%; Score 20; DB 7; Length 1626;
Best Local Similarity 90.9%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCACGATCTTGT 787

RESULT 51
US-10-369-493-32009/c
; Sequence 32009, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32009
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-369-493-32009

Query Match 92.6%; Score 20; DB 6; Length 1728;
Best Local Similarity 90.9%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||
Db 916 TGAAGGTACCGCGCATCTTGT 895

RESULT 52

US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1

Query Match 92.6%; Score 20; DB 7; Length 2256646;
Best Local Similarity 90.9%; Pred. No. 8.8;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 1640 TGAAGTGCCACGGATGTGTT 1619

RESULT 53

US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 92.6%; Score 20; DB 6; Length 9025608;
Best Local Similarity 90.9%; Pred. No. 9.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 6041755 TGAAGTGCCGCGGATCTTGTT 6041734

RESULT 54

US-10-500-586-56
; Sequence 56, Application US/10500586

; Publication No. US20050014157A1

; GENERAL INFORMATION:
; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIES
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSPR3
US-10-500-586-56

Query Match 90.7%; Score 19.6; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.1;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 1 AAGGTGCCRCGGATCTTGTT 20

RESULT 55

US-10-857-542-18/c
; Sequence 18, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
US-10-857-542-18

Query Match 85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 538 TGAATGTGCCACGAATCTTGTT 517

RESULT 56

US-10-857-542-27/c
; Sequence 27, Application US/10857542
; Publication No. US20050026188A1

```
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.IUS
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-27

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   ||||| ||:| |||||
Db 538 TGAAGTGCCACCAATCTTGT 517

RESULT 57
US-10-857-542-35/c
; Sequence 35, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.IUS
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-35

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   ||||| ||:| |||||
Db 538 TGAAGTGCCACCAATCTTGT 517

RESULT 58
US-10-857-542-38/c
; Sequence 38, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.IUS
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-38

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   ||||| ||:| |||||
Db 538 TGAAGTGCCACCAATCTTGT 517

RESULT 59
US-10-857-542-39/c
; Sequence 39, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.IUS
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-39

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   ||||| ||:| |||||
Db 538 TGAAGTGCCACCAATCTTGT 517

RESULT 60
US-10-857-542-41/c
; Sequence 41, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
```

; APPLICANT: Hemmingen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; TITLE OF INVENTION: Communities
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
US-10-857-542-41

Query Match 85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 538 TGAAGGTACCGAGATCTTGT 517
|||||

Search completed: April 2, 2006, 01:14:50
Job time : 68.2198 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:19:05 ; Search time 54.3836 Seconds
(without alignments)
1615.302 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaaggtagccggatctgtt 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	18.4	85.2	555	14	US-11-055-637-99	
C 2	18.4	85.2	1654	11	US-11-201-916-3	
C 3	18.3	1400	14	US-11-136-527-8176	Sequence 99, Appl	
C 4	18.3	9176	14	US-11-136-527-4080	Sequence 3, Appl	
C 5	17.4	80.6	399	6	US-09-925-065A-141335	Sequence 8176, Ap
C 6	17.4	80.6	401	10	US-10-301-480-141335	Sequence 4080, Ap
C 7	17.4	80.6	401	10	US-10-301-480-236251	Sequence 141335,
C 8	17.4	80.6	1587	9	US-10-897-981-11	Sequence 236251,
C 9	17.4	80.6	1683	14	US-11-131-479-37	Sequence 849660,
C 10	17.4	80.6	1836	11	US-11-096-568A-7645	Sequence 11, Appl
C 11	17.4	80.6	2590	9	US-11-096-568A-19419	Sequence 37, Appl
C 12	17.4	80.6	2619	9	US-10-932-182A-78771	Sequence 7645, Ap
C 13	17.2	79.6	2619	9	US-10-932-182A-78771	Sequence 19419, A
C 14	17.2	79.6	2619	9	US-10-932-182A-78771	Sequence 3, Appl
C 15	17.2	78.7	25	14	US-11-136-527-294718	Sequence 78771, A
C 16	17.7	78.7	1400	14	US-11-136-527-6229	Sequence 294718,
C 17	17.7	78.7	1415	14	US-11-136-527-2133	Sequence 6229, Ap
C 18	16.8	77.8	25	14	US-11-136-527-238844	Sequence 2133, Ap
					Sequence 238844,	

C 19	16.8	77.8	25	14	US-11-136-527-238846	Sequence 238846,
C 20	16.8	77.8	486	14	US-11-136-527-964	Sequence 964, App
C 21	16.8	77.8	486	14	US-11-136-527-964	Sequence 5060, Ap
C 22	16.8	77.8	547	6	US-09-925-065A-390792	Sequence 390792,
C 23	16.8	77.8	547	6	US-09-925-065A-390793	Sequence 390793,
C 24	16.8	77.8	547	6	US-09-925-065A-390794	Sequence 390794,
C 25	16.8	77.8	547	6	US-09-925-065A-390795	Sequence 390795,
C 26	16.8	77.8	552	14	US-11-055-637-112	Sequence 112, App
C 27	16.8	77.8	559	10	US-10-301-480-459081	Sequence 459081,
C 28	16.8	77.8	559	10	US-10-301-480-459082	Sequence 459082,
C 29	16.8	77.8	559	10	US-10-301-480-459083	Sequence 459083,
C 30	16.8	77.8	559	10	US-10-301-480-459084	Sequence 459084,
C 31	16.8	77.8	559	10	US-10-301-480-1072490	Sequence 1072490,
C 32	16.8	77.8	559	10	US-10-301-480-1072491	Sequence 1072491,
C 33	16.8	77.8	559	10	US-10-301-480-1072492	Sequence 1072492,
C 34	16.8	77.8	559	10	US-10-301-480-1072493	Sequence 1072493,
C 35	16.8	77.8	637	6	US-09-925-065A-697497	Sequence 697497,
C 36	16.8	77.8	637	6	US-09-925-065A-697498	Sequence 697498,
C 37	16.8	77.8	1562	11	US-11-096-568A-5292	Sequence 5292, Ap
C 38	16.8	77.8	1626	14	US-11-074-176-29	Sequence 29, Appl
C 39	16.8	77.8	1661	11	US-11-201-916-7	Sequence 7, Appli
C 40	16.8	77.8	3534	9	US-10-932-182A-940	Sequence 940, App
C 41	16.8	77.8	3534	9	US-10-932-182A-940	Sequence 940, App
C 42	16.6	76.9	25	8	US-10-310-914A-1061804	Sequence 1061804,
C 43	16.4	75.9	803	11	US-11-096-568A-1453	Sequence 1453, Ap
C 44	16.4	75.9	1402	11	US-11-072-512-1108	Sequence 1108, Ap
C 45	16.4	75.9	1750	14	US-11-091-883-407	Sequence 407, App
C 46	16.4	75.9	2886	11	US-11-050-857-678	Sequence 678, App
C 47	16.4	75.9	2886	11	US-11-051-720-55	Sequence 55, Appl
C 48	16.4	75.9	3100	11	US-11-050-857-679	Sequence 679, App
C 49	16.4	75.9	3164	11	US-11-051-720-56	Sequence 56, Appl
C 50	16.4	75.9	3164	11	US-11-050-857-677	Sequence 677, App
C 51	16.4	75.9	3164	11	US-11-051-720-54	Sequence 54, Appl
C 52	16.4	75.9	3254	11	US-11-050-857-680	Sequence 680, App
C 53	16.4	75.9	3254	11	US-11-051-720-57	Sequence 57, Appl
C 54	16.4	75.9	3256	11	US-11-050-857-676	Sequence 676, App
C 55	16.4	75.9	3256	11	US-11-051-720-53	Sequence 53, Appl
C 56	16.4	75.9	3263	11	US-11-050-857-675	Sequence 675, App
C 57	16.4	75.9	3263	11	US-11-051-720-52	Sequence 52, Appl
C 58	16.4	75.9	6208	11	US-11-181-330-5	Sequence 5, Appli
C 59	16.4	75.9	6237	14	US-11-076-074-14	Sequence 14, Appl
C 60	16.4	75.9	6240	9	US-10-912-971-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-11-055-637-99/c
; Sequence 99, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ IDS NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-99

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Query Match      85.2%; Score 18.4; DB 14; Length 555;
Best Local Similarity 86.4%; Pred. No. 8.9;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCCGATCTTGT 22
    ||||| ||||| ||||| ||||| |||||
Db 538 TGAAGGTACCGCGATCTTGT 517

RESULT 2
US-11-201-916-3/c
; Sequence 3, Application US/11201916
; Publication No. US20060039922A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE
; TITLE OF INVENTION: HSP60 FAMILY
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/201,916
; FILING DATE: 11-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,737
; FILING DATE: 31-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 870109.408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1637
; US-11-201-916-3

Query Match      85.2%; Score 18.4; DB 11; Length 1654;
Best Local Similarity 86.4%; Pred. No. 9.9;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCCGATCTTGT 22
    ||||| ||||| ||||| ||||| |||||
Db 822 TGAAGGTTCCACGAATCTTGT 801

RESULT 3
US-11-136-527-8176
; Sequence 8176, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

Query Match      83.3%; Score 18; DB 14; Length 1400;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGGTGCCRCCGATCTTGT 21
    ||||| ||||| ||||| ||||| |||||
Db 1270 GAAGGTGCACGATCTTGT 1289

RESULT 4
US-11-136-527-4080
; Sequence 4080, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4080
; LENGTH: 9176
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-4080

Query Match      83.3%; Score 18; DB 14; Length 9176;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGGTGCCRCCGATCTTGT 21
    ||||| ||||| ||||| ||||| |||||
Db 9046 GAAGGTGCACGATCTTGT 9065

RESULT 5
US-09-925-065A-141335/c
; Sequence 141335, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
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; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141335
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-141335

Query Match 80.6%; Score 17.4; DB 6; Length 399;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 21
|||||||:|||||||
DB 324 TGAAGTGCTGCAGATCTTGT 304

RESULT 6

US-10-301-480-236251/c
; Sequence 236251, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236251
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-236251

Query Match 80.6%; Score 17.4; DB 10; Length 401;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 21
|||||||:|||||||
DB 326 TGAAGTGCTGCAGATCTTGT 306

RESULT 7

US-10-301-480-849660/c
; Sequence 849660, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 849660
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-849660

Query Match 80.6%; Score 17.4; DB 10; Length 401;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 21
|||||||:|||||||
DB 326 TGAAGTGCTGCAGATCTTGT 306

RESULT 8

US-10-897-981-11/c
; Sequence 11, Application US/10897981
; Publication No. US20060019354A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Armentrout, Richard W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USING A
; FILE OF INVENTION: REGULATOR OF BIOPOLYMER PRODUCTION
; FILE REFERENCE: 850136.421
; CURRENT APPLICATION NUMBER: US/10/897,981
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Sphingomonas sp.
US-10-897-981-11

Query Match 80.6%; Score 17.4; DB 9; Length 1587;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
DB 471 GAAGTGTCGCGGATGTGT 451

RESULT 9

US-11-131-479-37/c
; Sequence 37, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Coding Region Encoding IBV NP Protein
US-11-131-479-37

Query Match 80.6%; Score 17.4; DB 14; Length 1683;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
DB 462 GAAGTGCCGCGGATGTGT 442

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RESULT 10
US-11-096-568A-7645/c
; Sequence 7645, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 7645
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1836)
; OTHER INFORMATION: Ceres Seq. ID no. 15174547
US-11-096-568A-7645

Query Match      80.6%; Score 17.4; DB 11; Length 1836;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCCRCGGATCTTGT 22
Db      413 GAAGGTGTCACGGATGTTGT 393

RESULT 11
US-11-096-568A-19419/c
; Sequence 19419, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19419
; LENGTH: 1997
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1997)
; OTHER INFORMATION: Ceres Seq. ID no. 12373118
US-11-096-568A-19419

Query Match      80.6%; Score 17.4; DB 11; Length 1997;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCCRCGGATCTTGT 22
Db      569 GAAGGTGTCACGGATGTTGT 549

RESULT 12
US-10-897-981-3
; Sequence 3, Application US/10897981
; Publication No. US20060019354A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Armentrout, Richard W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USING A
; TITLE OF INVENTION: REGULATOR OF BIOPOLYMER PRODUCTION
```

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; FILE REFERENCE: 850136.421
; CURRENT APPLICATION NUMBER: US/10/897,981
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Spingomonas sp.
US-10-897-981-3

Query Match      80.6%; Score 17.4; DB 9; Length 2590;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCCRCGGATCTTGT 22
Db      1402 GAAGGTGTCGCGATGTTGT 1422

RESULT 13
US-10-932-182A-78771/c
; Sequence 78771, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78771
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78771

Query Match      79.6%; Score 17.2; DB 9; Length 2619;
Best Local Similarity 86.4%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TGAAGTGCCRCGGATCTTGT 22
Db      2408 TGAAGTTGCCCGGATGTTGT 2387

RESULT 14
US-10-932-182A-78771/c
; Sequence 78771, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78771
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78771
```

Query Match 79.6%; Score 17.2; DB 9; Length 2619;
Best Local Similarity 86.4%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGCGATCTTGT 22
|||||:|||||:|||||:|||||
Db 2408 TGAAGTTGCCCGCGATCTTGT 2387

RESULT 15

US-11-136-527-294718/c
; Sequence 294718, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 294718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-294718

Query Match 78.7%; Score 17; DB 14; Length 25;
Best Local Similarity 89.5%; Pred. No. 38;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGCGATCTTGT 21
|||||:|||||:|||||
Db 21 AAGGTGCCACCGATCTTGT 3

RESULT 16

US-11-136-527-6229/c
; Sequence 6229, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6229
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6229

Query Match 78.7%; Score 17; DB 14; Length 1400;
Best Local Similarity 89.5%; Pred. No. 55;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGCGATCTTGT 21
|||||:|||||:|||||
Db 436 AAGGTGCCACCGATCTTGT 418

RESULT 17

US-11-136-527-2133/c

; Sequence 2133, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2133
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2133

Query Match 78.7%; Score 17; DB 14; Length 1415;
Best Local Similarity 89.5%; Pred. No. 55;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGCGATCTTGT 21
|||||:|||||:|||||
Db 451 AAGGTGCCACCGATCTTGT 433

RESULT 18

US-11-136-527-238844/c
; Sequence 238844, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-238844

Query Match 77.8%; Score 16.8; DB 14; Length 25;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGCGATCTTGT 22
|||||:|||||:|||||
Db 25 TGAAGTGCCCAAGATCTTGT 4

RESULT 19

US-11-136-527-238846/c
; Sequence 238846, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-238846

Query Match 77.8%; Score 16.8; DB 14; Length 25;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||: |||||
DB 23 TGAAGTGCCCAAGATCTTGT 2

RESULT 20
US-11-136-527-964
; Sequence 964, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 964
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-964

Query Match 77.8%; Score 16.8; DB 14; Length 486;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||: |||||
DB 211 TGAAGTGCCCAAGATCTTGT 232

RESULT 21
US-11-136-527-5060/c
; Sequence 5060, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5060
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5060

Query Match 77.8%; Score 16.8; DB 14; Length 486;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||: |||||
DB 276 TGAAGTGCCCAAGATCTTGT 255

RESULT 22
US-09-925-065A-390792/c
; Sequence 390792, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390792
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390792

Query Match 77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||: |||||
DB 221 TGAAGTGGAAGTCTTGT 200

RESULT 23
US-09-925-065A-390793/c
; Sequence 390793, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390793
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390793

```
Query Match          77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 221 TGAAGTGGAACTGATCTTGT 200

RESULT 24
US-09-925-065A-390794/c
; Sequence 390794, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390794
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390794

Query Match          77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 221 TGAAGTGGAACTGATCTTGT 200

RESULT 25
US-09-925-065A-390795/c
; Sequence 390795, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390795
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390795

; ORGANISM: Homo sapiens
US-09-925-065A-390795

Query Match          77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 221 TGAAGTGGAACTGATCTTGT 200

RESULT 26
US-11-055-637-112/c
; Sequence 112, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-112

Query Match          77.8%; Score 16.8; DB 14; Length 552;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 538 TGAAGTACCACGAATCTTGT 517

RESULT 27
US-10-301-480-459081/c
; Sequence 459081, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459081
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459081

Query Match          77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
```

```
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 28
US-10-301-480-459082/c
; Sequence 459082, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459082
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459082

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 29
US-10-301-480-459083/c
; Sequence 459083, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459083
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459083

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 30
US-10-301-480-459084/c
; Sequence 459084, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459084
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459084

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 31
US-10-301-480-1072490/c
; Sequence 1072490, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072490
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072490

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 32
US-10-301-480-1072491/c
; Sequence 1072491, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072491
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072491
```

```
; Sequence 459084, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459084
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459084

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 31
US-10-301-480-1072490/c
; Sequence 1072490, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072490
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072490

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGACTCTTGT 22
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 32
US-10-301-480-1072491/c
; Sequence 1072491, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072491
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072491
```

; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072491
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072491

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
||||||| : |||||
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 33

US-10-301-480-1072492/c
; Sequence 1072492, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072492
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072492

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
||||||| : |||||
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 34

US-10-301-480-1072493/c
; Sequence 1072493, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072493
; LENGTH: 559
; TYPE: DNA

; ORGANISM: Homo sapien
US-10-301-480-1072493

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
||||||| : |||||
Db 226 TGAAGTGGAACTGATCTTGT 205

RESULT 35

US-09-925-065A-697497/c
; Sequence 697497, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697497
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697497

Query Match 77.8%; Score 16.8; DB 6; Length 637;
Best Local Similarity 81.8%; Pred. No. 65;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
||||||| : |||||
Db 388 TGAAGTGGAACTGATCTTGT 367

RESULT 36

US-09-925-065A-697498/c
; Sequence 697498, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 697498
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-697498

Query Match          77.8%; Score 16.8; DB 6; Length 637;
Best Local Similarity 81.8%; Pred. No. 65;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 388 TGAAGTGGAAGTGAATCTTGT 367

RESULT 37
US-11-096-568A-5292
; Sequence 5292, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5292
; LENGTH: 1562
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1562)
; OTHER INFORMATION: Ceres Seq. ID no. 14307879
US-11-096-568A-5292

Query Match          77.8%; Score 16.8; DB 11; Length 1562;
Best Local Similarity 81.8%; Pred. No. 71;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 1260 TGAAGTGCCAGGAGATCTTGT 1281

RESULT 38
US-11-074-176-29/c
; Sequence 29, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAnuliffe, Olivia
; APPLICANT: Peril, Andrea Accarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1626)
; FEATURE:
```

```
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: ORF 406; GroEL - 60 kDa chaperonin
US-11-074-176-29

Query Match          77.8%; Score 16.8; DB 14; Length 1626;
Best Local Similarity 81.8%; Pred. No. 71;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 808 TGAAGTACCAGCAATCTTGT 787

RESULT 39
US-11-201-916-7/c
; Sequence 7, Application US/11201916
; Publication No. US20060039922A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE
; TITLE OF INVENTION: HSP60 FAMILY
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/201,916
; FILING DATE: 11-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,737
; FILING DATE: 31-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 870109.408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1649
US-11-201-916-7

Query Match          77.8%; Score 16.8; DB 11; Length 1661;
Best Local Similarity 81.8%; Pred. No. 71;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 822 TGAAGTACCAGCAATCTTGT 801

RESULT 40
US-110-932-182A-940
```

; Sequence 940, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-940

Query Match 77.8%; Score 16.8; DB 9; Length 3534;
Best Local Similarity 81.8%; Pred. No. 77;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1929 TAAAGTGCCGCGGAATTGTT 1950

RESULT 41
US-10-932-182A-940
; Sequence 940, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-940

Query Match 77.8%; Score 16.8; DB 9; Length 3534;
Best Local Similarity 81.8%; Pred. No. 77;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1929 TAAAGTGCCGCGGAATTGTT 1950

RESULT 42
US-10-310-914A-1061804/c
; Sequence 1061804, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1061804
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1061804

Query Match 76.9%; Score 16.6; DB 8; Length 25;
Best Local Similarity 94.1%; Pred. No. 61;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGGTGCCGCGGATCTTGT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 19 AGGTGCCGCGGATCTTGT 3

RESULT 43
US-11-096-568A-1453/c
; Sequence 1453, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1453
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (1)-(803)
; OTHER INFORMATION: Ceres Seq. ID no. 14308995
US-11-096-568A-1453

Query Match 75.9%; Score 16.4; DB 11; Length 803;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCGCGGATCTTGT 21
| | | | | | | | | | | | | | | | | | | | | |
Db 171 GACGTCGCGTGATCTTGT 152

RESULT 44
US-11-072-512-1108/c
; Sequence 1108, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512

; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1108
; LENGTH: 1402
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-1108

Query Match 75.9%; Score 16.4; DB 11; Length 1402;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 170 TGGAGGTGACGGGATCTTG 151

RESULT 45

US-11-091-883-407/c
; Sequence 407, Application US/11091883
; Publication No. US20060024693A1

; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.

; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; FILE REFERENCE: 53942US

; CURRENT APPLICATION NUMBER: US/11/091,883

; CURRENT FILING DATE: 2005-03-29

; PRIOR APPLICATION NUMBER: 60/556,875

; PRIOR FILING DATE: 2004-03-29

; NUMBER OF SEQ ID NOS: 513

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 407

; LENGTH: 1750

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-091-883-407

Query Match 75.9%; Score 16.4; DB 14; Length 1750;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 172 TGGAGGTGACGGGATCTTG 153

RESULT 46

US-11-050-857-678/c
; Sequence 678, Application US/11050857
; Publication No. US20060040278A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 1847.1005

; CURRENT APPLICATION NUMBER: US/11/050,857

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1150

; SEQ ID NO 678

; LENGTH: 2886

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-050-857-678

Query Match 75.9%; Score 16.4; DB 11; Length 2886;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 360 TGGAGGTGACGGGATCTTG 341

RESULT 47

US-11-051-720-55/c

; Sequence 55, Application US/11051720

; Publication No. US20060046257A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 1847.1002

; CURRENT APPLICATION NUMBER: US/11/051,720

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1780

; SEQ ID NO 55

; LENGTH: 2886

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-051-720-55

Query Match 75.9%; Score 16.4; DB 11; Length 2886;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 360 TGGAGGTGACGGGATCTTG 341

RESULT 48

US-11-050-857-679/c

; Sequence 679, Application US/11050857

; Publication No. US20060040278A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 1847.1005

; CURRENT APPLICATION NUMBER: US/11/050,857

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1150

; SEQ ID NO 679

; LENGTH: 3100

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-050-857-679

Query Match 75.9%; Score 16.4; DB 11; Length 3100;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 360 TGGAGGTGACGGGATCTTG 341

RESULT 49

US-11-051-720-56/c

; Sequence 56, Application US/11051720

; Publication No. US20060046257A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 56
LENGTH: 3100
TYPE: DNA
ORGANISM: Homo sapiens
US-11-051-720-56

Query Match 75.9%; Score 16.4; DB 11; Length 3100;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGGCGATCTTG 341

RESULT 50
US-11-050-857-677/c
Sequence 677, Application US/11050857
Publication No. US20060040278A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
FILE REFERENCE: 1847.1005
CURRENT APPLICATION NUMBER: US/11/050,857
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1150
SEQ ID NO 677
LENGTH: 3164
TYPE: DNA
ORGANISM: Homo sapiens
US-11-050-857-677

Query Match 75.9%; Score 16.4; DB 11; Length 3164;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGGCGATCTTG 341

RESULT 51
US-11-051-720-54/c
Sequence 54, Application US/11051720
Publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 54
LENGTH: 3164
TYPE: DNA
ORGANISM: Homo sapiens
US-11-051-720-54

Query Match 75.9%; Score 16.4; DB 11; Length 3164;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGGCGATCTTG 341

RESULT 52
US-11-050-857-680/c
Sequence 680, Application US/11050857
Publication No. US20060040278A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
FILE REFERENCE: 1847.1005
CURRENT APPLICATION NUMBER: US/11/050,857
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1150
SEQ ID NO 680
LENGTH: 3254
TYPE: DNA
ORGANISM: Homo sapiens
US-11-050-857-680

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGGCGATCTTG 341

RESULT 53
US-11-051-720-57/c
Sequence 57, Application US/11051720
Publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 57
LENGTH: 3254
TYPE: DNA
ORGANISM: Homo sapiens
US-11-051-720-57

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGGCGATCTTG 341

RESULT 54
US-11-050-857-676/c
Sequence 676, Application US/11050857
Publication No. US20060040278A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
FILE REFERENCE: 1847.1005
CURRENT APPLICATION NUMBER: US/11/050,857
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1150
SEQ ID NO 676
LENGTH: 3256
TYPE: DNA
ORGANISM: Homo sapiens
US-11-050-857-676

Query Match 75.9%; Score 16.4; DB 11; Length 3256;

Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRGGATCTTG 20
||| ||| : ||| |||
Db 360 TGGAGGTGACGCGGATCTTG 341

RESULT 55

US-11-051-720-53/c

; Sequence 53, Application US/11051720

; Publication No. US20060046257A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS

; FILE REFERENCE: 1847.1002

; CURRENT APPLICATION NUMBER: US/11/051,720

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1780

; SEQ ID NO 53

; LENGTH: 3256

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-051-720-53

Query Match

Best Local Similarity 75.9%; Score 16.4; DB 11; Length 3256;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRGGATCTTG 20
||| ||| : ||| |||
Db 360 TGGAGGTGACGCGGATCTTG 341

RESULT 56

US-11-050-857-675/c

; Sequence 675, Application US/11050857

; Publication No. US20060040278A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS

; FILE REFERENCE: 1847.1005

; CURRENT APPLICATION NUMBER: US/11/050,857

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1150

; SEQ ID NO 675

; LENGTH: 3263

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-050-857-675

Query Match

Best Local Similarity 75.9%; Score 16.4; DB 11; Length 3263;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRGGATCTTG 20
||| ||| : ||| |||
Db 360 TGGAGGTGACGCGGATCTTG 341

RESULT 57

US-11-051-720-52/c

; Sequence 52, Application US/11051720

; Publication No. US20060046257A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS

; FILE REFERENCE: 1847.1002

; CURRENT APPLICATION NUMBER: US/11/051,720

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1780

; SEQ ID NO 52

; LENGTH: 3263

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-051-720-52

Query Match

Best Local Similarity 75.9%; Score 16.4; DB 11; Length 3263;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRGGATCTTG 20
||| ||| : ||| |||
Db 360 TGGAGGTGACGCGGATCTTG 341

RESULT 58

US-11-181-330-5/c

; Sequence 5, Application US/11181330

; Publication No. US20060035283A1

; GENERAL INFORMATION:

; APPLICANT: CHILDREN'S MEDICAL CENTER CORPORATION

; TITLE OF INVENTION: NEUROPROTECTIVE THERAPEUTICS AND ASSAYS FOR IDENTIFYING

; FILE REFERENCE: CMA-3.25

; CURRENT APPLICATION NUMBER: US/11/181,330

; PRIOR FILING DATE: 2005-07-14

; PRIOR APPLICATION NUMBER: PCT/US04/01209

; PRIOR FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: 60/440,679

; PRIOR FILING DATE: 2003-01-17

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 5

; LENGTH: 6208

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-181-330-5

Query Match

Best Local Similarity 75.9%; Score 16.4; DB 11; Length 6208;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 22
||| ||| : ||| |||
Db 748 ATGGTCTCGCGATCTTGT 729

RESULT 59

US-11-076-074-14/c

; Sequence 14, Application US/11076074

; Publication No. US20060024749A1

; GENERAL INFORMATION:

; APPLICANT: CIS Biotech, Inc.

; TITLE OF INVENTION: Rapid multiple panel of biomarkers in laboratory blood tests for

; FILE REFERENCE: 08805.105001

; CURRENT APPLICATION NUMBER: US/11/076,074

; CURRENT FILING DATE: 2005-03-09

; PRIOR APPLICATION NUMBER: US/09/922,011

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 6237

; TYPE: DNA

; ORGANISM: homo sapiens

US-11-076-074-14

Query Match

Best Local Similarity 75.9%; Score 16.4; DB 14; Length 6237;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 22
| | | | | : | | | | |
Db 778 ATGGTGCTGCGGATCTTGT 759

RESULT 60
US-10-912-971-5/c
; Sequence 5, Application US/10912971
; Publication No. US20060029546A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING ANTI-SCHIZOPHRENIC AGENTS
; FILE REFERENCE: 30847/40237
; CURRENT APPLICATION NUMBER: US/10/912,971
; CURRENT FILING DATE: 2004-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-912-971-5

Query Match 75.9%; Score 16.4; DB 9; Length 6240;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 22
| | | | | : | | | | |
Db 778 ATGGTGCTGCGGATCTTGT 759

Search completed: April 1, 2006, 22:39:10
Job time : 56.3836 secs

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 BA000030_88 8800001 8910000
 BA000030_89 8900001 9010000
 BA000030_90 9000001 9025608

Continuation (49 of 91) of BA000030 from base 4800001 (BA000030 Streptomyces avermitilis
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Best Local Similarity 97.6%; Pred. No. 2.2e-34;
 Matches 410; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 AAGAAGACGACGAGCGTCCCGGTGACGATGACGACACCGGACCGCTTCTCGCCAGGCG 60
 DB 55587 AAGAAGACGACGAGCGTCCCGGTGACGATGACGACACCGGACCGCTTCTCGCCAGGCG 55528
 QY 61 CTCGTACGAGGCGCTCGCAACGTCGCGCGGTCGCAACCGCATGCTCTCAAGCGC 120
 DB 55527 CTCGTCCGAGGCGCTCGCAACGTCGCGCGGTCGCAACCGCATGCTCTCAAGCGC 55468
 QY 121 GGCATCGAAGGCGCGTCCGAGCGCTCTCCGCGCCCTGCTCGAGCAGCGAAGGATGTC 180
 DB 55467 GGTATCGAAGGCGCGTCCGAGCGCTCTCCGCGCCCTGCTCGAGCAGCGAAGGATGTC 55408
 QY 181 GAGACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGCGCCGACACCGATCGGC 240
 DB 55407 GAGACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGCGCCGACACCGATCGGC 55348
 QY 241 GAGCTCATCGCGAGCGATGACAGGTCGCGCAAGGAGGCGTCATCACCGTCGAGGAG 300
 DB 55347 GAGCTCATCGCGAGCGATGACAGGTCGCGCAAGGAGGCGTCATCACCGTCGAGGAG 55288
 QY 301 TCCGAGCCTTCGGTCTGAGCTGAGCTTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 360
 DB 55287 TCCGAGCCTTCGGTCTGAGCTGAGCTTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 55228
 QY 361 ATCTCGGCGTACTTCCGACCGACATGAGCGGATGAGCGCTCGCTCGACGACCGCTAC 420
 DB 55227 ATCTCGGCGTACTTCCGACCGACATGAGCGGATGAGCGCTCGCTCGACGACCGCTAC 55168

RESULT 2

STMGROELY

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

source

gene

CDS

STMGROELY 1814 bp DNA linear BCT 26-APR-1993
 Streptomyces albus open reading frame (GROEL2) gene, complete cds.
 M76658
 M76658.1 GI:153293
 heat shock protein.
 Streptomyces albus
 Streptomyces albus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomyceinae; Streptomycetaceae; Streptomyces.
 1 (bases 1 to 1814)
 Mazodier, P., Guglielmi, G., Davies, J. and Thompson, C. J.
 Characterization of the groEL-like genes in Streptomyces albus
 J. Bacteriol. 173 (22), 7382-7386 (1991)
 1682304
 Original source text: Streptomyces albus (strain G) DNA.
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 AEMDKVGEVITVEESQTGLELETEGMPFDKGYISAYPATDMERWASLDDPYI
 LIVNSKIGNVOLLPLEKVMQSGKPLLIADVEGELASTLVNKNKIGTFFKSAVAKA
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ALPLTFTEAVIADKPEKAAAAPGMPGGDMDF

ORIGIN	Query Match	Score	DB 1;	Length	DB 2;
	Best Local Similarity	96.0%;	Pred. No. 1.2e-32;		
	Matches	403;	Conservative	0;	Mismatches 17; Indels 0; Gaps 0;
QY	1	AAGAAGACGAGCGATCGTCCCGTGCACCGTACGACACCGCGACCGTCTTCGCCCGCAGGCG	60		
DB	332	AAGAAGACGAGCGATCGTCCCGTGCACCGTACGACACCGCGACCGTCTTCGCCCGCAGGCG	391		
QY	61	CTCGTACGAGGCGCTCGGCAACGTCGCGCGCGTGCACACCGATGCTTCAAGCGC	120		
DB	392	CTCGTCCGCGAGGCTCGGCAACGTCGCGCGCGTGCACACCGATGCTTCAAGCGC	451		
QY	121	GCATCGAGAAGCGCTCGAGCGCTCTCCGGCGCCCTCTGGAGCGCGGAGGATGTC	180		
DB	452	GGATCGAGAAGCGCTCGAGCGCTCTCTCCGGCGCCCTCTGGAGCGCGGAGGATGTC	511		
QY	181	GAGACCAAGGAGCAGATCGTCTCCAGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC	240		
DB	512	GAGACCAAGGAGCAGATCGTCTCCAGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC	571		
QY	241	GAGTCTATCGCGAGCGATGACAAAGTTCGCGCAAGGAGGCGTCAATCAGTTCGAGGAG	300		
DB	572	GAGTCTATCGCGAGCGATGACAAAGTTCGCGCAAGGAGGCGTCAATCAGTTCGAGGAG	631		
QY	301	TCCGAGACCTTCGCTGAGCTCGAGCTCACCGAGGATGCGTTCGACAGGCGCTAC	360		
DB	632	TCCGAGACCTTCGCTGAGCTCGAGCTCACCGAGGATGCGTTCGACAGGCGCTAC	691		
QY	361	ATCTCGGCGTATCTCGCCACCGACATGAGCGGATGAGGCGCTCGTCGACGACCCGTCAC	420		
DB	692	ATCTCGGCGTATCTCGCCACCGACATGAGCGGATGAGGCGCTCGTCGACGACCCGTCAC	751		

SC0939119 299050 bp DNA linear BCT 16-APR-2005
Streptomyces coelicolor A3(2) Complete genome; segment 16/29.
AL939119 AL160331 AL353816 AL356612 AL357432 AL357524 AL358692
AL358818 AL35998 AL391406 AL391541 AL392149 AL392150 AL392178
AL645882
AL939119.1 GI:24427855
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
1
Bentley, S.D., Chater, K.F., Cerdano-Tarraga, A.M., Challis, G.L.,
Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H.,
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,
Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S.,
Huang, C.H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S.,
Rabinowitz, E., Rajandream, M.A., Rutherford, K., Rutter, S.,
Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S.,
Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrall, B.G.,
Parkhill, J., and Hopwood, D.A.
Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)
Nature 417 (6885), 141-147 (2002)
1200953
2 (bases 1 to 299050)
Bentley, S.D.
Direct Submission
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: sds@sanger.ac.uk
On or before Oct 30, 2002 this sequence version replaced
gi:7242748, gi:7636006, gi:8248766, gi:8249971, gi:8388712,

gi:8439477, gi:8894718, gi:9857143, gi:9886716, gi:10129746,
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/strain="A3(2)"
/db_xref="taxon:100226"
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(EMBL:AL109848)." 2004. .5126
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2004. .5126
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/note="rrnA, 23S ribosomal RNA. Coordinates based on
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/gene="rrnA"
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complement(5412. .6080)
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/note="SCO72A.09c, possible two-component system response
regulator, len: 222aa; similar to many eg. FR:086632
(EMBL:AL031155) possible two-component regulator from
Streptomyces coelicolor (222 aa) fasta scores; opt: 973,
z-score: 1128.5, E(): 0, 69.1% identity in 220 aa overlap.
Contains pfam match to entry PF00072 response reg,
Response regulator receiver domain, pfam match to entry
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and Prosite match to PS00622 Bacterial regulatory
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/note="Pfam match to entry PF00196 GerE, Bacterial
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2.6e-14"
complement(5475. .5558)
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signature"
complement(5736. .6077)
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regulator receiver domain, score 126.30, E-value 5.7e-34"
complement(6077. .7447)

CDS	<pre>/gene="SCO4124" /notes="synonym: SCD72A.10c" complement(6077..7447) /genes="SCO4124" /notes="SCD72A.10c, possible two-component sensor kinase, len: 456aa; similar to many eg. TR:O86631 (EMBL:AL031155) putative two-component sensor kinase from Streptomyces coelicolor (429 aa) fasta scores; opt: 929, z-score: 995.1, E(): 0, 42.7% identity in 422 aa overlap. Contains pfam match to entry PF00512 signal, Histidine kinase and possible membrane-spanning hydrophobic regions. Contains possible hydrophobic membrane spanning regions" /codon_start=1 /transl_table=11 /product="putative two-component sensor kinase" /protein_id="CAB92377.1" /db_xref="GI:8052436" /db_xref="GOA:Q9KYB6" /db_xref="InterPro:IPR003594" /db_xref="InterPro:IPR011712" /db_xref="UniProt/TREMBL:Q9KYB6" /translation="MRATVPGYIAHLIYGPRTDARPARTDHGRMEPVKVPEDRA AEPTVYQVRNRIIRAFDRHPLLDLTITGFWLAALVDGTGMRVADHPGPV GLVLSLAVSVVWRRSHRGALITLPAALVSWSGAALQALLQLLVHIALR LPLRNWAVVAVPTCVSVARYGDSAGSNQOLGVALGVAALIGITVTRRGY TEALDRARLETERDQVRLAAARARIAREMDIIGHNLSVITGLADGGRYAAK SPRAQALDAIGTTRQALGELRLDLVLRDDQDGTPEPELAPQPPALTDLDRLLD GVRRAGLVNTKVGPELPGKQLTVRIQEALNTLKHAGPDATAHLSYSGGG AATLVTDGRTAPLPSRTSGRGLPGMRERTSLYGLTEAGRPAPQGRVRLHL PEESPQ" complement(6095..6670) /genes="SCO4124" /notes="Pfam match to entry PF00512 signal, Histidine kinase, score -41.40, E-value 0.0087" 7473..8006 /genes="SCO4125" /notes="synonym: SCD72A.11" 7473..8006 /gene="SCO4125" /notes="SCD72A.11, possible acetyltransferase, len: 177 aa; weakly similar to many eg. TR:AAD52985 (EMBL:AF140221) aminoglycoside 6'-N-acetyltransferase from Xanthomonas maltophilia (153 aa) fasta scores; opt: 128, z-score: 164.9, E(): 0.1, 28.7% identity in 115 aa overlap. Contains Pfam match to entry PF00583 Acetyltransf, Acetyltransferase (GNAT) family." /codon_start=1 /transl_table=11 /product="putative acetyltransferase" /protein_id="CAB92378.1" /db_xref="GI:8052437" /db_xref="GOA:Q9KYB5" /db_xref="InterPro:IPR000182" /db_xref="UniProt/TREMBL:Q9KYB5" /translation="MIRSHADEWPVKELRLRLRDPVADLAVLYETREAAAPDSY WQRRARGAGAGAAQVAVGGLWLTGLTVLVEAGTWDWAGFVRRQGVGV FVPEWRGSGITKALDAGLEWANGVEMRLIVHPNTRAQATRKAGAPSGRTV PLEGGPDHLEVYLER" 7476..7934 /genes="SCO4125" /notes="Pfam match to entry PF00583 Acetyltransf, Acetyltransferase (GNAT) family, score 34.50, E-value 2.4e-06" complement(8054..9541) /genes="SCO4126" /notes="synonym: SCD72A.12c" complement(8054..9541) /gene="SCO4126" /notes="SCD72A.12c, possible membrane protein, len: 495aa; similar in regions to others from actinomycetes eg. TR:Q9X8A2 (EMBL:AL049645) hypothetical protein from Streptomyces coelicolor (427 aa) fasta scores; opt: 266, z-score: 260.7, E(): 4.7e-07, 27.7% identity in 296 aa</pre>
misc_feature	
gene	
CDS	<pre>/gene="SCO4127" /notes="synonym: SCD72A.13c" complement(9615..11030) CDS</pre>
Query Match	92.4%; Score 388; DB 1; Length 299050;
Best Local Similarity	95.2%; Pred. No. 7.4e-33;
Matches	400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY	1 AAGAGACGAGCGAGCGTCCGCGGTGACGGTACGACACCGCGACCGTCTTCCGCCAGGCG 60
DB	180896 AAGAAGACGAGCGAGCGTCCGCGGTGACGGTACGACACCGCGACCGTCTTCCGCCAGGCG 180955
QY	61 CTCGTACGCGAGGCGCTGCGCAACGTGCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 120
DB	180956 CTGCTCAAGGAGGCGCTGCGCAACGTGCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 181015
QY	121 GGCATCGAAGAGGCGCTGAGCGCGTCTCCGCGCGGTCTGCGAGCAGCGGAGGATGTC 180
DB	181016 GGTATCGAAGAGGCGCTGAGCGCGTCTCCGCGCGGTCTGCGAGCAGCGGAGGATGTC 181075
QY	181 GAGACCAAGGAGCGATGCTTCCAGCGCTCCATCTCCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 240
DB	181076 GAGACCAAGGAGCGATGCTTCCAGCGCTCCATCTCCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 181135
QY	241 GAGCTCATCGCGAGGCGATGCAACAGGTGCGCAAGGAGGCGGTCTATCACCGTTCGAGGAG 300
DB	181136 GAGCTCATCGCGAGGCGATGCAACAGGTGCGCAAGGAGGCGGTCTATCACCGTTCGAGGAG 181195
QY	301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGGTTCGACACGCGCTAC 360
DB	181196 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGGTTCGACACGCGCTAC 181255
QY	361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTGAGCGGTTCGACACGCGCTAC 420
DB	181256 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTGAGCGGTTCGACACGCGCTAC 181315
RESULT 4	
SLGROEL2G	SLGROEL2G 2192 bp DNA linear BCT 18-APR-2005
LOCUS	S.lividans groEL2 gene.
DEFINITION	X95971
ACCESSION	X95971.1 GI:2558615
VERSION	GROEL2 protein; promoter region.
KEYWORDS	Streptomyces lividans
SOURCE	Streptomyces lividans
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE	1
AUTHORS	de Leon, P., Marco, S., Isiegas, C., Marina, A., Carrascoa, J.L. and Mellado, R.P.
TITLE	Streptomyces lividans groES, groEL1 and groEL2 genes
JOURNAL	Microbiology (Reading, Engl.) 143 (Pt 11), 3563-3571 (1997)
PUBMED	9387235
REFERENCE	2 (bases 1 to 2192)

AUTHORS	Mellado, R.P.	RESULT 5	AY691305
TITLE	Direct Submission	LOCUS	AY691305
JOURNAL	Submitted (27-FEB-1996) R.P. Mellado, Centro Nacional de Biotecnologia (CSIC), Campus de la Universidad Autonoma, Cantoblanco, 28049 Madrid, SPAIN	DEFINITION	Streptomyces thermoviolaceus subsp. thermoviolaceus 60 kDa chaperonin (cpn60) gene, partial cds.
FEATURES	Location/Qualifiers	ACCESSION	AY691305
source	1. .2192	VERSION	AY691305
	/organism="Streptomyces lividans"	KEYWORDS	AY691305.1 GI:51103898
	/mol_type="genomic DNA"	SOURCE	Streptomyces thermoviolaceus subsp. thermoviolaceus
	/strain="TK21"	ORGANISM	Streptomyces thermoviolaceus subsp. thermoviolaceus
-35_signal	/db_xref="taxon:1916"		Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyetaceae; Streptomyces.
-10_signal	283..288	REFERENCE	1 (bases 1 to 552)
mRNA	/note="groEL2 promoter"	AUTHORS	Hill, J.E., Penny, S.L., Crowell, K.G., Goh, S.H. and Hemmingsen, S.M.
gene	306..311	TITLE	cpnDB: a chaperonin sequence database
	/note="groEL2 promoter"	JOURNAL	Genome Res. 14 (8), 1659-1675 (2004)
	320	PUBMED	15289485
	/note="transcription start site"	REFERENCE	2 (bases 1 to 552)
gene	455..1904	AUTHORS	Hill, J.E., Van Kessel, A.G., Dumonceaux, T.J. and Hemmingsen, S.M.
RBS	/gene="GroEL2"	CONSTRM	cpnDB - a chaperonin sequence database
CDS	455..459	TITLE	Direct Submission
	/gene="GroEL2"	JOURNAL	Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada
	471..1904	FEATURES	Location/Qualifiers
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	/transl_table=11		/mol_type="genomic DNA"
	/product="GroEL2 protein"		/strain="ATCC 19283"
	/protein_id="CAA65226.1"		/sub_species="thermoviolaceus"
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	/db_xref="UniProt/Swiss-Prot:O33658"		/note="type strain of Streptomyces thermoviolaceus subsp. thermoviolaceus"
	/translation="MAKIAIFDEKARGLEGGMQLDAVKVTLGPKGRNVLEKKWG	gene	<1..>552
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	AEAMKVGEVITVEEFOTFGLLELETEGMGFDKGYISAVPATDMERMEASLDPPYI		/note="Hsp60, GroEL"
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	LKQIPSTAVSRAAWSRRCATSPWATA"		/db_xref="GI:51103899"
ORIGIN			/translation="ATVLAQALVKEGLNVAAGNPMALKRGIKAEVAVSTALDDQA
	Query Match 91.6%; Score 384.8; DB 1; Length 2192;		KEVETKQIASTASISAADTQIGELIEMKDKVKEGVITVEESQTFGLELELTGMR
	Best Local Similarity 94.8%; Pred. No. 7.6e-32;		FDKGYISAVPATDMERMEAVLDPPYIILANSKISAVKDLLPLEKVMQSGKPLLIIE
	Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;		DVEGALSTLVNKGIRTFKSAV"
QY	1 AAGAAGACGACGACGTCGCCGCGTGAACGTCGCCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120	QY	40 GCGACCGCTTCGCGCCAGCGCGCTGTACGCGAGGGCGCTCGCGCAACGTCGCGCGCGGTGCC 99
DB	702 AAGAAGACGACGACGTCGCCGCGTGAACGTCGCCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 761	DB	1 GCGACCGCTTCGCGCCAGCGCGCTGTGTGAAGAGGGTCTGCGCAACGTCGCGCGCGGTGCC 60
QY	61 CTGCTACGCGAGCGGCTGCGCAACGTCGCCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120	QY	100 AACCCGATGGCTCTCAAGCGCGGCGATCGAAGAGCGCGTTCGAGGGCGTCTCCGGGCGCCCTG 159
DB	762 CTGGTCAAGGAAGGCTGCGCAACGTCGCCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 821	DB	61 AACCCGATGGCGCTCAAGCGCGGATCGAAGAGCGCGTTCGAGGGCTGTCTCCACCGCGCTG 120
QY	121 GCATCGAAGCGCGTTCGAGCGCGTCTCGCGCGGCTGCTCGAGAGCGCGGAGGATGTC 180	QY	160 CTGGAGCAGCGGAGGATGTGAGCAACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCC 219
DB	822 GGTATCGAAGCGCGTTCGAGCGCGTCTCGCGCGGCTGCTCGAGAGCGCGGAGGATGTC 881	DB	121 CTGACACGAGGAGGAGGATGTGAGCAACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCC 180
QY	181 GAGACCAAGGAGCAGATGCTTCCAGCGCTCCATCTCGCGCGGCGGAGGAGGATGTC 240	QY	220 GCGCGCAGACCCAGATCGCGGAGCTCATCCCGAGGCGATGCGCAAGGTCGCGCAAGGAA 279
DB	882 GAGACCAAGGAGCAGATGCTTCCAGCGCTCCATCTCGCGCGGCGGAGGAGGATGTC 941	DB	181 GCGCGCAGACCCAGATCGCGGAGCTCATCCCGAGGCGATGCGCAAGGTCGCGCAAGGAA 240
QY	241 GAGCTCATCGCGAGGCGATGAGCAAGGTCGCGCAAGGAGGAGGATGTCATCAGCGTCGAGGAG 300	QY	280 GCGCTCATCAGCGTCGAGGAGTCCAGACCTTCGCTTCGAGGCTGAGAGCTCAACCGAGGT 339
DB	942 GAGCTCATCGCGAGGCGATGAGCAAGGTCGCGCAAGGAGGAGGATGTCATCAGCGTCGAGGAG 1001		
QY	301 TCCAGACCTTCGCTTCGAGCTGAGAGTCAACCGAGGATGAGCTTCGCAAGGCGGTAC 360		
DB	1002 TTCCAGACCTTCGCTTCGAGCTGAGAGTCAACCGAGGATGAGCTTCGCAAGGCGGTAC 1061		
QY	361 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGGTGCTTCGAGACCGCTAC 420		
DB	1062 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGGTGCTTCGAGACCGCTAC 1121		

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Db 241 GCGGTCAATCCGTCGAGGAGTCGACACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 300
Qy 340 ATGGCTTTCACAGGCTACATCTCGGCTACTTCCGACACCATGAGCGCGATGGAG 399
Db 301 ATGGCTTTCACAGGCTACATCTCGGCTACTTCCGACACCATGAGCGCGATGGAG 360
Qy 400 GCGTGCCTCGACGACCGCTAC 420
Db 361 GCGTGCCTCGACGACCGCTAC 381

RESULT 6
AF233387 4713 bp DNA linear BCT 04-FEB-2004
LOCUS Rhodococcus equi GroEL (groEL), gene, complete cds, and unknown
DEFINITION
ACCESSION AF233387
VERSION AF233387.1 GI:15321579
KEYWORDS
SOURCE Rhodococcus equi (Corynebacterium equi)
ORGANISM Rhodococcus equi
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
REFERENCE 1 (bases 1 to 4713)
AUTHORS Vanniasinkam, T., Barton, M.D. and Heuzenroeder, M.W.
TITLE The immunogenicity of Rhodococcus equi GroEL2-based vaccines in a
murine model
JOURNAL Vet. Immunol. Immunopathol. 98 (1-2), 91-100 (2004)
REFERENCE 2 (bases 1 to 4713)
AUTHORS Vanniasinkam, T., Barton, M.D. and Heuzenroeder, M.W.
TITLE Characterization of the groEL gene of Rhodococcus equi
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 4713)
AUTHORS Vanniasinkam, T., Barton, M.D. and Heuzenroeder, M.W.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2000) Microbiology, University of South
Australia, Frome Road, Adelaide, SA 5000, Australia
FEATURES
source Location/Qualifiers
1. 4713
/organism="Rhodococcus equi"
/mol_type="genomic DNA"
/strain="ATCC6939"
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571..1068
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/translation="MCVREPTASASFLIRARVAFIPTIMSADKSPRPTVLRNC
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LRMLNVLVPSRTPSPDRIILRHGCLHSPLRSDDTIHTSCGVAALISMLASRVFTVG
SPVSG"
1176..1955
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ORIGIN
Query Match 76.4%; Score 320.8; DB 1; Length 4713;
Best Local Similarity 85.2%; Pred. No. 3e-25;
Matches 358; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCAGCGTCGCGGTACGCTGACGTCAGACCAACCGACCGACCGCTTCTCGCCAGGCG 60
Db 3065 AAGAAGACGAGCAGCGTCGCTGCTGACGCGACCAACGACCGCTACGCTCTCGCTCAGGCG 3124
Qy 61 CTCGTACGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Db 3125 CTCGTCCGCGAGGCGCTCGCGCAACGTCGCTGCGCGCGCAACCCGCTGGGTCTTGAAGCGC 3184
Qy 121 GGCATCGAGNAGGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCAGCGGAGGATGTC 180
Db 3185 GGCATCGAGNAGGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCAGCGGAGGATGTC 3244
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCTCGGCGCGCTCTCGGAGCAGCGGAGGATGTC 240
Db 3245 GAGACCAAGGAGCAGATCGCTTCCACGCGCGCTCTCGGCGCGCTCTCGGAGCAGCGGAG 3304
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGTCGGCAAGGAGGCGTATCATCACCGTCGAGGAG 300
Db 3305 GAGCTCATCGCGAGGCGATGGAACAAGTCGGCAAGGAGGCGTATCATCACCGTCGAGGAG 3364
Qy 301 TCCACAGCTTCGGTCTGGAGCTCGAGCTCAGCGAGGATGCGCTTCGACAGGCGTAC 360
Db 3365 TCGAAGCTTCCTCGGCTTCGAGCTCGAGCTCAGCGAGGATGCGCTTCGACAGGCGTAC 3424
Qy 361 ATCTCGGCGTACTTCCGACCGACATGAGCGGATGAGGCGGCTCGCTTCGACAGCGGCTAC 420
Db 3425 ATCTCGCTGTACTTCCGACCGACCGAGCGGTTCAGGAGCGGCTCTCGAGGATCGGTAC 3484

RESULT 7
AF456472
LOCUS AP456472 1651 bp DNA linear BCT 05-NOV-2002
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DEFINITION Mycobacterium sp. 'graecum DL049' heat shock protein 65 (hsp65)
ACCESSION AF456472
VERSION AF456472.1 GI:24571116
SOURCE Mycobacterium sp. 'graecum DL049'
ORGANISM Mycobacterium sp. 'graecum DL049'
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1651)
AUTHORS Ucko, M., Colorni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED 12406715
REFERENCE 2 (bases 1 to 1651)
AUTHORS Ucko, M., Colorni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2001) Genetics, IOLR the National Center for Mariculture, P.O. Box 1212, Eilat 88112, Israel
LOCATION/Qualifiers
FEATURES
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        Query Match 75.2%; Score 316; DB 1; Length 1651;
        Best Local Similarity 84.5%; Pred. No. 1.3e-24;
        Matches 355; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCCGGTACCGGTACGACACCGACCGACCGTCTTCGCCCGAGCG 60
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DB 254 AAGAAGACTGACGACGTCGCAGCGAGCGGACACCAACCGCACCGTCTTCGCCCGAGCA 313
    |||
QY 61 CTCGTACGCGAGGGCTGCGCAACGTGCGCGCGTGCACACCGCATGGCTCTCAAGCGC 120
    |||
DB 314 CTCGTGCGCGAGGGCTGCGCAACGTGCGCGCGCGCGCGCAACCGCATGGCTGGAAGCGC 373
    |||
QY 121 GGCATCGAGAGGCGCGTGCAGGCGCTCTCCGCGCGCGCTGCGGACGCGAGGAGATGTC 180
    |||
DB 374 GGCATCGAGAGGCGCGTGCAGGCGCTCTCCGCGCGCGCTGCGGACGCGAGGAGATGTC 433
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QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCTCCATCTCGCGCGCGCGACACCGCATGGCT 240
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DB 434 GAGACCAAGGAGCAGATCTCCGCCACGCGGAGGATCTCGCGCGCGGATCTCCAGATCGGC 493
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QY 241 GAGCTCATCGCGCGAGCGGATGGAAGGTGCGCAAGGTGCGCAAGGAGGCGTCTATCACCGTCGAGGAG 300
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Db 494 GAGCTCATCGCGAGGCGCATGGAAGGTGCGCAACGAGGGGTGTCTATCACCGTCGAGGAG 553
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DB 554 TCCACACACTTCGGCTCGAGCTCGAGCTCACCGAGGGCATGCGCTTTCGACAAAGGGCTAC 613
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QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGAGTGGAGGGCGTCTCGACGACCGCGTAC 420
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DB 614 ATCTCGGCTTACTTCGTGACCGAGCGCGGAGGAGCGTCTCTGGAGGAGCGGTCAT 673
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RESULT 8
AF352578 1623 bp DNA linear BCT 13-MAR-2001
LOCUS Tsukamurella paurometabola heat shock protein 60 (hsp60) gene,
DEFINITION complete cds.
ACCESSION AF352578
VERSION AF352578.1 GI:13310800
KEYWORDS Tsukamurella paurometabola
SOURCE Tsukamurella paurometabola
ORGANISM Tsukamurella paurometabola
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Tsukamurellaceae; Tsukamurella.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Zimmermann, O.S. and Koechel, H.G.
JOURNAL Tsukamurella paurometabola heat shock protein 60 (hsp60) gene
Unpublished
REFERENCE 2 (bases 1 to 1623)
AUTHORS Zimmermann, O.S. and Koechel, H.G.
JOURNAL Direct Submission
Submitted (23-FEB-2001) Virology, Univ. Goettingen, Kreuzberggring
57, Goettingen D-37075, Germany
LOCATION/Qualifiers
FEATURES
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        Best Local Similarity 84.3%; Pred. No. 2e-24;
        Matches 354; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCCGGTACCGGTACGACACCGACCGTCTTCGCCCGAGCGC 60
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DB 232 AAGAAGACCGACGACGTCGCCGGGAGCGGACGACACCGCACCGTCTTCGCCCGAGCGC 291
    |||
QY 61 CTCGTACGCGAGGGCTGCGCAACGTGCGCGCGCGTGCACACCGCATGGCTCTCAAGCGC 120
    |||
DB 292 CTCGTGCGCGAGGGCTGCGCAACATGGCTGCGGTCGCAACCGCTGGGCTCAAGCGC 351
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QY 121 GGCATCGAGAGGCGCGTGCAGGCGCTCTCCGCGCGCGCTGCTGAGGAGCGGCGAAGATGTC 180
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Db      352  GGCATCGAAGGCGCTCGAGGCGGTGACCGAGCACCTGCTCAAGGAGCGCAAGGAGGTC 411
Qy      181  GAGACCAAGAGAGAGATCGTTTCCAGGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db      412  GAGACCAAGAGAGAGATCGTTTCCAGGCGCTCCATCTCCGCGCGCGACACCCAGATCGGT 471
Qy      241  GAGCTCATCGCCGAGGCGATGGAACAAGTTCGGCAAGTTCGGCAAGGCGCTCATCACCGTCGAGGAG 300
Db      472  GAGCTCATCGCCGAGGCGATGGAACAAGTTCGGCAAGGCGCTCATCACCGTCGAGGAG 531
Qy      301  TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGATGATCGCTTCGACCAAGGCGTAC 360
Db      532  AGCAACACCTTCGGTTCGGAGCTGGAGCTCACCGAGGATGATCGCTTCGACCAAGGCGTTC 591
Qy      361  ATCTCGGCGTACTTCGCCACCGATGAGCGATGAGCGCTCGCTTCGACCAAGGCGTAC 420
Db      592  ATCTCGGCGTACTTCGCCACCGATGAGCGATGAGCGCTCGCTTCGAGGAGCGCTTAC 651

RESULT 9
AF281650      1624 bp      DNA      linear      BCT 02-APR-2002
LOCUS      Mycobacterium avium heat shock protein Hsp65 gene, partial cds.
DEFINITION
ACCESSION      AF281650
VERSION
KEYWORDS
SOURCE
ORGANISM      Mycobacterium avium
                Mycobacterium avium
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                avium complex (MAC).
REFERENCE
AUTHORS      Nagabhushanam, V., Praszkier, J. and Cheers, C.
TITLE      Molecular and immunological characterization of Mycobacterium avium
                65 kDa heat shock protein (Hsp65)
JOURNAL      Immunol. Cell Biol. 79 (5), 454-461 (2001)
PUBMED      11564153
REFERENCE
AUTHORS      Nagabhushanam, V., Praszkier, J. and Cheers, C.
TITLE      Direct Submission
JOURNAL      Submitted (23-JUN-2000) Microbiology and Immunology, Melbourne
                University, Royal Parade, Melbourne, Victoria 3052, Australia
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                RIEDAVRNKAAVEEGIVAGGGVALLHAIIPALDELKLEGEATGANIVRVALEAPLQ
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ORIGIN
Query Match      74.9%; Score 314.4; DB 1; Length 1624;
Best Local Similarity 84.3%; Pred. No. 2e-24; Mismatches 0; Indels 0; Gaps 0;
Matches 354; Conservative 0;

Qy      1  AAGAAGACCGACGCTCGCGGCTGACGGTACGACACCGACCGACCGCTTCGCGCCAGGCG 60
Db      232  AAGAAGACCGACGCTCGCGGCTGACGGTACGACCGACCGACCGCGCTTCGCGCCAGGCG 291

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Qy      61  CTCGTACCGAGGCGCTCGCAACCTTCGCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 120
Db      292  TTGGTCCGCGAGGGGCTTCGCAACCTTCGCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 351
Qy      121  GGCATCGAAGAGCGGCTCGAGGCGCTTCGCGCGCGGTGCCAACCCCGATGCTCTCAAGCGC 180
Db      352  GGCATCGAAGAGCGGCTCGAAGAGCTTCGCGAGACCTTCGCTCAAGTCGCGCAAGGAGGTC 411
Qy      181  GAGACCAAGAGAGATCGTTTCCAGGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db      412  GAGACCAAGAGAGATCGTTTCCAGGCGCTCCATCTCCGCGCGCGACACCGATCGATCGGC 471
Qy      241  GAGCTCATCGCCGAGGCGATGGAACAAGTTCGGCAAGTTCGGCAAGGCGCTCATCACCGTCGAGGAG 300
Db      472  GAGCTCATCGCCGAGGCGATGGAACAAGTTCGGCAAGGCGCTCATCACCGTCGAGGAG 531
Qy      301  TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGATGATCGCTTCGACCAAGGCGTAC 360
Db      532  TCCAGACCTTCGGCTTCGAGCTTCGAGCTCACCGAGGATGATCGCTTCGACCAAGGCGTAC 591
Qy      361  ATCTCGGCGTACTTCGCCACCGATGAGCGATGAGCGCTCGCTTCGACCAAGGCGTAC 420
Db      592  ATCTCGGCGTACTTCGCCACCGATGAGCGATGAGCGCTCGCTTCGAGGAGCGCTTAC 651

RESULT 10
AX802868      1701 bp      DNA      linear      PAT 24-NOV-2003
LOCUS      Sequence 21 from Patent WO03058248.
DEFINITION
ACCESSION      AX802868
VERSION      AX802868.1 GI:38501565
KEYWORDS      Mycobacterium avium subsp. paratuberculosis
SOURCE      Mycobacterium avium subsp. paratuberculosis
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                avium complex (MAC).
REFERENCE
AUTHORS      Willemsen, P.T., Westerveen, S.F., Bakker, D., van Zijderveld, F.G. and
                Thole, J.E.
TITLE      Paramycobacterial diagnostics and vaccines
JOURNAL      Patent: WO 03058248-A 21 17-JUL-2003;
                ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid B.V.
                (NL)
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Query Match      74.9%; Score 314.4; DB 6; Length 1701;
Best Local Similarity 84.3%; Pred. No. 1.9e-24;

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Query Match 74.9%; Score 314.4; DB 1; Length 1751;
Best Local Similarity 84.3%; Pred. No. 1.9e-24;
Matches 354; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Db	356	A	A	G	A	G	A	C	C	G	A	C	G	T	T	C	C	C	G	G	T	G	A	C	G	T	T	C	G	C	C	A	G	G	C	G	415
QY	61	C	T	C	G	T	A	C	G	A	G	G	G	C	T	G	C	G	C	C	G	G	T	G	C	C	A	A	C	C	G	A	T	G	C	120	
Db	416	T	T	G	G	T	C	C	G	A	G	G	C	T	G	C	C	A	A	C	C	G	C	G	C	C	A	A	C	C	C	G	T	T	C	475	
QY	121	G	G	C	A	T	C	G	A	A	G	C	C	G	T	C	T	C	G	G	C	C	T	G	T	C	G	A	G	C	G	A	A	G	A	180	
Db	476	G	G	C	A	T	C	G	A	A	G	C	C	G	T	C	A	C	C	G	A	G	A	C	C	T	G	T	C	A	G	T	C	A	535		
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Db	536	G	A	G	A	C	A	G	A	G	C	A	G	A	T	C	T	C	C	A	G	G	C	C	A	T	C	C	G	C	C	G	C	A	C	595	
QY	241	G	A	G	C	T	C	A	T	C	C	G	A	G	G	C	T	G	C	A	A	G	G	C	G	T	C	A	T	C	A	C	C	G	T	300	
Db	596	G	A	C	T	G	A	T	C	C	C	G	A	G	G	C	T	G	C	A	A	G	G	C	G	T	C	A	T	C	A	C	C	G	T	655	
QY	301	T	C	C	A	G	A	C	T	T	C	G	G	T	G	A	G	C	T	C	A	C	C	G	A	G	G	T	A	T	C	G	C	T	G	360	
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QY	361	A	T	C	C	G	G	T	A	T	T	C	C	C	A	C	G	A	C	A	T	G	A	G	C	G	G	A	T	G	A	G	C	C	G	420	
Db	716	A	T	C	C	G	G	T	A	T	T	C	C	C	A	C	G	A	C	C	C	C	A	G	G	C	T	C	A	G	A	G	C	C	G	775	

MP115989 2641 bp DNA linear BCT 02-MAR-2000
Mycobacterium paratuberculosis 65 kDa heat shock protein PTB65K
gene, complete cds.

ACCESSION	U15989
VERSION	U15989.1 GI:559802

KEYWORDS

SOURCE .
SOURCE Mycobacterium avium subsp. paratuberculosis
ORGANISM Mycobacterium avium subsp. paratuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).

1 (bases 1 to 2641)
el-Zaataari, F.A., Naseer, S.A., Engstrand, L., Burch, P.E., Hachem, C.Y., Whipple, D.L. and Graham, D.Y.

TITLE Nucleotide sequence analysis and seroreactivities of the 65K heat shock protein from *Mycobacterium paratuberculosis*
JOURNAL Clin. Diagn. Lab. Immunol. 2 (6), 657-664 (1995)

PUBMED 8574825
REFERENCE 2 (bases 1 to 2641)
AUTHORS El-Zaatar, F.A.K.

TITLE	Direct Submission
JOURNAL	Submitted (17-OCT-1994) Fouad A.K. El-Zaatari, Medicine/Digestive Diseases, Baylor College of Medicine and VA Medical Center. 2002

FEATURES

Location/Qualifiers

Holcombe Blvd., Houston, TX 77030, USA

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RESULT 14
AE017241
LOCUS
DEFINITION
Mycobacterium avium subsp. paratuberculosis str. k10, section 15 of
16 of the complete genome.
ACCESSION
AE017241 AE016958
VERSION
AE017241.1 GI:41398721
KEYWORDS
SOURCE
Mycobacterium avium subsp. paratuberculosis str. k10.
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Qy 1 AAGAAGACGACGACGTCGCGGTGACGTAACGACCGACCGGTCGCGCCAGGCG 60
Db 157794 AAGAAGACGACGACGTCGCGGTGACGTAACGACCGACCGGTCGCGCCAGGCG 157853

Qy 61 CTGCTACGCGAGGCGCTCGGCAAGCTCGCGCGCGTGCACCGGTCCTCAAGCGC 120
Db 157854 TTGGTCCGCGAGGCGCTCGGCAAGCTCGCGCGCGTGCACCGGTCCTCAAGCGC 157913

Qy 121 GGCATCAGAGAGGCGCTCGAGGCGCTCTCGCGCGCGTCTGAGGAGGCGGAGGATGTC 180
Db 157914 GGCATCAGAGAGGCGCTCGAGGAGTCAACGAGACCTCTGTAAGTCCGACGAGGATGTC 157973

Qy 181 GAGACCAAGGACGACGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACCCAGATCGGC 240
Db 157974 GAGACCAAGGACGACGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACCGATCGGC 158033

Qy 241 GAGCTCATCGCGAGGCGATGGAAGAAGTTCGGGAAGGAGGCGTTCATCAGCTCGAGGAG 300
Db 158034 GAGCTCATCGCGAGGCGATGGAAGAAGTTCGGGAAGGAGGCGTTCATCAGCTCGAGGAG 158093

Qy 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACCGGAGGTATGCGCTTCGACCAAGGGGCTAC 360
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Db 158094 TCCAACACCTTCGCGCTCGAGCTCGAGCTCACCGAGGGTATGCGTTCGACCAAGGGTAC 158153
Qy 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGCGCTCGCTCGACGACCGCTAC 420
Db 158154 ATCTCGGCGTACTTCGCTACGACCGCGAGCGTTCGAGGAGCGTCTCGAGGAGCGCTTC 158213

RESULT 15
TTU90204
LOCUS TTU90204 1620 bp DNA linear BCT 21-MAR-1997
DEFINITION Tsukamurella tyrosinosolvens heat shock protein 60 (hsp60) gene, complete cds.
ACCESSION U90204
VERSION U90204.1 GI:1899189
KEYWORDS Tsukamurella tyrosinosolvens
ORGANISM Tsukamurella tyrosinosolvens
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
REFERENCE 1 (bases 1 to 1620)
AUTHORS Zimmermann,O., Pinkenburg,O. and Koehler,H.G.
TITLE Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock protein 60
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1620)
AUTHORS Zimmermann,O., Pinkenburg,O. and Koehler,H.G.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1997) Med. Microbiology, University, Kreuzberg 57, Goettingen D-37075, Germany
FEATURES
Location/Qualifiers
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Query Match 74.1%; Score 311.2; DB 1; Length 1620;
Best Local Similarity 83.8%; Pred. No. 4.3e-24;
Matches 352; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCGGTGACGTAACGACCGACCGGTCGCGCCAGGCG 60
Db 232 AAGAAGACGACGACGTCGCGGTGACGTAACGACCGACCGGTCGCGCCAGGCG 291

Qy 61 CTGCTACGCGAGGCGCTCGGCAAGCTCGCGCGCGTGCACCGGTCCTCAAGCGC 120
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DB 352 GGATCGAGAGAGCCGTCGAGGCGGTCCTCGGCGCCCTGCTGAGAGCAGGCGAAGGATGTC 411
QY 181 GAGACCAAGAGAGCAGATCGCTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
DB 412 GAGACCAAGAGAGCAGATCGCTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 471
QY 241 GAGCTCATCGCGAGCGCATGGACAAGGTCGCGCAAGGAGGCGTCATCAACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGCGCATGGACAAGGTCGCGCAAGGAGGCGTCATCAACCGTCGAGGAG 531
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DB 532 AGCAACACCTTCGGCTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACAGGCGCTAC 591
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DB 592 ATCTCGGGCTACTTCCGACCGCATGAGGAGGCGTCGCTTCGACAGGCGCTAC 651
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RESULT 16
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LOCUS Nocardia asteroides heat shock protein 60 (hsp60) gene, complete cds.
DEFINITION AF352019
ACCESSION AF352019.1 GI:13591780
VERSION AF352019.1
KEYWORDS Nocardia asteroides
SOURCE Nocardia asteroides
ORGANISM Nocardia asteroides
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Nocardia.

REFERENCE 1 (bases 1 to 1629)
Zimmermann, O.S. and Koehel, H.G.
AUTHORS Direct Submission
TITLES Submitted (21-FEB-2001) Department of Virology, University of
Goettingen, Kreuzbergstr 57, Goettingen D-37075, Germany
JOURNAL

FEATURES

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ORIGIN

Query Match 73.7%; Score 309.6; DB 1; Length 1629;
Best Local Similarity 83.6%; Pred. No. 6.2e-24;
Matches 351; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGAGCTCGCGGTCACCGTACGACACCGGACCGGTCCTCGCCAGGCG 60
DB 232 AAGAAGACGAGAGCTCGCGGTCACCGTACGACACCGGACCGGTCCTCGCGCTCAGGCG 291

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QY 61 CTCGTACGCGAGGCGCTCGGCAACGTCGCGCGCGTGCACACCCGATGGCTCTCAAGCGC 120
DB 292 CTGGTGCAGGAGGCGCTCGCAACGTCGCGCGCGCGGCAACCCGCTGGGTGCAAGCGC 351
QY 121 GGCATCGAGAGAGGCGCTCGAGGCGGCTCTCCGCGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAGAGAGGCGCTCGAGGCGGCTCACCGCAAGCTGCTGACACCGCCCAAGGAGGTC 411
QY 181 GAGACCAAGAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGAGAGCAGATCGCGCTACCGCGGTATCTCGCGCGCGACCGCGGCTCATCGGT 471
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DB 472 GAGCTCATCGCGAGGCGCATGGACAAGGTCGCGCAAGGAGGCGTCATCAACCGTCGAGGAG 531
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DB 532 AGCAACACCTTCGGCTCGAGCTCGAGCTCACCGAGGAGGCGTCATCAACCGTCGAGGAG 591
QY 361 ATCTCGGGCTACTTCCGACCGCATGAGGAGGCGTCGCTTCGACAGGCGCTAC 420
DB 592 ATCTCGGGCTACTTCCGACCGCATGAGGAGGCGTCGCTTCGACAGGATCGGTAC 651
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RESULT 17
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LOCUS Sequence 113 from patent US 5968524.
DEFINITION AR080017
ACCESSION AR080017
VERSION AR080017.1 GI:10006752
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1569)
Watson, J.D. and Tan, P.L.J.
AUTHORS Methods and compounds for the treatment of immunologically-mediated
TITLES psoriasis
JOURNAL Patent: US 5968524-A 113 19-OCT-1999;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGAGCTCGCGGTCACCGTACGACACCGGACCGGTCCTCGCCAGGCG 60
DB 232 AAGAAGACGAGAGCTCGCGGTCACCGTACGACACCGGACCGGTCCTCGCTCAGGCT 291
QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTCGCAACCCGATGGCTCTCAAGCGC 120
DB 292 CTGGTTCGCAAGGCGCTCGCAACGTCGCGCGCGCGCAACCCGCTCGGCTCAAGCGT 351
QY 121 GGCATCGAGAGGCGCTCGAGGCGGCTCTCCGCGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAGAGGCGCTCGAGGCGGTCATCCACAGTCGCTGCTGTAAGTCGCGCAAGGAGGTC 411
QY 181 GAGACCAAGAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGAGAGCAGATTCGTCACCGCGCGGATTTCCGCGCGGGAACCCAGATCGGC 471
QY 241 GAGCTCATCGCGAGGCGATGGACAAGGTCGCGCAAGGAGGCGTCATCAACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGGCGATGGACAAGGTCGCGCAAGGAGGCGTCATCAACCGTCGAGGAG 531
QY 301 TCCACAGCTTCGGCTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACAGGCGCTAC 360
DB 532 TCGAACACCTTCGGCGCTCGAGCTCAGGCTCAGGAGGATGCGCTTCGACAGGCGCTAC 591

QY 361 ATCTCGGCTACTTCGCCACCGACATGAGCGGATGGAGCGCTCGCTCGACGACCGCTAC 420
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Db 592 ATCTCGGCTACTTCGTGACCGACCGCGGAGCGGCGGAGCGCTCTCGAGGATCCCTAC 651
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RESULT 18
AR085943
LOCUS AR085943 1569 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 113 from patent US 5985287.
ACCESSION AR085943
VERSION AR085943.1 GI:10012709
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 113 16-NOV-1999;
FEATURES Location/Qualifiers
source 1.1569
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGCTCGCGGTCAGCGTACGACACCGACCGGCGCTTCGCGCCAGGCG 60
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Db 232 AAGAAGACGACGACGCTCGCGGTCAGCGTACGACACCGACCGGCGCTTCGCTCAGGCT 231
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QY 61 CTCGTACGACGAGGCGCTCGCGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGCGC 120
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Db 292 CTGGTTCCGCAAGGCGCTCGCGCAACGTCGCGCGGCGCAACCCGCTCGCGCTCAAGCGT 351
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QY 121 GGCATCGAGAGGCGCTCGAGGCGCTCGCGGCGCTCGCGGCGCTCGCGGCGGAGGATGTC 180
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Db 352 GGCATCGAGAGGCGCTCGAGGCGCTCGCGGCGCTCGCGGCGCTCGCGGCGGAGGATGTC 180
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QY 181 GAGACCAAGGACGATCGCTTCACCGGCTTCATCTCCGCGCGCGGCGGACACCCAGATCGGC 240
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Db 412 GAGACCAAGGACGATTCCTGCCACCGCGGCGGATTCGCGCGGCGGACACCCAGATCGGC 471
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QY 241 GAGCTCATCTCGCGAGCGATGACAAAGGTCGCGAGGAAGGCGTCTATCACCCTCGAGGAG 300
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Db 472 GAGCTCATCTCGCGAGCGCATGACAAAGGTCGCGAGGCGTCTATCACCCTCGAGGAG 531
|||||

QY 301 TCCAGACCTTCGCTCGAGCTGAGGCTCAGGAGTCCAGGCGTATCGCTTCGACAGGCGCTAC 360
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Db 532 TCGAACACCTTCGCGCTCGAGCTCGAGCTCAGGAGGATGCGCTTCGACAGGCGCTAC 591
|||||

QY 361 ATCTCGGCTACTTCGCCACCGACATGAGCGATGAGGCGCTCGCTCGACGACCGCTAC 420
|||||
Db 592 ATCTCGGCTACTTCGTGACCGGCGGAGCGCGGAGGAGCGCTCTCGAGGATCCCTAC 651
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RESULT 19
AR121709
LOCUS AR121709 1569 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 113 from patent US 6160093.
ACCESSION AR121709
VERSION AR121709.1 GI:14105285
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial

infections
Patent: US 6160093-A 113 12-DEC-2000;
FEATURES Location/Qualifiers
source 1.1569
/organism="unknown"
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ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGCTCGCGGTCAGCGTACGACACCGACCGGCGCTTCGCGCCAGGCG 60
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Db 232 AAGAAGACGACGACGCTCGCGGTCAGCGTACGACACCGACCGGCGCTTCGCTCAGGCT 231
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QY 61 CTCGTACGACGAGGCGCTCGCGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGCGC 120
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Db 292 CTGGTTCCGCAAGGCGCTCGCGCAACGTCGCGCGGCGCAACCCGCTCGCGCTCAAGCGT 351
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QY 121 GGCATCGAGAGGCGCTCGAGGCGCTCGCGGCGCTCGCGGCGCTCGCGGCGGAGGATGTC 180
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Db 352 GGCATCGAGAGGCGCTCGAGGCGCTCGCGGCGCTCGCGGCGCTCGCGGCGGAGGATGTC 180
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QY 181 GAGACCAAGGACGATCGCTTCACCGGCTTCATCTCCGCGCGCGGCGGACACCCAGATCGGC 240
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Db 412 GAGACCAAGGACGATTCCTGCCACCGCGGCGGATTCGCGCGGCGGACACCCAGATCGGC 471
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QY 241 GAGCTCATCTCGCGAGCGATGACAAAGGTCGCGAGGAAGGCGTCTATCACCCTCGAGGAG 300
|||||
Db 472 GAGCTCATCTCGCGAGCGCATGACAAAGGTCGCGAGGCGTCTATCACCCTCGAGGAG 531
|||||

QY 301 TCCAGACCTTCGCTCGAGCTGAGGCTCAGGAGTCCAGGCGTATCGCTTCGACAGGCGCTAC 360
|||||
Db 532 TCGAACACCTTCGCGCTCGAGCTCGAGCTCAGGAGGATGCGCTTCGACAGGCGCTAC 591
|||||

QY 361 ATCTCGGCTACTTCGCCACCGACATGAGCGATGAGGCGCTCGCTCGACGACCGCTAC 420
|||||
Db 592 ATCTCGGCTACTTCGTGACCGGCGGAGCGCGGAGGAGCGCTCTCGAGGATCCCTAC 651
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RESULT 20
BD218118
LOCUS BD218118 1569 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218118.1 GI:33027888
VERSION JP 2002514385-A/43.
KEYWORDS Mycobacterium vaccae
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for their use
JOURNAL Patent: JP 2002514385-A 43 21-MAY-2002;
COMMENT GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Mycobacterium vaccae
PN JP 2002514385-A/43
PD 21-MAY-2002
PP 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC

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G01N33/58//
PC (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
CC Compositions derived from mycobacterium
vacciae and methods for
their use
FH Key Location/Qualifiers
FT source 1..1569
/organism="Mycobacterium vaccae".
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source Location/Qualifiers
1..1569
/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"
/db_xref="taxon:1810"
ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGAGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 60
DB 232 AAGAAGACGAGCGAGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 291
QY 61 CTCGTACGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 120
DB 292 CTGGTTCCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 351
QY 121 GGCATCGAGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 180
DB 352 GGCATCGAGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 411
QY 181 GAGACCAAGGAGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 240
DB 412 GAGACCAAGGAGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 471
QY 241 GAGCTCATCGCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 300
DB 472 GAGCTCATCGCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 531
QY 301 TCCAGACCTTCGCTCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 360
DB 532 TCCAGACCTTCGCTCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 591
QY 361 ATCTCGGGTTACTTCGTCAGCGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 420
DB 592 ATCTCGGGTTACTTCGTCAGCGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 651
RESULT 21
LOCUS AR213755 1569 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 113 from patent US 6406704.
ACCESSION AR213755
VERSION AR213755.1 GI:23311042
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 113 18-JUN-2002;
Genesis Research and Development Corporation Limited;;
NZX;
FEATURES
source Location/Qualifiers
1..1569
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGAGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 60
DB 232 AAGAAGACGAGCGAGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 291
QY 61 CTCGTACGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 120
DB 292 CTGGTTCCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 351
QY 121 GGCATCGAGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 180
DB 352 GGCATCGAGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 411
QY 181 GAGACCAAGGAGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 240
DB 412 GAGACCAAGGAGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 471
QY 241 GAGCTCATCGCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 300
DB 472 GAGCTCATCGCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 531
QY 301 TCCAGACCTTCGCTCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 360
DB 532 TCCAGACCTTCGCTCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 591
QY 361 ATCTCGGGTTACTTCGTCAGCGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 420
DB 592 ATCTCGGGTTACTTCGTCAGCGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 651
RESULT 22
LOCUS AR365987 1569 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 113 from patent US 6328978.
ACCESSION AR365987
VERSION AR365987.1 GI:34598240
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Watson,J.D., Tan,P.I.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 113 11-DEC-2001;
Genesis Research & Development Corp. Ltd.; Parnell;
NZX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGAGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 60
DB 232 AAGAAGACGAGCGAGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 291
QY 61 CTCGTACGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 120
DB 292 CTGGTTCCGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 351
QY 121 GGCATCGAGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 180
DB 352 GGCATCGAGAGGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 411
QY 181 GAGACCAAGGAGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 240
DB 412 GAGACCAAGGAGCGCGTCCCGGTGACGATAGACACCGCGACCGTTCTCCGCCAGGCG 471
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KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1626)
AUTHORS	Tan, P., Skinner, M. and Prestidge, R.
TITLE	Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL	Patent: US 5985287-A 159 16-NOV-1999;
FEATURES	Location/Qualifiers
source	1..1626
ORIGIN	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity	83.3%; Pred. No. 9.2e-24;
Matches	350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY	1 AAGAAGCGGACGACGTCGCGGTGACGCGTACGACCAACCGCGACCGCTTCTCGCCCGAGGCG 60
Db	232 AAGAAGCGGACGACGTCGCGGGCGACGCGACCAACCGCGACCGTCTCGCTCAGGCT 291
QY	61 CTCGTACGCGAGGGCGCTGGCAACCTCGCCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
Db	292 CTGGTTCCGGAAGGCGCTCGCAACCTCGCAGCGCGCGCAACCCCGCTCGGCTCAAGCGT 351
QY	121 GGCATCGAGAAGCGCGTTCGAGGCCGCTCTCCGCGCGCTCTGCTGGAGCAGCGCAAGGATGTC 180
Db	352 GGCATCGAGAGGCTGTGAGGGCTGTACCCAGTCTGCTGTAAGTTCGGCCAGGAGGTC 411
QY	181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCATCTCGCGCGCGACACCCAGATCGGC 240
Db	412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCGCGCGACACCCAGATCGGC 471
QY	241 GAGCTCATCGCGAGGCGATGAGCAAGGTTCGCAAGGAAGGCGTATCATCCGTCGAGGAG 300
Db	472 GAGCTCATCGCGAGGCGATGAGCAAGGTTCGCAAGGAGGCGTATCATCCGTCGAGGAG 531
QY	301 TCCAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 360
Db	532 TCGAACACCTTCGGCTGAGCTCAGCTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 591
QY	361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCCGTCAC 420
Db	592 ATCTCGGCGTACTTCGTGACCGACCGCGAGCGCGAGGAAGCGCTCTCGAGGATCCCTAC 651
RESULT 27	
BD218146	
LOCUS	1626 bp DNA linear PAT 17-JUL-2003
DEFINITION	Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION	BD218146
VERSION	BD218146.1 GI:33027916
KEYWORDS	JP 2002514385-A/71.
SOURCE	Mycobacterium vaccae
ORGANISM	Mycobacterium vaccae
REFERENCE	1 (bases 1 to 1626)
AUTHORS	Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
TITLE	Compositions derived from mycobacterium vaccae and methods for their use
JOURNAL	Patent: JP 2002514385-A 71 21-MAY-2002;
COMMENT	GENESIS RESEARCH AND DEVELOPMENT CORP LTD
	OS Mycobacterium vaccae
	PN JP 2002514385-A/71
	PD 21-MAY-2002
	PF 23-DEC-1998 JP 2000525553
	PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
	23-DEC-1997 US 08/996624,11-JUN-1998 US 09/995855 PR
	17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
	TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
	PI L PRESTIDGE
	PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
	PC A61P17/00,
	PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
	PC C07K19/00,
	PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
	G01N33/68//
	PC (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
	CC Compositions derived from mycobacterium
	vaccae and methods for
	their use
	CC Key
	Location/Qualifiers
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source	1..1626
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Query Match      73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACACCGACCGGTCCTCGCCCGAGGCG 60
DB 232 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACACCGACCGGTCCTCGCTCAGGCT 291
QY 61 CTGCTACGCGAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 120
DB 292 CTGGTTCCGCAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 351
QY 121 GGCATCGAGAAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 180
DB 352 GGCATCGAGAAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 411
QY 181 GAGACCAAGGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCCCGAGGCG 240
DB 412 GAGACCAAGGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCCCGAGGCG 471
QY 241 GAGCTCATCGCGAGGCGTCGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 300
DB 472 GAGCTCATCGCGAGGCGTCGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 531
QY 301 TCCGACACCTTCGGTTCGAGCTGAGCTCAGCGAGGTCATCCGCTCGCAAGGCGTCAC 360
DB 532 TCGAACACCTTCGGTTCGAGCTGAGCTCAGCGAGGTCATCCGCTCGCAAGGCGTCAC 591
QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGTCGTCGCGCGGTGACGGTACGACACCGGTCAC 420
DB 592 ATCTCGGCGTACTTCGCGACCGACATGAGCGGTCGTCGCGCGGTGACGGTACGACACCGGTCAC 651

RESULT 29
AR366015 LOCUS 1626 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 159 from patent US 6328978.
ACCESSION AR366015
VERSION AR366015.1 GI:34598268
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 159 11-DEC-2001;
Genesis Research & Development Corp. Ltd.; Parnell;
NZX;

FEATURES
source 1..1626
/mol_type="genomic DNA"

ORIGIN
Query Match      73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCCCGAGGCG 60
DB 232 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 291
QY 61 CTGCTACGCGAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 120
DB 292 CTGGTTCCGCAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 351
QY 121 GGCATCGAGAAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 180
DB 352 GGCATCGAGAAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 411
QY 181 GAGACCAAGGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCCCGAGGCG 240
DB 412 GAGACCAAGGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCCCGAGGCG 471
QY 241 GAGCTCATCGCGAGGCGTCGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 300
DB 472 GAGCTCATCGCGAGGCGTCGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 531
QY 301 TCCGACACCTTCGGTTCGAGCTGAGCTCAGCGAGGTCATCCGCTCGCAAGGCGTCAC 360
DB 532 TCGAACACCTTCGGTTCGAGCTGAGCTCAGCGAGGTCATCCGCTCGCAAGGCGTCAC 591
QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGTCGTCGCGCGGTGACGGTACGACACCGGTCAC 420
DB 592 ATCTCGGCGTACTTCGCGACCGACATGAGCGGTCGTCGCGCGGTGACGGTACGACACCGGTCAC 651

RESULT 28
AR213783 LOCUS 1626 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 159 from patent US 6406704.
ACCESSION AR213783
VERSION AR213783.1 GI:23311070
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 159 18-JUN-2002;
Genesis Research and Development Corporation Limited;;
NZX;

FEATURES
source 1..1626
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ORIGIN
Query Match      73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCCCGAGGCG 60
DB 232 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 291
QY 61 CTGCTACGCGAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCAAGCGC 120
DB 292 CTGGTTCCGCAAGGCGCTGCGCAACGTCGCGCGGTGACGGTACGACACCGGTCCTCGCTCAGGCT 351
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RESULT 30
AR080018
LOCUS AR080018 647 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 115 from patent US 5968524.
ACCESSION AR080018
VERSION AR080018.1 GI:10006753
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Watson, J.D. and Tan, P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL Patent: US 5968524-A 115 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGAGCTCGCGGTGACGGGTAGCACCGGACCGGACCGGCTTCTCGCCCGAGGG 60
Db |||||
QY 232 AAGAAGACGGACGAGCTCGCGGGGACGCGACACCGACCGGCTGCTCGCTCAGGCT 291
Db |||||
QY 61 CTCGTACGCGAGGGCTCGCGCAACGTCGCCCGGTGCGCAACCGCGATGGCTCTCAAGGCG 120
Db |||||
QY 292 CTGGTTGCGAAGGCGCTCGCGCAACGTCGACGCGCGCGCAACCGCGCTCGGCTCAAGCGT 351
Db |||||
QY 121 GGCATCGAAGGCGCTCGAGCGGCTCTCGCGGCGCTCTCGGAGCGAGCGAGGATGTC 180
Db |||||
QY 352 GGCATCGAAGGCGCTCGAGGCTGTCAACCGTGGCTGTGAAAGTCCGCGCAAGGAGGTC 411
Db |||||
QY 181 GAGACCAAGGACGAGATCGCTTCCACGGCTCTCATCTCCGCGCGCGACACCGAGATCGGC 240
Db |||||
QY 412 GAGACCAAGGACGAGATTTCTGCCACCGCGGGATTTCCGCGCGGACACCGAGATCGGC 471
Db |||||
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Db |||||
QY 472 GAGCTCATCGCGAGGGCCATGCAAGGTGCGCAACGAGGGTGTATCATCAGCTCGAGGAG 531
Db |||||
QY 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCAGCGAGGGTATGCGTTTCGACNAGGGCTAC 360
Db |||||
QY 532 TCGAACACCTTCGGCTTCGAGCTCAGCTCAGCGAGGGTATGCGCTTCGACNAGGGCTAC 591
Db |||||
QY 361 ATCTCGGGGTACTTCCGACCGACATGAGCGGATGAGGGGTGCTCGACGAGCC 416
Db |||||
QY 592 ATCTCGGGTACTTCTGTGACCGACCGCGGAGCGCGGAGGCGCTCCTCGAGGATCC 647
Db |||||

RESULT 31
AR085944
LOCUS AR085944 647 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 115 from patent US 5985287.
ACCESSION AR085944
VERSION AR085944.1 GI:10012710
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 115 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="unassigned DNA"

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ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGAGCTCGCGGTGACGGGTAGCACCGGACCGGACCGGCTTCTCGCCCGAGGG 60
Db |||||
QY 232 AAGAAGACGGACGAGCTCGCGGGGACGCGACACCGACCGGCTGCTCGCTCAGGCT 291
Db |||||
QY 61 CTCGTACGCGAGGGCTCGCGCAACGTCGCCCGGTGCGCAACCGCGATGGCTCTCAAGGCG 120
Db |||||
QY 292 CTGGTTGCGAAGGCGCTCGCGCAACGTCGACGCGCGCGCAACCGCGCTCGGCTCAAGCGT 351
Db |||||
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Db |||||
QY 352 GGCATCGAAGGCGCTCGAGGCTGTCAACCGTGGCTGTGAAAGTCCGCGCAAGGAGGTC 411
Db |||||
QY 181 GAGACCAAGGACGAGATCGCTTCCACGGCTCTCATCTCCGCGCGCGACACCGAGATCGGC 240
Db |||||
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Db |||||
QY 241 GAGCTCATCGCGAGGGCGATGCAAGGTGCGGCAAGGAGGCGTCAATCAGCTCGAGGAG 300
Db |||||
QY 472 GAGCTCATCGCGAGGGCCATGCAAGGTGCGCAACGAGGGTGTATCATCAGCTCGAGGAG 531
Db |||||
QY 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCAGCGAGGGTATGCGTTTCGACNAGGGCTAC 360
Db |||||
QY 532 TCGAACACCTTCGGCTTCGAGCTCAGCTCAGCGAGGGTATGCGCTTCGACNAGGGCTAC 591
Db |||||
QY 361 ATCTCGGGGTACTTCCGACCGACATGAGCGGATGAGGGGTGCTCGACGAGCC 416
Db |||||
QY 592 ATCTCGGGTACTTCTGTGACCGACCGCGGAGCGCGGAGGCGCTCCTCGAGGATCC 647
Db |||||

RESULT 32
AR121710
LOCUS AR121710 647 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 115 from patent US 6160093.
ACCESSION AR121710
VERSION AR121710.1 GI:14105286
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Viesser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 115 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGAGCTCGCGGTGACGGGTAGCACCGGACCGGACCGGCTTCTCGCCCGAGGG 60
Db |||||
QY 232 AAGAAGACGGACGAGCTCGCGGGGACGCGACACCGACCGGCTGCTCGCTCAGGCT 291
Db |||||
QY 61 CTCGTACGCGAGGGCTCGCGCAACGTCGCCCGGTGCGCAACCGCGATGGCTCTCAAGGCG 120
Db |||||
QY 292 CTGGTTGCGAAGGCGCTCGCGCAACGTCGACGCGCGCGCAACCGCGCTCGGCTCAAGCGT 351
Db |||||
QY 121 GGCATCGAAGGCGCTCGAGCGGCTCTCGCGGCGCTCTCGGAGCGAGCGAGGATGTC 180
Db |||||
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QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
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QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCACCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGATGCGCTTCGACAAAGGCGTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACGAGGATGCGCTTCGACAAAGGCGTAC 591
QY 361 ATCTCGCGTACTTCCGCCCGGACATGAGCGGATGAGGCGCTCGTCCGACGACCC 416
Db 592 ATCTCGGGTTACTTTCGTGACCGACCGCGCGGAGCGCTCGTCCGAGGATCC 647

RESULT 33
LOCUS BD218119 647 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218119
VERSION 1 GI:33027889
KEYWORDS JP 2002514385-A/44.
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE Corynebacterineae; Actinobacteridae; Actinomycetales;
AUTHORS Bacteria; Actinobacteria; Mycobacteriaceae; Mycobacterium.
TITLE 1 (bases 1 to 647)
Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
Compositions derived from mycobacterium vaccae and methods for
their use
JOURNAL Patent: JP 2002514385-A 44 21-MAY-2002;
GENESTS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT OS Mycobacterium vaccae
PN JP 2002514385-A/44
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
A61P17/00,
PC A61P17/06, A61P31/00, A61P37/04, C07K14/35, C07K16/12,
C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC (C12N15/09, C12R1.32), C12N15/00, C12N5/00, (C12N15/00, C12R1.32)
CC Compositions derived from mycobacterium
vaccae and methods for
their use
FH Key Location/Qualifiers
FT source 1..647
/organism="Mycobacterium vaccae".
FEATURES Location/Qualifiers
source 1..647
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ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGACGTCGCGGGCGACGGACACCAACCGCGTCTCGTCCGAGGCG 60
Db 232 AAGAAGACGAGACGTCGCGGGCGACGGACACCAACCGCGTCTCGTCCGAGGCT 291
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QY 61 CTCTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCCAACCCGATGCTCTCAAGCGC 120
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Db 352 GGCATCGAAGAGGCTTCGAGGCTGTCAACCCAGTCTGCTGAAGTTCGGCCCAAGGAGTTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTTCGCCACCGCGCGATTTCCCGCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCACCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGATGCGCTTCGACAAAGGCGTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACGAGGATGCGCTTCGACAAAGGCGTAC 591
QY 361 ATCTCGCGTACTTCCGCCCGGACATGAGCGGATGAGGCGCTCGTCCGACGACCC 416
Db 592 ATCTCGGGTTACTTTCGTGACCGACCGCGCGGAGCGCTCGTCCGAGGATCC 647

RESULT 34
LOCUS AR213756 647 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 115 from patent US 6406704.
ACCESSION AR213756
VERSION AR213756.1 GI:23311043
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 647)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6406704-A 115 18-JUN-2002;
GENESTS Research and Development Corporation Limited;;
NZX;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGACGTCGCGGGCGACGGTACGAGTACGACACCGCGACCGCTTTCGCGCCAGGCG 60
Db 232 AAGAAGACGAGACGTCGCGGGCGACGGTACGAGTACGACACCGCGACCGCTTTCGCTCGAGCT 291
QY 61 CTCTACGCGAGGCGCTTCGCAACGTCGCGCGCGGTGCCAACCCGATGCTCTCAAGCGC 120
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Db 352 GGCATCGAAGAGGCTTCGAGGCTGTCAACCCAGTCTGCTGAAGTTCGCGCAAGGAGGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
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QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCACCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGATGCGCTTCGACAAAGGCGTAC 360
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Db 532 TCGAACACCTTCGGCTTCAGCTCGAGCTCACCAGGGTATGCGCTTCGACCAAGGCTAC 591
QY 361 ATCTCGCGTACTTCGACCGACCATGAGCGGATGAGCGCTCGCTCGACGACCC 416
Db 592 ATCTCGGGTTACTTCGTGACCGAGCGCGAGCGCCAGGAGCGCTTCGTGAGGATCC 647

RESULT 35
AR365988
LOCUS
DEFINITION
ACCESSION
AR365988
VERSION
AR365988.1 GI:34598241
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 647)
AUTHORS
Watson, J.D., Tan, P.L.J. and Prestidge, R.
TITLE
Methods for the treatment of immunologically-mediated skin disorders
JOURNAL
Patent: US 6328978-A 115 11-DEC-2001;
Genesis Research & Development Corp. Ltd.; Parnell;
NZX;

FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAGACCGAGCGAGCTCGCGGTGACGCTAGCACCGGACCGTTTCGCCCGCAGGG 60
Db 232 AAGAAGACCGAGCGAGCTCGCGGGCGACGCGCACCCACCGCTGCTCGCTCAGGCT 291
QY 61 CTGCTACCGGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
Db 292 CTGGTTCGGAAGGCTCGCAACGTCGCGCGGTGCGCAACCCGCTCGGCTCAAGGCT 351
QY 121 GGCATCGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTGCTGAGCAGCGAAGGATGTC 180
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QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCTCATCTCGCGCGCGCACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCGCGCGCACCCAGATCGGC 471
QY 241 GAGCTCATCGCGGAGGCGATGACCAAGGTCGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 300
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QY 301 TCCGAGACCTTCGGCTTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACCAAGGCTTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACCAAGGCTTAC 591
QY 361 ATCTCGGGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGTCGACGACCC 416
Db 592 ATCTCGGGTACTTCGTGACCGAGCGCGAGCGCCAGGAGCGCTCTCGAGGATCC 647

RESULT 36
BD008541
LOCUS
DEFINITION
BD008541
ACCESSION
BD008541.1 GI:18635914
VERSION
JP 2001503969-A/44.
KEYWORDS
SOURCE
unidentified

BD008541
Compounds and methods for treatment and diagnosis of Mycobacterial infections.
BD008541
BD008541.1 GI:18635914
JP 2001503969-A/44.
unidentified

RESULT 37
AP006618_55/c
WPCOMMENT

Sequence split into 61 fragments LOCUS AP006618 Accession AP006618
Fragment Name Begin End
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AP006618_01 100001 210000
AP006618_02 200001 310000
AP006618_03 300001 410000
AP006618_04 400001 510000

ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 647)
AUTHORS
Tan, P., Hiyaama, J., Visser, E.S., Skinner, M.A., Scott, L.M. and Prestidge, R.L.
TITLE
Compounds and methods for treatment and diagnosis of Mycobacterial infections
JOURNAL
Patent: JP 2001503969-A 44 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT
OS Unidentified
PN JP 2001503969-A/44
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI LINDA M SCOTT.
PI ROSS L PRESTIDGE
PC A61K39/04, A61K35/74, C07K14/35, C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..647
/organism="Unidentified".

FEATURES
source
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ORIGIN

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAGACCGAGCGAGCTCGCGGTGACGCTAGCACCGGACCGTTTCGCCCGCAGGG 60
Db 232 AAGAAGACCGAGCGAGCTCGCGGGCGACGCGCACCCACCGCTGCTCGCTCAGGCT 291
QY 61 CTGCTACCGGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
Db 292 CTGGTTCGGAAGGCTCGCAACGTCGCGCGGTGCGCAACCCGCTCGGCTCAAGGCT 351
QY 121 GGCATCGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTGCTGAGCAGCGAAGGATGTC 180
Db 352 GGCATCGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTGCTGAGTCCGCGAAGGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCTCATCTCGCGCGCGCACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCGCGCGCACCCAGATCGGC 471
QY 241 GAGCTCATCGCGGAGGCGATGACCAAGGTCGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 300
Db 472 GAGCTCATCGCGGAGGCGATGACCAAGGTCGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 531
QY 301 TCCGAGACCTTCGGCTTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACCAAGGCTTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACCAAGGCTTAC 591
QY 361 ATCTCGGGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGTCGACGACCC 416
Db 592 ATCTCGGGTACTTCGTGACCGAGCGCGAGCGCCAGGAGCGCTCTCGAGGATCC 647

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Continuation (56 of 61) of AP006618 from base 5500001 (AP006618 Nocardia farcinica IFM 1

Query Match 71.8%; Score 301.6; DB 1; Length 110000;
Best Local Similarity 82.4%; Pred. No. 1.1e-23;
Matches 346; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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61 CTCTGACGCGAGGCGCTGCGCAAGCTGCGCGCGTCCCAACCGATGGCTCTCAAGCGC 120
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QY 61 CTCGTACGAGGCGCTCGCAACGTCGCGCGCGTGCACACCCGATGGCTCTCAAGCGC 120
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Db 352 AGCATCGAGAGCGCTCGAGGCGCTCGAGGCGCTCGAGGCGCTCTCGACACCGCCAGAGGTC 411
QY 181 GAGACCAAGGAGGAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
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RESULT 39
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LOCUS
DEFINITION
Mycobacterium marinum isolate S4 heat shock protein 65 (hsp65)
gene, partial cds.
ACCESSION
AF456474
VERSION
AF456474.1 GI:24571122
KEYWORDS
Mycobacterium marinum
ORGANISM
Mycobacterium marinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE
Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL
Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED
12406715
REFERENCE
AUTHORS
Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2001) Genetics, IOLR the National Center for
Mariculture, P.O. Box 1212, Eilat 88112, Israel
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/note="sample kindly provided by Prof. Sandra Adams,
Institute of Aquaculture, University of Stirling,
Scotland"
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Institute of Aquaculture, University of Stirling,
Scotland"
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ORIGIN

Query Match
Best Local Similarity 71.4%; Score 300; DB 1; Length 1648;
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Db 614 ATCTCGGCGTACTTCGCCACCGAGCGCGGAGCGCTCAGGAGGCGCTCCTGGAGGACCGCTAC 673

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AF456468
LOCUS
DEFINITION
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65 (hsp65) gene, partial cds.
ACCESSION
AF456468
VERSION
AF456468.1 GI:24571104
KEYWORDS
Mycobacterium marinum
ORGANISM
Mycobacterium marinum
Bacteria; Actinobacteria;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE
Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL
Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED
12406715
REFERENCE
AUTHORS
Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2001) Genetics, IOLR the National Center for
Mariculture, P.O. Box 1212, Eilat 88112, Israel
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/isolation_source="isolated from European seabass spleen"
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Best Local Similarity 81.9%; Pred. No. 9.3e-23;
Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 1 AAGAAGCGAGACGTCGCGGTGACGTGACACACCGGACCGGTCCTCGGCCGAGGCG 60
DB 254 AAGAAGCGAGACGTCGCGGTGACGTGACACACCGGACCGGTCCTCGGCCGAGGCG 313
QY 61 CTGCTACGCGAGGCGCTCGCCACGTCGCGCGGTGCCAACCCGATGCTCTCAAGCGC 120
DB 314 CTGCTCAAGAGAGCGCTCGCCACGTCGCGCGGTGCCAACCCGCTCGGTCTGAAGCGC 373
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DEFINITION Mycobacterium marinum strain cyprinum CC240299 heat shock protein
65 (hsp65) gene, partial cds.
ACCESSION AF456469
VERSION AF456469.1 GI:24571107
KEYWORDS
SOURCE Mycobacterium marinum
ORGANISM Mycobacterium marinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Cornebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1648)
AUTHORS Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE Strain Variation in Mycobacterium marinum Fish Isolates
Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
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12406715
2 (bases 1 to 1648)
Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
Direct Submission
Submitted (10-DEC-2001) Genetics, IOUR the National Center for
Mariculture, P.O. Box 1212, Bilat 88112, Israel
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ORIGIN
Query Match 71.0%; Score 298.4; DB 1; Length 1648;
Best Local Similarity 81.9%; Pred. No. 9.3e-23;
Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 1 AAGAAGCGAGACGTCGCGGTGACGTGACACACCGGACCGGTCCTCGGCCGAGGCG 60
DB 254 AAGAAGCGAGACGTCGCGGTGACGTGACACACCGGACCGGTCCTCGGCCGAGGCG 313
QY 61 CTGCTACGCGAGGCGCTCGCCACGTCGCGCGGTGCCAACCCGATGCTCTCAAGCGC 120
DB 314 CTGCTCAAGAGAGCGCTCGCCACGTCGCGCGGTGCCAACCCGCTCGGTCTGAAGCGC 373
QY 121 GGCAATCGAGAGCGCTCGAGGCGCTCGCGCGCGCTCGTGGAGCAGCGAGGATGTC 180
DB 374 GGCAATCGAGAGCGCTCGAGGCGCTCGCGCGCGCTCGTGGAGCAGCGAGGATGTC 433
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACCAAGGATGTC 240
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DB 494 GAGCTATCGCGAGGCGCTCGAGGCGCTCGCGCGCGCTCGATCACCCTCGAGGAG 553
QY 301 TCCACACCTTCGCGCTCGAGGCGCTCGCGCGCGCTCGATCACCCTCGAGGAGCTAC 360
DB 554 TCCACACCTTCGCGCTCGAGGCGCTCGCGCGCGCTCGATCACCCTCGAGGAGCTAC 613
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DB 614 ATCTCGCGCTACTTCTCGTCAAGGAGGATGAGGCGCTCGTCAAGGAGGATGAGGAG 673
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AF456470
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LOCUS      AF456470                1648 bp    DNA        linear    BCT 05-NOV-2002
DEFINITION Mycobacterium marinum strain ATCC 927 heat shock protein 65 (hsp65)
            gene, partial cds.
ACCESSION  AF456470
VERSION    AF456470.1  GI:24571110
KEYWORDS   Mycobacterium marinum
SOURCE     Mycobacterium marinum
ORGANISM   Mycobacterium marinum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 1648)
AUTHORS    Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
            Knibb,W.R.
TITLE      Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL    Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED     12406715
REFERENCE  2 (bases 1 to 1648)
AUTHORS    Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
            Knibb,W.R.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2001) Genetics, IOIR the National Center for
            Mariculture, P.O. Box 1212, Eilat 88112, Israel
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            Best Local Similarity 81.9%; Pred. No. 9.3e-23;
            Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY      1  AAGAAGACGAGCGTCCCGGTGACGCGTACGACACCGCCACCGTTCGCCCCAGCGG 60
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DEFINITION
ACCESSION  AF456471
VERSION    AF456471.1  GI:24571113
KEYWORDS   Mycobacterium marinum
SOURCE     Mycobacterium marinum
ORGANISM   Mycobacterium marinum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 1648)
AUTHORS    Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
            Knibb,W.R.
TITLE      Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL    Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED     12406715
REFERENCE  2 (bases 1 to 1648)
AUTHORS    Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
            Knibb,W.R.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2001) Genetics, IOIR the National Center for
            Mariculture, P.O. Box 1212, Eilat 88112, Israel
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            Query Match      71.0%; Score 298.4; DB 1; Length 1648;
            Best Local Similarity 81.9%; Pred. No. 9.3e-23;
            Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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Best Local Similarity 81.4%; Pred. No. 2.7e-22;
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AE016822.18/c

WPCOMMENT

Sequence split into 26 fragments LOCUS AE016822 Accession AE016822

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Query Match 70.3%; Score 295.2; DB 1; Length 110000;
Best Local Similarity 81.4%; Pred. No. 5.3e-23;
Matches 342; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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DB 68189 GGTATCGAAGGCTGTCTGAGCGCTCTCACCGCGAGCTGTCTCGCAACGCGCAAGGAGGTC 68130
QY 181 GAGACCAAGGACGATCGTCTCACGGCTCTCACGGCTCTCACGGCGCGACACCCAGATCGCG 240
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QY 361 ATCTCGGCTTCTTCCGACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGCTAC 420
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RESULT 47

CQ816174

LOCUS

Sequence 3 from Patent WO2004041304.

DEFINITION

CQ816174

ACCESSION

VERSION

CQ816174.1

GI:48144533

KEYWORDS

SOURCE

Myobacterium tuberculosis

Myobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

tuberculosis complex.

1

Coates, A.R.

Pain relief agents

Patent: WO 2004041304-A 3 21-MAY-2004;

Helpierby Therapeutics Limited (GB)

Location/Qualifiers

1. 1623

/organism="Mycobacterium tuberculosis"

/db_type="unassigned DNA"

/mol_xref="taxon:1773"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 1623;

Best Local Similarity 81.2%; Pred. No. 3e-22;

Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTAGCACCACCGAGCGGCTTCCTCGCCCGAGCG 60

Db 232 AAGAGACCGATGACGTGCGCGGTGACGGACCAACGAGCCACCGTGTGCGCCAGGCG 291
Qy 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCCCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Db 292 TTGGTTCCGAGGCGCTGCGCAACGTCGCCCGCGGTGCCAACCCGCTCGGTCTCAACGCG 351
Qy 121 GGCATCGAGAGCGCGTCGAGGCGGTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
Db 352 GGCATCGAAGGCGGTGGAGAGGTCAACGAGACCCCTGCTCAAGGGCGCCAGAGGATC 411
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCCGCCGCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTCGGGCCACCGCAGCGATTTCGGGGGTGACCAAGTCCATCGGT 471
Qy 241 GAGCTATCGCGAGGCGATGACCAAGTGTGCGCAAGAGGCGGTCAATCACCCTCGAGGAG 300
Db 472 GACCTGATCGCGAGGCGATGACCAAGTGTGCGCAACGAGGGCGTCAATCACCCTCGAGGAG 531
Qy 301 TCCGAGACCTTCGCTCGGAGCTGAGCTCACCGAGGTATGCGTTCGACCAAGGCGTAC 360
Db 532 TCCAAACACCTTTGGGCTGCGAGCTGAGCTCACCGAGGTATGCGGTTCGACCAAGGCGTAC 591
Qy 361 ATCTCGGCGTACTTCGCCACCGCAGATGGAGCGGTGAGCGGTGCTCGACGACCGGTAC 420
Db 592 ATCTCGGGTACTTCGTGACCGACCGCGAGCGTCAAGGGCGGTCTCGAGGACCCCTAC 651

RESULT 48

AR266836
LOCUS AR266836 1623 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6495347.

AR266836
ACCESSION AR266836

AR266836.1 GI:29696202

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1623)

AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.

TITLE Induction of a Th1-like response in vitro

JOURNAL Patent: US 6495347-A 3 17-DEC-2002;

Stressgen Biotechnologies Corporation; Victoria;

CAX;

FEATURES Location/Qualifiers

source 1..1623

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 1623;

Best Local Similarity 81.2%; Pred. No. 3e-22;

Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAGACCGACGATGCGCGGTGACGGTACGACCAACCGCGGTCTTCGCCCGAGGCG 60

Db 232 AAGAGACCGATGACGTGCGCGGTGACGGTACGACCAACCGCGGTCTTCGCCCGAGGCG 291

Qy 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCCCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120

Db 292 TTGGTTCCGAGGCGCTGCGCAACGTCGCCCGCGGTGCCAACCCGCTCGGTCTCAACGCG 351

Qy 121 GGCATCGAGAGCGCGTTCGAGGCGGTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180

Db 352 GGCATCGAAGGCGGTGGAGAGGTCAACGAGACCCCTGCTCAAGGGCGCCAGAGGATC 411

Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCCGCCGCGACACCCAGATCGGC 240

Db 412 GAGACCAAGGAGCAGATTCGGGCCACCGCAGCGATTTCGGGGGTGACCAAGTCCATCGGT 471

Qy 241 GAGCTATCGCGAGGCGATGACCAAGTGTGCGCAAGAGGCGGTCAATCACCCTCGAGGAG 300

Db 472 GACCTGATCGCGAGGCGATGACCAAGTGTGCGCAACGAGGGCGTCAATCACCCTCGAGGAG 531

Qy 301 TCCGAGACCTTCGCTCGGAGCTGAGCTCACCGAGGTTATGCGTTCGACCAAGGCGTAC 360
Db 532 TCCAAACACCTTTGGGCTGCGAGCTCGAGCTCACCGAGGTTATGCGTTCGACCAAGGCGTAC 591
Qy 361 ATCTCGGCGTACTTCGCCACCGCAGATGGAGCGGTGAGCGGTGCTCGACGACCGGTAC 420
Db 592 ATCTCGGGTACTTCGTGACCGACCGCGAGCGTCAAGGGCGGTCTCGAGGACCCCTAC 651

RESULT 49

AR655543
LOCUS AR655543 1623 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 23 from patent US 6892139.

AR655543
ACCESSION AR655543

AR655543.1 GI:67587586

Unknown.

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1623)

AUTHORS Eisenberg, D., Rotstein, S.H. and Marcotte, E.M.

TITLE Determining the functions and interactions of proteins by

comparative analysis

JOURNAL Patent: US 6892139-A 23 10-MAY-2005;

The Regents of the University of California; Alameda, CA

FEATURES Location/Qualifiers

source 1..1623

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 1623;

Best Local Similarity 81.2%; Pred. No. 3e-22;

Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAGACCGACGATGCGCGGTGACGGTACGACCAACCGCGGTCTTCGCCCGAGGCG 60

Db 232 AAGAGACCGATGACGTGCGCGGTGACGGTACGACCAACCGCGGTCTTCGCCCGAGGCG 291

Qy 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCCCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120

Db 292 TTGGTTCCGAGGCGCTGCGCAACGTCGCCCGCGGTGCCAACCCGCTCGGTCTCAACGCG 351

Qy 121 GGCATCGAGAGCGCGTTCGAGGCGGTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180

Db 352 GGCATCGAAGGCGGTGGAGAGGTCAACGAGACCCCTGCTCAAGGGCGCCAGAGGATC 411

Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCCGCCGCGACACCCAGATCGGC 240

Db 412 GAGACCAAGGAGCAGATTCGGGCCACCGCAGCGATTTCGGGGGTGACCAAGTCCATCGGT 471

Qy 241 GAGCTATCGCGAGGCGATGACCAAGTGTGCGCAAGAGGCGGTCAATCACCCTCGAGGAG 300

Db 472 GACCTGATCGCGAGGCGATGACCAAGTGTGCGCAACGAGGGCGTCAATCACCCTCGAGGAG 531

Qy 301 TCCGAGACCTTCGCTCGGAGCTGAGCTCACCGAGGTTATGCGTTCGACCAAGGCGTAC 360

Db 532 TCCAAACACCTTTGGGCTGCGAGCTCGAGCTCACCGAGGTTATGCGTTCGACCAAGGCGTAC 591

Qy 361 ATCTCGGCGTACTTCGCCACCGCAGATGGAGCGGTGAGCGGTGCTCGACGACCCCGTAC 420

Db 592 ATCTCGGGTACTTCGTGACCGACCGCGAGCGTCAAGGGCGGTCTCGAGGACCCCTAC 651

RESULT 50

AX073911
LOCUS AX073911 1623 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104344.

AX073911

AX073911

AX073911.1 GI:12710171

synthetic construct

SOURCE

ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE Siegel, M., Chu, N.R. and Mizzen, L.A.
AUTHORS Induction of a th1-like response in vitro
TITLE Patent: WO 0104344-A 3 18-JAN-2001;
JOURNAL Stressgen Biotechnologies Corporation (CA)
FEATURES Location/Qualifiers
source 1. .1623
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion sequence"
1. .1623
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC28419.1"
/db_xref="GI:12710172"
/translation="MAKTIAYDEBARRGLERGINLADAVKVTLPKGRNVLEKKWG
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LIVSSKVSIVKDLLPLEKVIAGKPELIIAEDVEGEALSTLVNKGIRTFKSVAVKA
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ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 1623;
Best Local Similarity 81.2%; Pred. No. 3e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGNAGACGACGACGTCGCGGTGACGTCAGCACCGCGACCGTTCCTGCCCCAGGGC 60
DB 232 AAGNAGACGATGACGTCGCGGTGACGTCAGCACCGCGACCGTTCCTGCCCCAGGGC 291
QY 61 CTCGTACGCGAGGGCTCGCAACGTCGCGCGCGTGCACACCGATGCTCTCAAGGCG 120
DB 292 TTGGTTCGCGAGGGCTCGCAACGTCGCGCGCGTGCACACCGATGCTCTCAAGGCG 351
QY 121 GGCATCGAGAGCGCGTCGAGCCGCTCTCCGCGCGCTCTCGAGCAGCGCGAAGGATGTC 180
DB 352 GGCATCGAGAGCGCGTCGAGAGGTCACCGAGACCGTCTCAAGGGCGCAAGGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCGATCGGC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCCACCGCAGCGATTCGCGCGGTGACCGATCGGT 471
QY 241 GAGCTCATCGCGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531
DB 472 GACCTGATCGCGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 360
DB 532 TCCAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGGTCGCTCGACGACCGCGTAC 420
DB 592 ATCTCGGCGTACTTCGTCGACCGACCGCGAGCGTTCAGGAGGCGGTCCTCGAGGAGCCCTTAC 651
RESULT 51
AR266846
LOCUS AR266846 1920 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 16 from patent US 6495347.
ACCESSION AR266846
VERSION AR266846.1 GI:29696212
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE Siegel, M., Chu, N.R. and Mizzen, L.A.
AUTHORS Induction of a th1-like response in vitro
TITLE Patent: WO 0104344-A 3 18-JAN-2001;
JOURNAL Stressgen Biotechnologies Corporation (CA)
FEATURES Location/Qualifiers
source 1. .1623
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion sequence"
1. .1623
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/codon_start=1
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ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 1623;
Best Local Similarity 81.2%; Pred. No. 3e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGNAGACGACGACGTCGCGGTGACGTCAGCACCGCGACCGTTCCTGCCCCAGGGC 60
DB 232 AAGNAGACGATGACGTCGCGGTGACGTCAGCACCGCGACCGTTCCTGCCCCAGGGC 291
QY 61 CTCGTACGCGAGGGCTCGCAACGTCGCGCGCGTGCACACCGATGCTCTCAAGGCG 120
DB 292 TTGGTTCGCGAGGGCTCGCAACGTCGCGCGCGTGCACACCGATGCTCTCAAGGCG 351
QY 121 GGCATCGAGAGCGCGTCGAGCCGCTCTCCGCGCGCTCTCGAGCAGCGCGAAGGATGTC 180
DB 352 GGCATCGAGAGCGCGTCGAGAGGTCACCGAGACCGTCTCAAGGGCGCAAGGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCGATCGGC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCCACCGCAGCGATTCGCGCGGTGACCGATCGGT 471
QY 241 GAGCTCATCGCGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531
DB 472 GACCTGATCGCGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 360
DB 532 TCCAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGGTCGCTCGACGACCGCGTAC 420
DB 592 ATCTCGGCGTACTTCGTCGACCGACCGCGAGCGTTCAGGAGGCGGTCCTCGAGGAGCCCTTAC 651
RESULT 51
AR266846
LOCUS AR266846 1920 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 16 from patent US 6495347.
ACCESSION AR266846
VERSION AR266846.1 GI:29696212
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 1920)
Siegel, M., Chu, N.R. and Mizzen, L.A.
Induction of a th1-like response in vitro
Patent: US 6495347-A 16 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria;
CAX;
FEATURES Location/Qualifiers
source 1. .1920
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 1920;
Best Local Similarity 81.2%; Pred. No. 2.8e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGNAGACGACGACGTCGCGGTGACGTCAGCACCGCGACCGTTCCTGCCCCAGGGC 60
DB 232 AAGNAGACGATGACGTCGCGGTGACGTCAGCACCGCGACCGTTCCTGCCCCAGGGC 291
QY 61 CTCGTACGCGAGGGCTCGCAACGTCGCGCGCGTGCACACCGATGCTCTCAAGGCG 120
DB 292 TTGGTTCGCGAGGGCTCGCAACGTCGCGCGCGTGCACACCGATGCTCTCAAGGCG 351
QY 121 GGCATCGAGAGCGCGTCGAGCCGCTCTCCGCGCGCTCTCGAGCAGCGCGAAGGATGTC 180
DB 352 GGCATCGAGAGCGCGTCGAGAGGTCACCGAGACCGTCTCAAGGGCGCAAGGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCGATCGGC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCCACCGCAGCGATTCGCGCGGTGACCGATCGGT 471
QY 241 GAGCTCATCGCGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531
DB 472 GACCTGATCGCGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 360
DB 532 TCCAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGGTCGCTCGACGACCGCGTAC 420
DB 592 ATCTCGGCGTACTTCGTCGACCGACCGCGAGCGTTCAGGAGGCGGTCCTCGAGGAGCCCTTAC 651
RESULT 52
AX073924
LOCUS AX073924 1920 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 16 from Patent WO0104344.
ACCESSION AX073924
VERSION AX073924.1 GI:12710184
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
Siegel, M., Chu, N.R. and Mizzen, L.A.
Induction of a th1-like response in vitro
Patent: WO 0104344-A 16 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
FEATURES Location/Qualifiers
source 1. .1920
/organism="synthetic construct"
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1. .1920
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1424 GCGTTGATCGCGAGCCCTGGACAGGTGCGCAAGAGGCGTTCATCAGCGTCGAGGAG 1483
301 TCCAGACCTTCGCTCGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
1484 TCCAAACACCTTCGCTTCGGAATCGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 1543
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RESULT 57
AR266848
LOCUS AR266848 2847 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 20 from patent US 6495347.
ACCESSION AR266848
VERSION AR266848.1 GI:29696214
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2847)
AUTHORS Siegel, M., Chu, N.R., and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: US 6495347-A 20 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria;
CA;

FEATURES
source
1. .2847
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 2847;
Best Local Similarity 81.2%; Pred. No. 2.5e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
1 AAGAGACGACGACGCTCGCGGTGACGTTACGACACCGGACCGGTCCTCGCCCGAGGCG 60
292 AAGAAGACCGATGACGTCGCGGTGACGACGACCGGACCGGTCCTCGCCCGAGGCG 351
61 CTGCTACGCGAGGCGCTCGCGCAAGCTCGCGCGGTCGCAACCGGATGCGCTCTCAAGCGC 120
352 TTGGTTCCGAGGCGCTCGCGCAAGCTCGCGCGGTCGCAACCGGATGCGCTCTCAAGCGC 411
121 GGATCGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCGCGGTCGCAAGGAGATGTC 180
412 GGCATCGAAAGGCGCTCGAGAGGTCACCGAGACCGCTCTCAAGGCGCGCAAGGAGGTC 471
181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCCGCGCGACACCCAGATCGGC 240
472 GAGACCAAGGAGCAGATTCGCGGCCACCGGACGCAATTCGCGCGGTGACCAATCGGTC 531
241 GAGCTATCCCGGAGGCGATGAGCAAGGTCGCAAGGAGGCGTTCATCAGCGTCGAGGAG 300
532 GACCTGATCCCGAGGCGATGAGCAAGGTCGCAAGGAGGCGTTCATCAGCGTCGAGGAG 591
301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
592 TCCAAACACCTTCGCTTCGGAATCGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 651
361 ATCTCGGCTACTTCGCGCCAGCATGAGGAGGATGAGGCGCTCGCTCGAGGAGCCGCTAC 420
652 ATCTCGGCTACTTCGCTCACCGAGCGCGAGGCGGAGAGCGCTCTCGAGGAGCCCTAC 711

RESULT 58

AX073928
LOCUS AX073928 2847 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 20 from Patent WO0104344.
ACCESSION AX073928
VERSION AX073928.1 GI:12710188
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Siegel, M., Chu, N.R., and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: WO 0104344-A 20 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
LOCATION/Qualifiers
FEATURES
source
1. .2847
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="fusion sequence"
1. .2847
/note="unnamed protein product"
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/db_xref="GI:12710189"
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ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 2847;
Best Local Similarity 81.2%; Pred. No. 2.5e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
1 AAGAGACGACGACGCTCGCGGTGACGTTACGACACCGGACCGGTCCTCGCCCGAGGCG 60
292 AAGAAGACCGATGACGTCGCGGTGACGACGACCGGACCGGTCCTCGCCCGAGGCG 351
61 CTGCTACGCGAGGCGCTCGCGCAAGCTCGCGCGGTCGCAACCGGATGCGCTCTCAAGCGC 120
352 TTGGTTCCGAGGCGCTCGCGCAAGCTCGCGCGGTCGCAACCGGATGCGCTCTCAAGCGC 411
121 GGATCGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCGCGGTCGCAAGGAGATGTC 180
412 GGCATCGAAAGGCGCTCGAGAGGTCACCGAGACCGCTCTCAAGGCGCGCAAGGAGGTC 471
181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCCGCGCGACACCCAGATCGGC 240
472 GAGACCAAGGAGCAGATTCGCGGCCACCGGACGCAATTCGCGCGGTGACCAATCGGTC 531
241 GAGCTATCCCGGAGGCGATGAGCAAGGTCGCAAGGAGGCGTTCATCAGCGTCGAGGAG 300
532 GACCTGATCCCGAGGCGATGAGCAAGGTCGCAAGGAGGCGTTCATCAGCGTCGAGGAG 591
301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
592 TCCAAACACCTTCGCTTCGGAATCGAGCTCACCGAGGATGCGCTTCGAGGAGCCCTAC 651

QY 61 CTGTACGCGAGGCGCTGCGCAACGTCGCGCGGTCGCCAACCGGATGGCTCTCAAGCGC 120
DB 543 TTGGTTCCGAGAGGCGCTGCGCAACGTCGCGCGGTCGCCAACCGGATGGCTCTCAAGCGC 602
QY 121 GGCAATCGAGAAGGCGCTGCGAGGCGCTCTCCGGCGCCCTCTGGAGCAGGCGCAAGGATGTC 180
DB 603 GGCAATCGAAAAGGCGCTGCGAGAGGTCACCGAGACCTCTGCTCAAGGCGCGCAAGGAGGTC 662
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCCGCGCGGACACCCAGATCGGC 240
DB 663 GAGACCAAGGAGCAGATTCGGCGCACCGCGCAGCGATTTCCGGCGGTCACCAAGTCATCGGT 722
QY 241 GAGCTCATCCCGGAGGCGATGGAAGGTCGCGCAAGGTCGCGCAAGGTCATCACCGTCGAGGAG 300
DB 723 GACCTGATCGCGGAGGCGATGGAAGGTCGCGCAAGGTCGCGCAAGGTCATCACCGTCGAGGAG 782
QY 301 TCCACAGACCTTCGGTCTGAGGCTGAGGCTCACCGAGGCTATGGCTTCGACAAAGGGCTAC 360
DB 783 TCCACACCTTTGGCTGAGGCTGAGGCTCACCGAGGCTATGGCTTCGACAAAGGGCTAC 842
QY 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCCGCTAC 420
DB 843 ATCTCGGCGTACTTCGCTGACCGACCGCGAGCGTCAGGAGGCGGTCCTGGAGGACCCCTAC 902

RESULT 60

I08847
LOCUS I08847 4380 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8805823.
ACCESSION I08847
VERSION I08847.1 GI:588446
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4380)
AUTHORS Huxson, R.N., Young, Richard A. and Shinnick, T.M.
TITLE MYCOBACTERIUM TUBERCULOSIS GENES ENCODING PROTEIN ANTIGENS
JOURNAL Patent: WO 8805823-A 5 11-AUG-1988;
FEATURES
source
1. .4380
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 4380;
Best Local Similarity 81.2%; Pred. No. 2.2e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGAGAGCGGACGAGCTGCGCGGTGACGGTACGACACCGGACCGTTCTCGCCAGGCG 60
DB 483 AAGAAGACCGATGACGTGCGCGGTGACGGCACCAACGCGCACCGTGTGGCCAGGCG 542
QY 61 CTGTACGCGAGGCGCTGCGCAACGTCGCGCGGTCGCCAACCGATGGCTCTCAAGCGC 120
DB 543 TTGGTTCCGAGAGGCGCTGCGCAACGTCGCGCGGTCGCCAACCGCTCGGTCTCAAGCGC 602
QY 121 GGCAATCGAGAAGGCGCTGCGAGGCGCTCTCCGGCGCCCTCTGGAGCAGGCGCAAGGATGTC 180
DB 603 GGCAATCGAAAAGGCGCTGCGAGAGGTCACCGAGACCTCTGCTCAAGGCGCGCAAGGAGGTC 662
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGGCGCGGACACCCAGATCGGC 240
DB 663 GAGACCAAGGAGCAGATTCGGCGCACCGCGCAGCGATTTCCGGCGGTCGACCATCGGT 722
QY 241 GAGCTCATCCCGGAGGCGATGGAAGGTCGCGCAAGGTCGCGCAAGGTCATCACCGTCGAGGAG 300
DB 723 GACCTGATCGCGGAGGCGATGGAAGGTCGCGCAAGGTCATCACCGTCGAGGAG 782
QY 301 TCCACAGACCTTCGGTCTGAGGCTGAGGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 360
DB 783 TCCACACCTTTGGGCTGACGCTGAGCTCACCGAGGCTATGCGGTTCCGACAAAGGGCTAC 842

QY 361 ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGCGGTCGCTCGACGACCCGCTAC 420
DB 843 ATCTCGGCGTACTTTCGTGACCGGACCGGAGCGTCAGAGGCGGTCCTGGAGGACCCCTAC 902

Search completed: April 1, 2006, 23:37:24
Job time : 2961.29 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 21:55:10 ; Search time 853.578 Seconds
(without alignments)
3279.340 Million cell updates/sec

Title: US-10-824-527-43
Perfect score: 420
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

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- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420	100.0	420	14	ADV99163
2	420	100.0	420	14	ADV99165
3	412	98.1	420	14	ADV99178
4	396	94.3	420	14	ADV99167
5	396	94.3	420	14	ADV99168
6	394.4	93.9	420	14	ADV99123
7	394.4	93.9	420	14	ADV99131
8	394.4	93.9	420	14	ADV99140
9	394.4	93.9	420	14	ADV99129
10	392.8	93.5	420	14	ADV99143
11	392.8	93.5	420	14	ADV99135
12	392.8	93.5	420	14	ADV99175
13	391.2	93.1	420	14	ADV99136
14	391.2	93.1	420	14	ADV99126
15	391.2	93.1	420	14	ADV99142
16	388	92.4	420	14	ADV99156
17	388	92.4	420	14	ADV99181
18	388	92.4	420	14	ADV99144
19	386.4	92.0	420	14	ADV99158

20	386.4	92.0	420	14	ADV99166	ADV99166	groEL2	ge
21	386.4	92.0	420	14	ADV99154	ADV99154	groEL2	ge
22	386.4	92.0	420	14	ADV99169	ADV99169	groEL2	ge
23	386.4	92.0	420	14	ADV99152	ADV99152	groEL2	ge
24	386.4	92.0	420	14	ADV99177	ADV99177	groEL2	ge
25	386.4	92.0	420	14	ADV99137	ADV99137	groEL2	ge
26	386.4	92.0	420	14	ADV99160	ADV99160	groEL2	ge
27	386.4	92.0	422	14	ADV99138	ADV99138	groEL2	ge
28	384.8	91.6	420	14	ADV99151	ADV99151	groEL2	ge
29	384.8	91.6	420	14	ADV99155	ADV99155	groEL2	ge
30	384.8	91.6	420	14	ADV99128	ADV99128	groEL2	ge
31	383.2	91.2	420	14	ADV99139	ADV99139	groEL2	ge
32	383.2	91.2	420	14	ADV99157	ADV99157	groEL2	ge
33	383.2	91.2	420	14	ADV99133	ADV99133	groEL2	ge
34	383.2	91.2	420	14	ADV99146	ADV99146	groEL2	ge
35	381.6	90.9	420	14	ADV99148	ADV99148	groEL2	ge
36	381.6	90.9	420	14	ADV99180	ADV99180	groEL2	ge
37	381.6	90.9	420	14	ADV99145	ADV99145	groEL2	ge
38	381.6	90.9	420	14	ADV99149	ADV99149	groEL2	ge
39	381.6	90.9	420	14	ADV99141	ADV99141	groEL2	ge
40	380	90.5	420	14	ADV99134	ADV99134	groEL2	ge
41	378.4	90.1	420	14	ADV99171	ADV99171	groEL2	ge
42	378.4	90.1	420	14	ADV99172	ADV99172	groEL2	ge
43	378.4	90.1	420	14	ADV99173	ADV99173	groEL2	ge
44	378.4	90.1	420	14	ADV99174	ADV99174	groEL2	ge
45	373.6	89.0	420	14	ADV99170	ADV99170	groEL2	ge
46	372	88.6	420	14	ADV99176	ADV99176	groEL2	ge
47	372	88.6	420	14	ADV99179	ADV99179	groEL2	ge
48	372	88.6	420	14	ADV99147	ADV99147	groEL2	ge
49	372	88.6	420	14	ADV99164	ADV99164	groEL2	ge
50	370.4	88.2	420	14	ADV99125	ADV99125	groEL2	ge
51	370.2	88.1	423	14	ADV99127	ADV99127	groEL2	ge
52	368.6	87.8	423	14	ADV99150	ADV99150	groEL2	ge
53	365.6	87.0	420	14	ADV99124	ADV99124	groEL2	ge
54	362.4	86.3	420	14	ADV99153	ADV99153	groEL2	ge
55	362.2	86.2	423	14	ADV99159	ADV99159	groEL2	ge
56	360.8	85.9	420	14	ADV99130	ADV99130	groEL2	ge
57	359.2	85.5	420	14	ADV99132	ADV99132	groEL2	ge
58	322.4	76.8	604	9	ACF04295	ACF04295	M phlei	h
59	320.8	76.4	420	14	ADV99161	ADV99161	Nucleotid	
60	320.8	76.4	1626	9	ACC70275	ACC70275	Nucleotid	

ALIGNMENTS

RESULT 1
ADV99163
ID ADV99163 standard; DNA; 420 BP.
XX AC ADV99163;
XX AC ADV99163;
DT 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 43.

Microorganism identification; microorganism detection; groEL2;
potato scab; gene; ds.
Streptomyces scabiei.
US2004265873-A1.
30-DEC-2004.
15-APR-2004; 2004US-00824527.
18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

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XX DR WPI; 2005-089568/10.
XX PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PR species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 43; 34pp; English.
XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 82 A; 141 C; 139 G; 58 T; 0 U; 0 Other;
Query Match 100.0%; Score 420; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 7.8e-61;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGTACGAGTACGACACCGGACCGGATCTTCGCCCGAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGTACGAGTACGACACCGGACCGGATCTTCGCCCGAGGCG 60
QY 61 CTGTCAGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGTCAGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGCAAGGATGTC 180
DB 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCGATCGCTTTCACGGCTCCATCTCCGCGCCGACACCGGATCGGC 240
DB 181 GAGACCAAGGAGCGATCGCTTTCACGGCTCCATCTCCGCGCCGACACCGGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGATGGAACAAGTCCGCAAGGCGCTCATCCCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGGAACAAGTCCGCAAGGCGCTCATCCCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGATGAGGCGGATGAGGCGGCTCGCTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGATGAGGCGGATGAGGCGGCTCGCTCGACGACCGGTAC 420
RESULT 2
ADV99165
ID ADV99165 standard; DNA; 420 BP.
XX AC ADV99165;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 45.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces scabiei.
XX PN US2004265873-A1.
XX XX
XX PD 30-DEC-2004.
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XX PR 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PT species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 45; 34pp; English.
XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 82 A; 141 C; 139 G; 58 T; 0 U; 0 Other;
Query Match 100.0%; Score 420; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 7.8e-61;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGTACGAGTACGACACCGGACCGGATCTTCGCCCGAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGTACGAGTACGACACCGGACCGGATCTTCGCCCGAGGCG 60
QY 61 CTGTCAGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGTCAGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGCAAGGATGTC 180
DB 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCGATCGCTTTCACGGCTCCATCTCCGCGCCGACACCGGATCGGC 240
DB 181 GAGACCAAGGAGCGATCGCTTTCACGGCTCCATCTCCGCGCCGACACCGGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGATGGAACAAGTCCGCAAGGCGCTCATCCCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGGAACAAGTCCGCAAGGCGCTCATCCCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGATGAGGCGGATGAGGCGGCTCGCTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGATGAGGCGGATGAGGCGGCTCGCTCGACGACCGGTAC 420
RESULT 3
ADV99178
ID ADV99178 standard; DNA; 420 BP.
XX AC ADV99178;
XX DT 24-MAR-2005 (first entry)
XX XX
XX DE groEL2 gene fragment, SEQ ID 58.
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XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX Streptomyces scabiei.
OS US2004265873-A1.
PN 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 4; SEQ ID NO 58; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 82 A; 142 C; 137 G; 59 T; 0 U; 0 Other;
SQ
Query Match 98.1%; Score 412; DB 14; Length 420;
Best Local Similarity 98.8%; Pred. No. 1.7e-59;
Matches 415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGGTGCGCAACCGATGGCTCTCAAGCGC 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGGTGCGCAACCGATGGCTCTCAAGCGC 60
QY 61 CTCGTACGCGAGGGCTGCGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
DB 61 CTCGTACGCGAGGGCTGCGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTGAGGCGCTCTCGGCGCCCTGCTGGAGCGGCGAAGGATGTC 180
DB 121 GGCATCGAGAGGCGCTGAGGCGCTCTCGGCGCCCTGCTGGAGCGGCGAAGGATGTC 180
QY 181 GAGACCAAGGACGATCGCTTCCAGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGACGATCGCTTCCAGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTTCATCAACCGTCGAGGAG 300
DB 241 GAGCTCATCGGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTTCATCAACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCTTAC 360
DB 301 TCCGAGACCTTCGCTCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCTTAC 360
QY 361 ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTTCGACGACCGGTAC 420
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RESULT 4
ADV99167
ID ADV99167 standard; DNA; 420 BP.
XX AC ADV99167;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 47.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces scabiei.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 4; SEQ ID NO 47; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 82 A; 139 C; 141 G; 58 T; 0 U; 0 Other;
SQ
Query Match 94.3%; Score 396; DB 14; Length 420;
Best Local Similarity 96.4%; Pred. No. 7.3e-57;
Matches 405; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGGTGCGCAACCGATGGCTCTCAAGCGC 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGGTGCGCAACCGATGGCTCTCAAGCGC 60
QY 61 CTCGTACGCGAGGGCTGCGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
DB 61 CTCGTACGCGAGGGCTGCGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTGAGGCGCTCTCGGCGCCCTGCTGGAGCGGCGAAGGATGTC 180
DB 121 GGCATCGAGAGGCGCTGAGGCGCTCTCGGCGCCCTGCTGGAGCGGCGAAGGATGTC 180
QY 181 GAGACCAAGGACGATCGCTTCCAGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGACGATCGCTTCCAGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTTCATCAACCGTCGAGGAG 300
DB 241 GAGCTCATCGGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTTCATCAACCGTCGAGGAG 300
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QY 301 TCCAGACCTTCGGTCTGAGCTGGAGCTCACGAGGATGCGCTTCGACAAAGGCTAC 360
 DB 301 TCCAGACCTTCGGTCTGAGCTGGAGCTCACGAGGATGCGCTTCGACAAAGGCTAC 360
 QY 361 ATCTCGCGTACTTCGCGCACCGACATGAGCGTATGAGGCGCTCTCGACGACCGGTAC 420
 DB 361 ATCTCGCGTACTTCGCGCACCGACATGAGCGTATGAGGCGCTCTCGACGACCGGTAC 420

RESULT 5
 ADV99168
 ID ADV99168 standard; DNA; 420 BP.
 XX
 AC ADV99168;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE groEL2 gene fragment, SEQ ID 48.
 XX
 KW Microorganism identification; microorganism detection; groEL2;
 KW potato scab; gene; ds.
 XX
 OS Streptomyces scabiei.
 XX
 PN US2004265873-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 15-APR-2004; 2004US-00824527.
 XX
 PR 18-APR-2003; 2003KR-00024656.
 PR 14-NOV-2003; 2003KR-00080580.
 XX
 PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX
 PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
 XX
 PF WPI; 2005-089568/10.
 XX
 PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.
 XX
 PS Claim 4; SEQ ID NO 48; 34pp; English.
 XX
 CC The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.
 XX
 SQ Sequence 420 BP; 82 A; 139 C; 141 G; 58 T; 0 U; 0 Other;
 Query Match 94.3%; Score 396; DB 14; Length 420;
 Best Local Similarity 96.4%; Pred. No. 7.3e-57;
 Matches 405; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCGTTCGCGTACGAGTACGACCGGACCGGCTTCGCGCCAGGCG 60
 DB 1 AAGAAGACGAGCGTTCGCGTACGAGTACGACCGGACCGGCTTCGCGCCAGGCG 60
 QY 61 CTGCTACGAGGCGCTTCGCGTACGAGTACGACCGGACCGGCTTCGCGCCAGGCG 120
 DB 61 CTGCTACGAGGCGCTTCGCGTACGAGTACGACCGGACCGGCTTCGCGCCAGGCG 120
 QY 121 GGCAATCAGAGAGCGCGTTCGAGCGCGCTTCGCGCGCCCTTCGCGAGCGGCGAAGGATGTC 180
 DB 121 GGCAATCAGAGAGCGCGTTCGAGCGCGCTTCGCGCGCCCTTCGCGAGCGGCGAAGGATGTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
 QY 241 GAGCTCATCGCGAGGCGATGGACCAAGTTCGCAAGGAAGGCGTATCATCCGTCGAGGAG 300
 DB 241 GAGCTCATCGCGAGGCGATGGACCAAGTTCGCAAGGAAGGCGTATCATCCGTCGAGGAG 300
 QY 301 TCCAGACCTTCGGTCTGAGCTGGAGCTCACGAGGATGCGCTTCGACAAAGGCTAC 360
 DB 301 TCCAGACCTTCGGTCTGAGCTGGAGCTCACGAGGATGCGCTTCGACAAAGGCTAC 360
 QY 361 ATCTCGCGTACTTCGCGCACCGACATGAGCGTATGAGGCGCTCTCGACGACCGGTAC 420
 DB 361 ATCTCGCGTACTTCGCGCACCGACATGAGCGTATGAGGCGCTCTCGACGACCGGTAC 420

RESULT 6
 ADV99123
 ID ADV99123 standard; DNA; 420 BP.
 XX
 AC ADV99123;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE groEL2 gene fragment, SEQ ID 3.
 XX
 KW Microorganism identification; microorganism detection; groEL2;
 KW potato scab; gene; ds.
 XX
 OS Streptomyces acrimycini.
 XX
 PN US2004265873-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 15-APR-2004; 2004US-00824527.
 XX
 PR 18-APR-2003; 2003KR-00024656.
 PR 14-NOV-2003; 2003KR-00080580.
 XX
 PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX
 PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
 XX
 PF WPI; 2005-089568/10.
 XX
 PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.
 XX
 PS Claim 3; SEQ ID NO 3; 34pp; English.
 XX
 CC The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.
 XX
 SQ Sequence 420 BP; 82 A; 145 C; 137 G; 56 T; 0 U; 0 Other;
 Query Match 93.9%; Score 394.4; DB 14; Length 420;
 Best Local Similarity 96.2%; Pred. No. 1.3e-56;
 Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCGTTCGCGTACGAGTACGACCGGACCGGCTTCGCGCCAGGCG 60
 DB 1 AAGAAGACGAGCGTTCGCGTACGAGTACGACCGGACCGGCTTCGCGCCAGGCG 60

Db 1 AAGGAGGACGACGACGCTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGCC 60
Qy 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGGAGCGCTCGAGGCGCTGCGGCGCGCTGCGGCGCGCTGCGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCGAGGAGCGCTCGAGGCGCTGCGGCGCGCTGCGGCGCGCTGCGGAGCAGGCGAAGGACGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTGCATCAACCGTTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTGCATCAACCGTTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
Db 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCCGTTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCCGTTAC 420

RESULT 7

ADV99131
ID ADV99131 standard; DNA; 420 BP.
XX AC ADV99131;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 11.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; db.
XX OS Streptomyces ambofaciens.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 11; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX SQ Sequence 420 BP; 84 A; 144 C; 137 G; 55 T; 0 U; 0 Other;
Query Match 93.9%; Score 394.4; DB 14; Length 420;
Best Local Similarity 96.2%; Pred. No. 1.3e-56;
Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCAGCGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGCC 60
Db 1 AAGAAGACGAGCAGCGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGCC 60
Qy 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGGAGCGCTCGAGGCGCTGCGGCGCGCTGCGGCGCGCTGCGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCGAGGAGCGCTCGAGGCGCTGCGGCGCGCTGCGGCGCGCTGCGGAGCAGGCGAAGGACGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTGCATCAACCGTTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTGCATCAACCGTTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
Db 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCCGTTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCCGTTAC 420

RESULT 8

ADV99140
ID ADV99140 standard; DNA; 420 BP.
XX AC ADV99140;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 20.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; db.
XX OS Streptomyces chartreusis.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 20; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and

CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.
 XX

SQ Sequence 420 BP; 82 A; 144 C; 136 G; 58 T; 0 U; 0 Other;
 Query Match 93.9%; Score 394.4; DB 14; Length 420;
 Best Local Similarity 96.2%; Pred. No. 1.3e-56;
 Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGTACGACACCGACCGGTCGCGCCAGGCG 60
 DB 1 AAGAAGACGACGACGTCGCGGTGACGTACGACACCGACCGGTCGCGCCAGGCG 60
 QY 61 CTGCTACGCGAGGCGCTGCGGACGTCGCGCGGTCGCGACCGGATGCTCTCAAGCGC 120
 DB 61 CTGCTCAAGGAGGCGCTGCGGACGTCGCGCGGTCGCGACCGGATGCTCTCAAGCGC 120
 QY 121 GGCATCGAAGAGCGCGTCGAGGCGCTCTCGCGCGGCTGCTGGAGCAGGCGAAGGATGTC 180
 DB 121 GGTATCGAGCGTCGCGTCGAGGCGCTCTCGCGCGGCTGCTGGAGCAGGCGAAGGATGTC 180
 QY 181 GAGACCAAGGACGACGTCGCTTCCACCGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGACGACGTCGCTTCCACCGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
 QY 241 GAGCTCATCGCGAGGCGATGGACAAAGTTCGGCAGGAGGCGTTCATCAGCGTCGAGGAG 300
 DB 241 GAGCTCATCGCGAGGCGATGGACAAAGTTCGGCAGGAGGCGTTCATCAGCGTCGAGGAG 300
 QY 301 TCCGACACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAAAGGCGTAC 360
 DB 301 TCCGACACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAAAGGCGTAC 360
 QY 361 ATCTCGCGCTACTTCGCGCACCGACATGCGGCGGATGAGGCGTCTCGACGACCCCGTAC 420
 DB 361 ATCTCGCGCTACTTCGCGCACCGACATGCGGCGGATGAGGCGTCTCGACGACCCCGTAC 420

RESULT 9

ADV99129
 ID ADV99129 standard; DNA; 420 BP.

AC ADV99129;

XX 24-MAR-2005 (first entry)

XX groEL2 gene fragment, SEQ ID 9.

XX Microorganism identification; microorganism detection; groEL2;
 XX potato scab; gene; ds.

XX Streptomyces alboniger.

XX US2004265873-A1.

XX 30-DEC-2004.

XX 15-APR-2004; 2004US-00824527.

XX 18-APR-2003; 2003KR-00024656.

XX 14-NOV-2003; 2003KR-00080580.

XX (KOREA-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX

WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 9; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 420 BP; 81 A; 141 C; 140 G; 58 T; 0 U; 0 Other;

Query Match 93.9%; Score 394.4; DB 14; Length 420;
 Best Local Similarity 96.2%; Pred. No. 1.3e-56;
 Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGTACGACACCGACCGGTCGCGCCAGGCG 60
 DB 1 AAGAAGACGACGACGTCGCGGTGACGTACGACACCGACCGGTCGCGCCAGGCG 60
 QY 61 CTGCTACGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCCGATGCTCTCAAGCGC 120
 DB 61 CTGCTCGCGAGGCGCTCTGCGCAACGTCGCGCGGTCGCAACCCGATGCTCTCAAGCGC 120
 QY 121 GGCATCGAAGAGCGCGTCGAGGCGCTCTCGCGCGGCTGCTGGAGCAGGCGAAGGATGTC 180
 DB 121 GGTATCGAGCGTCGCGTCGAGGCGCTCTCGCGCGGCTGCTGGAGCAGGCGAAGGATGTC 180
 QY 181 GAGACCAAGGACGACGTCGCTTCCACCGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGACGACGTCGCTTCCACCGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
 QY 241 GAGCTCATCGCGAGGCGATGGACAAAGTTCGGCAGGAGGCGTTCATCAGCGTCGAGGAG 300
 DB 241 GAGCTCATCGCGAGGCGATGGACAAAGTTCGGCAGGAGGCGTTCATCAGCGTCGAGGAG 300
 QY 301 TCCGACACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAAAGGCGTAC 360
 DB 301 TCCGACACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAAAGGCGTAC 360
 QY 361 ATCTCGCGCTACTTCGCGCACCGACATGCGGCGGATGAGGCGTCTCGACGACCCCGTAC 420
 DB 361 ATCTCGCGCTACTTCGCGCACCGACATGCGGCGGATGAGGCGTCTCGACGACCCCGTAC 420

RESULT 10

ADV99143
 ID ADV99143 standard; DNA; 420 BP.

XX ADV99143;

XX 24-MAR-2005 (first entry)

XX groEL2 gene fragment, SEQ ID 23.

XX Microorganism identification; microorganism detection; groEL2;
 XX potato scab; gene; ds.

XX Streptomyces cinereoruber.

XX US2004265873-A1.

XX 30-DEC-2004.

XX


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ADV99175
ID  ADV99175 standard; DNA; 420 BP.
XX  |||
AC  ATCCGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGGCTTCGACAGGGCTAC 360
XX  |||
XX  361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTTAC 420
XX  |||
DT  24-MAR-2005 (first entry)
XX  |||
DE  groEL2 gene fragment, SEQ ID 55.
XX  |||
KW  Microorganism identification; microorganism detection; groEL2;
KW  potato scab; gene; ds.
XX  |||
OS  Streptomyces bottropensis.
XX  |||
XX  US2004265873-A1.
XX  |||
XX  30-DEC-2004.
XX  |||
XX  15-APR-2004; 2004US-00824527.
XX  |||
XX  18-APR-2003; 2003KR-00024656.
XX  |||
XX  14-NOV-2003; 2003KR-00080580.
XX  |||
XX  (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX  |||
XX  Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX  WPI; 2005-089568/10.
XX  |||
XX  New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX  species, useful in identifying the genus Streptomyces, and for isolating
XX  or purifying natural products using such microorganisms.
XX  |||
XX  Claim 4; SEQ ID NO 55; 34pp; English.
XX  |||
XX  The present invention relates to novel primers STGROF1 (ADV99121) and
XX  STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX  Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX  derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX  Potato scab is a pathogenic disease caused by certain Streptomyces
XX  species. Primers ADV99121 and ADV99122 are useful in a method for
XX  identifying Streptomyces species, comprising amplifying groEL2 gene
XX  fragment of target strain, analyzing the nucleotide sequence of groEL2
XX  gene fragment amplified, and comparing the nucleotide sequence obtained
XX  with that of groEL2 gene fragment of a reference strain.
XX  |||
XX  Sequence 420 BP; 82 A; 141 C; 141 G; 56 T; 0 U; 0 Other;
XX  |||
XX  Query Match 93.5%; Score 392.8; DB 14; Length 420;
XX  Best Local Similarity 96.0%; Pred. No. 2.5e-56;
XX  Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX  |||
QY  1 AAGAAGACGACGACGTCGCGGTGACGAGTACGACACCGACCGACCGTTCGCGCCAGGCG 60
DB  1 AAGAAGACGACGACGTCGCGGTGACGAGTACGACACCGACCGACCGTTCGCGCCAGGCG 60
XX  |||
QY  61 CTGATCGAGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTC 120
DB  121 GGCATCGAGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTC 180
XX  |||
QY  181 GAGACCAAGGAGCAGATCGGTTCCACGGCTTCCATCTCCGCGCGGACACCCGATCGGC 240
DB  181 GAGACCAAGGAGCAGATCGGTTCCACGGCTTCCATCTCCGCGCGGACACCCGATCGGC 240
XX  |||
QY  241 GAGTCATCGCGAGGCGGTCGAGCAAGGTCGCGGCAAGGAGGCGTCATCATCGTCGAGGAG 300
DB  241 GAGTCATCGCGAGGCGGTCGAGCAAGGTCGCGGCAAGGAGGCGTCATCATCGTCGAGGAG 300
XX  |||
QY  301 TCCAGACCTTCGGTCTGGAGCTGGAGCTCACCAGGGGTATCGCTTCGACAGGGGCTAC 360
XX  |||

ADV99136
ID  ADV99136 standard; DNA; 420 BP.
XX  |||
AC  ADV99136;
XX  |||
XX  24-MAR-2005 (first entry)
XX  |||
DE  groEL2 gene fragment, SEQ ID 16.
XX  |||
XX  Microorganism identification; microorganism detection; groEL2;
XX  potato scab; gene; ds.
XX  |||
OS  Streptomyces capillarispiralis.
XX  |||
XX  US2004265873-A1.
XX  |||
XX  30-DEC-2004.
XX  |||
XX  15-APR-2004; 2004US-00824527.
XX  |||
XX  18-APR-2003; 2003KR-00024656.
XX  |||
XX  14-NOV-2003; 2003KR-00080580.
XX  |||
XX  (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX  |||
XX  Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX  WPI; 2005-089568/10.
XX  |||
XX  New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX  species, useful in identifying the genus Streptomyces, and for isolating
XX  or purifying natural products using such microorganisms.
XX  |||
XX  Claim 3; SEQ ID NO 16; 34pp; English.
XX  |||
XX  The present invention relates to novel primers STGROF1 (ADV99121) and
XX  STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX  Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX  derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX  Potato scab is a pathogenic disease caused by certain Streptomyces
XX  species. Primers ADV99121 and ADV99122 are useful in a method for
XX  identifying Streptomyces species, comprising amplifying groEL2 gene
XX  fragment of target strain, analyzing the nucleotide sequence of groEL2
XX  gene fragment amplified, and comparing the nucleotide sequence obtained
XX  with that of groEL2 gene fragment of a reference strain.
XX  |||
XX  Sequence 420 BP; 83 A; 142 C; 137 G; 58 T; 0 U; 0 Other;
XX  |||
XX  Query Match 93.1%; Score 391.2; DB 14; Length 420;
XX  Best Local Similarity 95.7%; Pred. No. 4.6e-56;
XX  Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX  |||
QY  1 AAGAAGACGACGACGTCGCGGTGACGAGTACGACACCGACCGACCGTTCGCGCCAGGCG 60
DB  1 AAGAAGACGACGACGTCGCGGTGACGAGTACGACACCGACCGACCGTTCGCGCCAGGCG 60
XX  |||
QY  61 CTGATCGAGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTC 120
DB  61 CTGATCGAGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTC 120
XX  |||
QY  121 GGCATCGAGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTC 180
DB  121 GGCATCGAGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGGTC 180
XX  |||
QY  181 GAGACCAAGGAGCAGATCGGTTCCACGGCTTCCATCTCCGCGCGGACACCCGATCGGC 240
DB  181 GAGACCAAGGAGCAGATCGGTTCCACGGCTTCCATCTCCGCGCGGACACCCGATCGGC 240
XX  |||
QY  241 GAGTCATCGCGAGGCGGTCGAGCAAGGTCGCGGCAAGGAGGCGTCATCATCGTCGAGGAG 300
DB  241 GAGTCATCGCGAGGCGGTCGAGCAAGGTCGCGGCAAGGAGGCGTCATCATCGTCGAGGAG 300
XX  |||
QY  301 TCCAGACCTTCGGTCTGGAGCTGGAGCTCACCAGGGGTATCGCTTCGACAGGGGCTAC 360
XX  |||
```

QY 181 GAGACCAAGGAGCAGATCGTTCCACGGGCTCATCTCCGCGCGGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGTTCCACGGGCTCATCTCCGCGCGGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCCGAGGCGATGACAAAGGTCGGCAAGGAGGGGTCTATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCCGAGGCGATGACAAAGGTCGGCAAGGAGGGGTCTATCACCCTCGAGGAG 300
QY 301 TCCACAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
DB 301 TCCACAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGTTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGTTCGACGACCGGTAC 420

RESULT 14

ADV99126
ID ADV99126 standard; DNA; 420 BP.

XX

AC ADV99126;

DT 24-MAR-2005 (first entry)

DE groEL2 gene fragment, SEQ ID 6.

XX

KW Microorganism identification; microorganism detection; groEL2;

KW potato scab; gene; ds.

XX

OS Streptomyces albireticuli.

XX

PN US2004265873-A1.

XX

PD 30-DEC-2004.

XX

PF 15-APR-2004; 2004US-00824527.

XX

PR 18-APR-2003; 2003KR-00024656.

XX

PR 14-NOV-2003; 2003KR-00080580.

XX

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX

PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX

DR WPI; 2005-089568/10.

XX

PT New primer specifically amplifying groEL2 gene fragment of Streptomyces

PT species, useful in identifying the genus Streptomyces, and for isolating

PT or purifying natural products using such microorganisms.

XX

PS Claim 3; SEQ ID NO 6; 34pp; English.

XX

CC The present invention relates to novel primers STGROF1 (ADV99121) and

CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of

CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment

CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces

CC species. Primers ADV99121 and ADV99122 are useful in a method for

CC identifying Streptomyces species, comprising amplifying groEL2 gene

CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC gene fragment amplified, and comparing the nucleotide sequence obtained

CC with that of groEL2 gene fragment of a reference strain.

XX

SQ Sequence 420 BP; 81 A; 144 C; 139 G; 56 T; 0 U; 0 Other;

XX

Query Match 93.1%; Score 391.2; DB 14; Length 420;

Best Local Similarity 95.7%; Pred. No. 4.6e-56;

Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCAGCTGCCGGTACCGGTACGACCGGACCGGTCTCGCCGAGCGG 60

DB 1 AAGAGACGAGCAGCTGCCGGTACCGGTACGACCGGACCGGTCTCGCCGAGCGG 60

QY 61 CTGCTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGCGC 120
DB 61 CTGCTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTCGAGCCGCTTCGCGCGCCCTGCTGGAGCAGCGAAGATGTC 180
DB 121 GGCATCGAGAGGCGCTCGAGCCGCTTCGCGCGCCCTGCTGGAGCAGCGAAGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACAGCGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCACAGCGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGATGACAAAGGTTCGCAAGGAGGCGTCTATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGACAAAGGTTCGCAAGGAGGCGTCTATCACCCTCGAGGAG 300
QY 301 TCCACAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
DB 301 TCCACAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGTTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGTTCGACGACCGGTAC 420

RESULT 15

ADV99142

ID ADV99142 standard; DNA; 420 BP.

XX

AC ADV99142;

DT 24-MAR-2005 (first entry)

DE groEL2 gene fragment, SEQ ID 22.

XX

KW Microorganism identification; microorganism detection; groEL2;

KW potato scab; gene; ds.

XX

OS Streptomyces cinnamonensis.

XX

PN US2004265873-A1.

XX

PD 30-DEC-2004.

XX

PF 15-APR-2004; 2004US-00824527.

XX

PR 18-APR-2003; 2003KR-00024656.

XX

PR 14-NOV-2003; 2003KR-00080580.

XX

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX

PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX

DR WPI; 2005-089568/10.

XX

PT New primer specifically amplifying groEL2 gene fragment of Streptomyces

PT species, useful in identifying the genus Streptomyces, and for isolating

PT or purifying natural products using such microorganisms.

XX

PS Claim 3; SEQ ID NO 22; 34pp; English.

XX

CC The present invention relates to novel primers STGROF1 (ADV99121) and

CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of

CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment

CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces

CC species. Primers ADV99121 and ADV99122 are useful in a method for

CC identifying Streptomyces species, comprising amplifying groEL2 gene

CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC gene fragment amplified, and comparing the nucleotide sequence obtained

CC with that of groEL2 gene fragment of a reference strain.

XX

SQ Sequence 420 BP; 80 A; 150 C; 132 G; 58 T; 0 U; 0 Other;
 Query Match 93.1%; Score 391.2; DB 14; Length 420;
 Best Local Similarity 95.7%; Pred. No. 4.6e-56;
 Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACCAACCGCAGCGTTCTCGCCAGGCG 60
 DB 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACCAACCGCAGCGTTCTCGCCAGGCG 60
 QY 61 CTCGTACGAGGCGCTGCGCAACGTCGCCCGCGTGCACCCGATGGCTCTCAAGCGC 120
 DB 61 CTCGTACGAGGCGCTGCGCAACGTCGCCCGCGTGCACCCGATGGCTCTCAAGCGT 120
 QY 121 GGCATCGAAGAGCGCTCGAGGCGCTCTCGGGCGCTCTCGGCGCGCTCTCGGCGCGGATGTC 180
 DB 121 GGTATCGAAGAGCGCTCGAGGCGCTCTCGGGCGCTCTCGGCGCGCTCTCGGCGCGGATGTC 180
 QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCCGCGCGCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCCGCGCGCGACACCCAGATCGGC 240
 QY 241 GAGCTCATTCGCCGAGGCGATGGACAAAGGTGCGCAAGGTCGCAAGGCGCTCATCACCGTCGAGGAG 300
 DB 241 GAGCTCATTCGCCGAGGCGATGGACAAAGGTGCGCAAGGTCGCAAGGCGCTCATCACCGTCGAGGAG 300
 QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGGTAC 360
 DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGGTAC 360
 QY 361 ATCTCGGCGTACTTCGGCCACCGATGGAGCGGTGCGTTCGACGACCGCGTAC 420
 DB 361 ATCTCGGCGTACTTCGGCCACCGATGGAGCGGTGCGTTCGACGACCGCGTAC 420

RESULT 16
 ADV99156
 ID ADV99156 standard; DNA; 420 BP.
 XX AC ADV99156;
 XX XX
 DT 24-MAR-2005 (first entry)
 XX groEL2 gene fragment, SEQ ID 36.
 XX Microorganism identification; microorganism detection; groEL2;
 KW potato scab; gene; ds.
 XX Streptomyces humiferus.
 OS
 XX US2004265873-A1.
 XX 30-DEC-2004.
 XX 15-APR-2004; 2004US-00824527.
 XX 18-APR-2003; 2003KR-00024656.
 PR 14-NOV-2003; 2003KR-00080580.
 XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
 XX WPI; 2005-089568/10.
 XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.
 XX Claim 3; SEQ ID NO 36; 34pp; English.
 PS The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of

CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.
 XX Sequence 420 BP; 84 A; 144 C; 136 G; 56 T; 0 U; 0 Other;

Query Match 92.4%; Score 388; DB 14; Length 420;
 Best Local Similarity 95.2%; Pred. No. 1.5e-55;
 Matches 400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACCAACCGCAGCGTTCTCGCCAGGCG 60
 DB 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACCAACCGCAGCGTTCTCGCCAGGCG 60
 QY 61 CTCGTACGAGGCGCTGCGCAACGTCGCCCGCGTGCACCCGATGGCTCTCAAGCGC 120
 DB 61 CTCGTACGAGGCGCTGCGCAACGTCGCCCGCGTGCACCCGATGGCTCTCAAGCGC 120
 QY 121 GGCATCGAAGAGCGCTCGAGGCGCTCTCCGGCGCTCTCGGCGCGCTCTCGGCGCGGATGTC 180
 DB 121 GGTATCGAAGAGCGCTCGAGGCGCTCTCCGGCGCTCTCGGCGCGCTCTCGGCGCGGATGTC 180
 QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCCGCGCGCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCCGCGCGCGACACCCAGATCGGC 240
 QY 241 GAGCTCATTCGCCGAGGCGATGGACAAAGGTGCGCAAGGTCGCAAGGCGCTCATCACCGTCGAGGAG 300
 DB 241 GAGCTCATTCGCCGAGGCGATGGACAAAGGTGCGCAAGGTCGCAAGGCGCTCATCACCGTCGAGGAG 300
 QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGGTAC 360
 DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGGTAC 360
 QY 361 ATCTCGGCGTACTTCGCCACCGATGGAGCGGTGCGTTCGACGACCGCGTAC 420
 DB 361 ATCTCGGCGTACTTCGCCACCGATGGAGCGGTGCGTTCGACGACCGCGTAC 420

RESULT 17
 ADV99181
 ID ADV99181 standard; DNA; 420 BP.
 XX AC ADV99181;
 XX XX
 DT 24-MAR-2005 (first entry)
 XX groEL2 gene fragment, SEQ ID 61.
 XX Microorganism identification; microorganism detection; groEL2;
 KW potato scab; gene; ds.
 XX Streptomyces acidiscabies.
 OS
 XX US2004265873-A1.
 XX 30-DEC-2004.
 XX 15-APR-2004; 2004US-00824527.
 XX 18-APR-2003; 2003KR-00024656.
 PR 14-NOV-2003; 2003KR-00080580.
 XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
 XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
XX Claim 4; SEQ ID NO 61; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROK2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 82 A; 143 C; 143 G; 52 T; 0 U; 0 Other;
Query Match 92.4%; Score 388; DB 14; Length 420;
Best Local Similarity 95.2%; Pred. No. 1.5e-55;
Matches 400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCCGCTGACGCTACGACACCGGACCGTTCGCCCGAGGCG 60
DB 1 AAGAAGACGACGACGTCGCCGCTGACGCTACGACACCGGACCGTTCGCCCGAGGCGA 60
QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCCGCGGTCGCAACCCGATGCTCTCAAGCGC 120
DB 61 CTGTTCGCGAGGCGCTCCGACGCTGCGCGCGGCGCAACCCGATGCTTCGAGCGC 120
QY 121 GGCATCGAGAAGCGCTCGAGGCGCTCTCCGCGCGCTCTGAGCAGCGGCAAGGATGTC 180
DB 121 GGCATCGAGAAGCGCTCGAGGCGCTCTCCGCGCGCTCTGAGCAGCGGCAAGGATGTC 180
QY 181 GAGACCAAGGACGATCGCTTCACGGCTTCATCTCCGCGCGGCAACCCGATGCTTC 240
DB 181 GAGACCAAGGACGATCGCTTCACGGCTTCATCTCCGCGCGGCAACCCGATGCTTC 240
QY 241 GAGCTCATCGCGAGGCGATGCAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGCAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATCGCTTCGACAAAGGCTTAC 360
DB 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATCGCTTCGACAAAGGCTTAC 360
QY 361 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420

RESULT 18

ADV99144
ID ADV99144 standard; DNA; 420 BP.
XX
XX ADV99144;
XX
XX 24-MAR-2005 (first entry)
XX
XX groEL2 gene fragment, SEQ ID 24.
XX
XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
XX Streptomyces cirratius.
OS
XX US2004265873-A1.
XX
XX 30-DEC-2004.
PD
XX 15-APR-2004; 2004US-00824527.

XX

PR 18-APR-2003; 2003KR-00024656.

PR 14-NOV-2003; 2003KR-00080580.

XX

(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

PA

Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

PI

WPI; 2005-089568/10.

XX

DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
XX Claim 3; SEQ ID NO 24; 34pp; English.

PS

The present invention relates to novel primers STGROF1 (ADV99121) and

CC

CC STGROK2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

SQ

Sequence 420 BP; 80 A; 147 C; 137 G; 56 T; 0 U; 0 Other;

Query Match

Best Local Similarity 92.4%; Score 388; DB 14; Length 420;

Matches

400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY

1 AAGAAGACGACGACGTCGCCGCTGACGCTACGACACCGGACCGTTCGCCCGAGGCG 60

DB

1 AAGAAGACGACGACGTCGCCGCTGACGCTACGACACCGGACCGTTCGCCCGAGGCG 60

QY

61 CTCGTACGCGAGGCGCTCGCAACGTCGCCGCGGTCGCAACCCGATGCTCTCAAGCGC 120

DB

61 CTGTTCGCGAGGCGCTCCGACGCTGCGCGCGGCGCAACCCGATGCTTCGAGCGC 120

QY

121 GGCATCGAGAAGCGCTCGAGGCGCTCTCCGCGCGCTCTGAGCAGCGGCAAGGATGTC 180

DB

121 GGCATCGAGAAGCGCTCGAGGCGCTCTCCGCGCGCTCTGAGCAGCGGCAAGGATGTC 180

QY

181 GAGACCAAGGACGATCGCTTCACGGCTTCATCTCCGCGCGGCAACCCGATGCTTC 240

DB

181 GAGACCAAGGACGATCGCTTCACGGCTTCATCTCCGCGCGGCAACCCGATGCTTC 240

QY

241 GAGCTCATCGCGAGGCGATGCAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300

DB

241 GAGCTCATCGCGAGGCGATGCAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300

QY

301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATCGCTTCGACAAAGGCTTAC 360

DB

301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATCGCTTCGACAAAGGCTTAC 360

QY

361 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420

DB

361 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420

RESULT 19

ADV99158

ID ADV99158 standard; DNA; 420 BP.

XX

ADV99158;

XX

24-MAR-2005 (first entry)

XX

groEL2 gene fragment, SEQ ID 38.

DE

Microorganism identification; microorganism detection; groEL2;

XX

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KW potato scab; gene; ds.
XX Streptomyces minutiscleroticus.
XX US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 38; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 80 A; 143 C; 141 G; 56 T; 0 U; 0 Other;
SQ
Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGGCGCCATCTCTCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGGCGCCATCTCTCGCCAGGCG 60
QY 61 CTGTCACGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGTCGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGCGCGTTCGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180
DB 121 GGCATCGAGAAGCGCGTTCGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGCGGATGCTCAAGCGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGCGGATGCTCAAGCGC 240
QY 241 GAGTCATCGCGAGGCGATGGAACAAGTCGGAAGGCGCTCATCCGCTCGAGGAG 300
DB 241 GAGTCATCGCGAGGCGATGGAACAAGTCGGAAGGCGCTCATCCGCTCGAGGAG 300
QY 301 TCCAGACCTTTCGGTTCGAGCTGAGCTACCGAGGGTATGCGCTTCGACAGGGGTAC 360
DB 301 TCCAGACCTTTCGGTTCGAGCTGAGCTACCGAGGGTATGCGCTTCGACAGGGGTAC 360
QY 361 ATCTCGCGTACTTTCGGCCACGATGAGCGGATGAGGCGTCTCGACGACCGCTAC 420
DB 361 ATCTCGCGTACTTTCGGCCACGATGAGCGGATGAGGCGTCTCGACGACCGCTAC 420
ADV99166 standard; DNA; 420 BP.
ADV99166;
24-MAR-2005 (first entry)
groEL2 gene fragment, SEQ ID 46.
Microorganism identification; microorganism detection; groEL2;
potato scab; gene; ds.
Streptomyces scabiei.
US2004265873-A1.
30-DEC-2004.
15-APR-2004; 2004US-00824527.
18-APR-2003; 2003KR-00024656.
14-NOV-2003; 2003KR-00080580.
(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
WPI; 2005-089568/10.
New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
Claim 4; SEQ ID NO 46; 34pp; English.
The present invention relates to novel primers STGROF1 (ADV99121) and
STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
Potato scab is a pathogenic disease caused by certain Streptomyces
species. Primers ADV99121 and ADV99122 are useful in a method for
identifying Streptomyces species, comprising amplifying groEL2 gene
fragment of target strain, analyzing the nucleotide sequence of groEL2
gene fragment amplified, and comparing the nucleotide sequence obtained
with that of groEL2 gene fragment of a reference strain.
Sequence 420 BP; 84 A; 142 C; 135 G; 59 T; 0 U; 0 Other;
Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGGCGCCATCTCTCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGGCGCCATCTCTCGCCAGGCG 60
QY 61 CTGTCACGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGTCGCGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGCGCGTTCGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180
DB 121 GGCATCGAGAAGCGCGTTCGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGCGGATGCTCAAGCGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGCGGATGCTCAAGCGC 240
QY 241 GAGTCATCGCGAGGCGATGGAACAAGTCGGAAGGCGCTCATCCGCTCGAGGAG 300
DB 241 GAGTCATCGCGAGGCGATGGAACAAGTCGGAAGGCGCTCATCCGCTCGAGGAG 300
QY 301 TCCAGACCTTTCGGTTCGAGCTGAGCTACCGAGGGTATGCGCTTCGACAGGGGTAC 360
DB 301 TCCAGACCTTTCGGTTCGAGCTGAGCTACCGAGGGTATGCGCTTCGACAGGGGTAC 360
QY 361 ATCTCGCGTACTTTCGGCCACGATGAGCGGATGAGGCGTCTCGACGACCGCTAC 420
DB 361 ATCTCGCGTACTTTCGGCCACGATGAGCGGATGAGGCGTCTCGACGACCGCTAC 420
RESULT 20
ADV99166
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Db 301 TCCAGACCTTCGGTCTGGAGCTGGAACCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCGCCAGCATGAGACGGATGAGAGCGTTCGCTTCGACGACCGCGTAC 420
Db 361 ATCTCGGCGTACTTCGCGCCAGCATGAGACGGATGAGAGCGTTCGCTTCGACGACCGCGTAC 420

RESULT 21
ADV99154
ID ADV99154 standard; DNA; 420 BP.
XX
AC ADV99154;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 34.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces griseolus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 34; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 84 A; 142 C; 135 G; 59 T; 0 U; 0 Other;

Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCCGCGACGCTGACGATGACGACCGGTCCTCGCCAGCGG 60
Db 1 AAGAAGACGACGACGTCGCCGCGACGCTGACGATGACGACCGGTCCTCGCCAGCGG 60

Qy 61 CTCGTACCGGAGGCGTCCGCACTCGCGCGGTCGCAACCCGATGCTTCGAGCGC 120
Db 61 CTCGTCCGAGGCGGCTCGCAACGTCGCGCGGTCGCAACCCGATGCTTCGAGCGT 120

Qy 121 GGCATCGAAGAGCGCTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGAAGATGTC 180
Db 121 GGCATCGAAGAGCGCTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGAAGATGTC 180

Qy 181 GAGACCAAGGACGATCGCTTCCACGGCCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
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Db 181 GAGACCAAGGACGATCGCTTCGACCGGCTTCATCTCCGCGCGCGACACCCGATCGGC 240
Qy 241 GAGCTTCATCGCCGAGCGATGACCAAGGTTCGCAAGGAGGCGTTCATCACCGCTCGAGGAG 300
Db 241 GCCAAGATCGCCGAGCGATGACCAAGGTTCGCAAGGAGGCGTTCATCACCGCTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCGCCAGCATGAGACGGATGAGAGCGTTCGCTTCGACGACCGCGTAC 420
Db 361 ATCTCGGCGTACTTCGCGCCAGCATGAGACGGATGAGAGCGTTCGCTTCGACGACCGCGTAC 420

RESULT 22
ADV99169
ID ADV99169 standard; DNA; 420 BP.
XX
AC ADV99169;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 49.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces scabiei.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 4; SEQ ID NO 49; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 83 A; 137 C; 140 G; 60 T; 0 U; 0 Other;

Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCCGCGACGCTGACGATGACGACCGGTCCTCGCCAGCGG 60
Db 1 AAGAAGACGACGACGTCGCCGCGACGCTGACGATGACGACCGGTCCTCGCCAGCGG 60
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PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
DR
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 40; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
XX Sequence 420 BP; 82 A; 146 C; 137 G; 55 T; 0 U; 0 Other;
XX
XX Query Match 92.0%; Score 386.4; DB 14; Length 420;
XX Best Local Similarity 95.0%; Pred. No. 2.8e-55;
XX Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX
QY 1 AAGAAGACGACGACGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCAAGGCG 60
DB 1 AAGAAGACGACGACGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCAAGGCG 60
QY 61 CTGCTACGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 180
DB 121 GGTATCGAGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 180
QY 181 GAGACCAAGGACGAGATCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 240
DB 181 GAGACCAAGGACGAGATCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 240
QY 241 GAGCTCATCGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 300
DB 241 GAGCTCATCGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 300
QY 301 TCCGACGCTTCCGCTTGGAGCTGAGCTCACCGAGGGTATCGCTTTCGACAAAGGGCTAC 360
DB 301 TCCGACGCTTCCGCTTGGAGCTGAGCTCACCGAGGGTATCGCTTTCGACAAAGGGCTAC 360
QY 361 ATCTCGCGTACTTTCGCCACCGATGAGCGGATGAGCGGCTCGCTTCGACGACCGCGTAC 420
DB 361 ATCTCGCGTACTTTCGCCACCGATGAGCGGATGAGCGGCTCGCTTCGACGACCGCGTAC 420
XX
XX RESULT 27
XX ID ADV99138 standard; DNA; 422 BP.
XX AC
XX ADV99138;
XX
XX 24-MAR-2005 (first entry)
XX
XX groEL2 gene fragment, SEQ ID 18.
XX
XX Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
XX
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Streptomyces catenulae.
US2004265873-A1.
30-DEC-2004.
15-APR-2004; 2004US-00824527.
18-APR-2003; 2003KR-00024656.
14-NOV-2003; 2003KR-00080580.
(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
WPI; 2005-089568/10.
New primer specifically amplifying groEL2 gene fragment of Streptomyces
species, useful in identifying the genus Streptomyces, and for isolating
or purifying natural products using such microorganisms.
Claim 3; SEQ ID NO 18; 34pp; English.
The present invention relates to novel primers STGROF1 (ADV99121) and
STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
Potato scab is a pathogenic disease caused by certain Streptomyces
species. Primers ADV99121 and ADV99122 are useful in a method for
identifying Streptomyces species, comprising amplifying groEL2 gene
fragment of target strain, analyzing the nucleotide sequence of groEL2
gene fragment amplified, and comparing the nucleotide sequence obtained
with that of groEL2 gene fragment of a reference strain.
Sequence 422 BP; 81 A; 145 C; 139 G; 57 T; 0 U; 0 Other;
Query Match 92.0%; Score 386.4; DB 14; Length 422;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
1 AAGAAGACGACGACGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCAAGGCG 60
1 AAGAAGACGACGACGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCAAGGCG 60
61 CTGCTACGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 120
61 CTGCTCGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 120
121 GGCATCGAGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 180
121 GGCATCGAGACCGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 180
181 GAGACCAAGGACGAGATCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 240
181 GAGACCAAGGACGAGATCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 240
241 GAGCTCATCGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 300
241 GAGCTCATCGCGAGGCGCTTCCGACGCTCGCGCGGTGACGACCGGATGGCTCTCAAGCGC 300
301 TCCGACGCTTCCGCTTGGAGCTGAGCTCACCGAGGGTATCGCTTTCGACAAAGGGCTAC 360
301 TCCGACGCTTCCGCTTGGAGCTGAGCTCACCGAGGGTATCGCTTTCGACAAAGGGCTAC 360
361 ATCTCGCGTACTTTCGCCACCGATGAGCGGATGAGCGGCTCGCTTCGACGACCGCGTAC 420
361 ATCTCGCGTACTTTCGCCACCGATGAGCGGATGAGCGGCTCGCTTCGACGACCGCGTAC 420
RESULT 28
ADV99151
ID ADV99151 standard; DNA; 420 BP.
```

XX ADV99151;
XX 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 31.
XX Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
XX Streptomyces fulvissimus.
XX US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 31; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 84 A; 146 C; 137 G; 53 T; 0 U; 0 Other;
Query Match 91.6%; Score 384.8; DB 14; Length 420;
Best Local Similarity 94.8%; Pred. No. 5.2e-55;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGACGTCCGCGGTGACGCGTACGACCGACCGACCGACCGTCTCGCCAGGCG 60
DB 1 AAGAAGACGGACGACGTCCGCGGTGACGCGTACGACCGACCGACCGACCGTCTCGCCAGGCG 60
QY 61 CTCGTACCGAGGGCTTGGCAACGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 120
DB 61 CTCGTACCGAGGGCTTGGCAACGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 120
QY 121 GGCATCGAGAGGCGTTCGAGGCGGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 180
DB 121 GGCATCGAGAGGCGTTCGAGGCGGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 180
QY 181 GAGACCAAGGACGATCGCTTTCACGGCTTCATCTCCGCGCGCGACACCGATCGGC 240
DB 181 GAGACCAAGGACGATCGCTTTCACGGCTTCATCTCCGCGCGCGACACCGATCGGC 240
QY 241 GAGCTCATCGCGAGCGATGACCAAGTTCGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGATGACCAAGTTCGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 360

QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACGACCCGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACGACCCGTAC 420
RESULT 29
ADV99155
ID ADV99155 standard; DNA; 420 BP.
XX AC ADV99155;
XX 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 35.
XX Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
XX Streptomyces griseoviridis.
XX US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 35; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 84 A; 142 C; 138 G; 56 T; 0 U; 0 Other;
Query Match 91.6%; Score 384.8; DB 14; Length 420;
Best Local Similarity 94.8%; Pred. No. 5.2e-55;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGACGTTCGCGGTGACGCGTACGACCGACCGACCGTCTCGCCAGGCG 60
DB 1 AAGAAGACGGACGACGTTCGCGGTGACGCGTACGACCGACCGACCGTCTCGCCAGGCG 60
QY 61 CTCGTACCGAGGGCTTGGCAACGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 120
DB 61 CTCGTACCGAGGGCTTGGCAACGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 120
QY 121 GGCATCGAGAGGCGGTTCGAGGCGGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 180
DB 121 GGCATCGAGAGGCGGTTCGAGGCGGTTCGCGCGGTGCAACCGCATGGCTCTCAAGGCG 180
QY 181 GAGACCAAGGACGATCGCTTTCACGGCTTCATCTCCGCGCGCGACACCGATCGGC 240

Db	181	GAGACCAAGGAGCAGATCGCTCCACGGCTCCATCTCCGCGCGCGCACACCCAGATCGGC	240
QY	241	GAGCTATCCGCGGCGGATGACACAGGTCCGCAAGGAGCGCTCATCACCGTCGAGGAG	300
Db	241	GAGCTATCCGCGGCGGATGACACAGGTCCGCAAGGAGCGCTCATCACCGTCGAGGAG	300
QY	301	TCCGAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGCAAGGCGCTAC	360
Db	301	TCCGAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGCAAGGCGCTAC	360
QY	361	ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGACGACCCGCTAC	420
Db	361	ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGACGACCCGCTAC	420
RESULT 30			
ID	ADV99128	ADV99128 standard; DNA; 420 BP.	
XX	ADV99128;		
DT	24-MAR-2005	(first entry)	
XX	groEL2 gene fragment, SEQ ID 8.		
DE	Microorganism identification; microorganism detection; groEL2;		
KW	potato scab; gene; ds.		
OS	Streptomyces albobrisesolus.		
XX	US2004265873-A1.		
PN	30-DEC-2004.		
PD	15-APR-2004; 2004US-00824527.		
PF	18-APR-2003; 2003KR-00024656.		
PR	14-NOV-2003; 2003KR-00080580.		
XX	(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.		
PI	Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;		
XX	WPI; 2005-089568/10.		
XX	New primer specifically amplifying groEL2 gene fragment of Streptomyces		
PT	species, useful in identifying the genus Streptomyces, and for isolating		
PT	or purifying natural products using such microorganisms.		
XX	Claim 3; SEQ ID NO 8; 34pp; English.		
XX	The present invention relates to novel primers STGROF1 (ADV99121) and		
CC	STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of		
CC	Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment		
CC	derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).		
CC	Potato scab is a pathogenic disease caused by certain Streptomyces		
CC	species. Primers ADV99121 and ADV99122 are useful in a method for		
CC	identifying Streptomyces species, comprising amplifying groEL2 gene		
CC	fragment of target strain, analyzing the nucleotide sequence of groEL2		
CC	gene fragment amplified, and comparing the nucleotide sequence obtained		
CC	with that of groEL2 gene fragment of a reference strain.		
XX	Sequence 420 BP; 83 A; 144 C; 137 G; 56 T; 0 U; 0 Other;		
QY	Query Match	91.6%;	Score 384.8; DB 14; Length 420;
Db	Best Local Similarity	94.8%;	Pred. No. 5.2e-55;
QY	Matches 398; Conservative	0;	Mismatches 22; Indels 0; Gaps 0;
QY	1	AAGAAGACGACGACGTCGCGGTCGACGTCACGACCGGACCGCTTCGCCGACGGCG	60
Db	1	AAGAAGACGACGACGTCGCGGTCGACGTCACGACCGGACCGCTTCGCCGACGGCG	60
QY	61	CTGCTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCCAACCGATGGCTCTCAAGCGC	120

Db	61	CTGGTCAAGGAGGCGCTCGCGCAACGTCGCGCGCGCGCGCAACCGATGGGCCCTTGAAGCGC	120
QY	121	GSCATCCGAGAAAGGCGCTCGAGGCGCTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC	180
Db	121	GGTATCCGAGAGGCGCTCGAGGCGCTCTCCGGCGCCCTCTCGAGCAGGCGAAGGAGGTG	180
QY	181	GAGACCAAGGAGCAGATCGCTTCACCGCTTCATCTCCGCGCGCGACACCCAGATCGGC	240
Db	181	GAGACCAAGGAGCAGATCGCTTCACCGCTTCATCTCCGCGCGCGACACCCAGATCGGC	240
QY	241	GAGCTCATCCGCGGCGATGGACAAGGTCCGCAAGGAGCGCTCATCACCGTCGAGGAG	300
Db	241	GAGCTCATCCGCGGCGCATGGACAAGGTCCGCAAGGAGCGCTCATCACCGTCGAGGAG	300
QY	301	TCCGAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGCAAGGCGCTAC	360
Db	301	TCCGAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGCAAGGCGCTAC	360
QY	361	ATCTCGCGGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGACGACCCGCTAC	420
Db	361	ATCTCGCGGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGACGACCCGCTAC	420
RESULT 31			
ID	ADV99139	ADV99139 standard; DNA; 420 BP.	
XX	ADV99139;		
DT	24-MAR-2005	(first entry)	
XX	groEL2 gene fragment, SEQ ID 19.		
DE	Microorganism identification; microorganism detection; groEL2;		
KW	potato scab; gene; ds.		
OS	Streptomyces cellulosa.		
XX	US2004265873-A1.		
XX	30-DEC-2004.		
PF	15-APR-2004; 2004US-00824527.		
PR	18-APR-2003; 2003KR-00024656.		
PR	14-NOV-2003; 2003KR-00080580.		
XX	(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.		
XX	Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;		
XX	WPI; 2005-089568/10.		
XX	New primer specifically amplifying groEL2 gene fragment of Streptomyces		
PT	species, useful in identifying the genus Streptomyces, and for isolating		
PT	or purifying natural products using such microorganisms.		
XX	Claim 3; SEQ ID NO 19; 34pp; English.		
XX	The present invention relates to novel primers STGROF1 (ADV99121) and		
CC	STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of		
CC	Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment		
CC	derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).		
CC	Potato scab is a pathogenic disease caused by certain Streptomyces		
CC	species. Primers ADV99121 and ADV99122 are useful in a method for		
CC	identifying Streptomyces species, comprising amplifying groEL2 gene		
CC	fragment of target strain, analyzing the nucleotide sequence of groEL2		
CC	gene fragment amplified, and comparing the nucleotide sequence obtained		
CC	with that of groEL2 gene fragment of a reference strain.		
XX	Sequence 420 BP; 82 A; 140 C; 141 G; 57 T; 0 U; 0 Other;		

Query Match 91.2%; Score 383.2; DB 14; Length 420;
Best Local Similarity 94.5%; Pred. No. 9.6e-55;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGCTCGCGGTGACGCTACGACACCGCGCGCGCTTCGCGCCGAGGCG 60
DB 1 AAGNAGACGAGCGCTCGCGGTGACGCTACGACACCGCGCGCGCTTCGCGCCGAGGCG 60
QY 61 CTCGTACGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
DB 61 CTGGTCAAGGAGGCGCTCGCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGAGCGAGGATGTC 180
DB 121 GGTATCGAGAGCGCTCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGAGCGAGGACGTCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTCCATCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTCCATCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCTATCAACCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCTATCAACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGGTTGCGCAAGGCGCTAC 360
DB 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGGTTGCGCAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGCTCGACGACCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGCTCGACGACCGCTAC 420

RESULT 32
ADV99157
ID ADV99157 standard; DNA; 420 BP.
XX
AC ADV99157;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 37.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces hygroscopicus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 37; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 80 A; 146 C; 137 G; 57 T; 0 U; 0 Other;
Query Match 91.2%; Score 383.2; DB 14; Length 420;
Best Local Similarity 94.5%; Pred. No. 9.6e-55;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGCTCGCGGTGACGCTACGACACCGCGCGCGCTTCGCGCCGAGGCG 60
DB 1 AAGAAGACGAGCGCTCGCGGTGACGCTACGACACCGCGCGCGCTTCGCGCCGAGGCG 60
QY 61 CTCGTACGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
DB 61 CTGGTCCGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGAGCGAGGATGTC 180
DB 121 GGTATCGAGCGCTCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGAGCGAGGACGTCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTCCATCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GAGACCAAGGAGCAGATCGCTTCGAGCGCTCCATCTCCGCGCGCTGACACCGCGATGCGC 240
QY 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCTATCAACCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGACAAAGGTGCGCAAGGAGGCGTCTATCAACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGGTTGCGCAAGGCGCTAC 360
DB 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGGTTGCGCAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGCTCGACGACCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCTCGCTCGACGACCGCTAC 420

RESULT 33
ADV99133
ID ADV99133 standard; DNA; 420 BP.
XX
AC ADV99133;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 13.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces anandii.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 37; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 13; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 420 BP; 81 A; 150 C; 135 G; 54 T; 0 U; 0 Other;

Query Match 91.2%; Score 383.2; DB 14; Length 420;
Best Local Similarity 94.5%; Pred. No. 9.6e-55;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCGCGGTGACGCTACGACACCGCGACCGTCTCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGCGGTGACGCTACGACACCGCGACCGTCTCGCCAGGCG 60
Qy 61 CTGCTACGACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTACGACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCAGAGAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGCGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCAGAGAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGCGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGACGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGACGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGCGACAGCTGCGCAGGAGCGCTCATCAGCGTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGCGACAGCTGCGCAGGAGCGCTCATCAGCGTCGAGGAG 300
Qy 301 TCCGACACCTTCGCTCTGGAGCTGAGCTCACCAGGCGTATCGCTTTCGACAAAGGGCTAC 360
Db 301 TCCGACACCTTCGCTCTGGAGCTGAGCTCACCAGGCGTATCGCTTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGCGCTACTTCGCCACCGACATCGAGCGGATGAGGCGCTCGCTCGACGACCCGCTAC 420
Db 361 ATCTCGCGCTACTTCGCCACCGACATCGAGCGGATGAGGCGCTCGCTCGACGACCCGCTAC 420

RESULT 34

ADV99146
ID ADV99146 standard; DNA; 420 BP.

XX AC ADV99146;

XX 24-MAR-2005 (first entry)

XX groEL2 gene fragment, SEQ ID 26.

XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.

XX Streptomyces collinus.

XX US2004265873-A1.

XX 30-DEC-2004.

XX 15-APR-2004; 2004US-00824527.

XX 18-APR-2003; 2003KR-00024656.

PR 14-NOV-2003; 2003KR-00080580.

PA (KOR-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 26; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 420 BP; 82 A; 145 C; 135 G; 58 T; 0 U; 0 Other;

Query Match 91.2%; Score 383.2; DB 14; Length 420;

Best Local Similarity 94.5%; Pred. No. 9.6e-55;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCGCGGTGACGCTACGACACCGCGACCGTCTCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGCGGTGACGCTACGACACCGCGACCGTCTCGCCAGGCG 60

Qy 61 CTGCTACGACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120

Db 61 CTGCTACGACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120

Qy 121 GGCATCAGAGAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGCGAGCAGGCGAAGGATGTC 180

Db 121 GGCATCAGAGAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGCGAGCAGGCGAAGGATGTC 180

Qy 181 GAGACCAAGGACGACGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240

Db 181 GAGACCAAGGACGACGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240

Qy 241 GAGCTCATCGCGAGGCGATGCGACAGCTGCGCAGGAGCGCTCATCAGCGTCGAGGAG 300

Db 241 GAGCTCATCGCGAGGCGATGCGACAGCTGCGCAGGAGCGCTCATCAGCGTCGAGGAG 300

Qy 301 TCCGACACCTTCGCTCTGGAGCTGAGCTCACCAGGCGTATCGCTTTCGACAAAGGGCTAC 360

Db 301 TCCGACACCTTCGCTCTGGAGCTGAGCTCACCAGGCGTATCGCTTTCGACAAAGGGCTAC 360

Qy 361 ATCTCGCGCTACTTCGCCACCGACATCGAGCGGATGAGGCGCTCGCTCGACGACCCGCTAC 420

Db 361 ATCTCGCGCTACTTCGCCACCGACATCGAGCGGATGAGGCGCTCGCTCGACGACCCGCTAC 420

RESULT 35

ADV99148

ID ADV99148 standard; DNA; 420 BP.

XX AC ADV99148;

XX 24-MAR-2005 (first entry)

XX groEL2 gene fragment, SEQ ID 28.

XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.

XX

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OS Streptomyces diastaticus.
PN US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 28; 34pp; English.
XX The present invention relates to novel primers STGR0F1 (ADV99121) and
CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 81 A; 146 C; 137 G; 56 T; 0 U; 0 Other;

Query Match 90.9%; Score 381.6; DB 14; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGCGGACGACGTCCCGGTGACGTACGACCGCGACCGACCGTCTCGCCCGAGCGG 60
DB 1 AAGAAGCGGACGACGTCCCGGTGACGTACGACCGCGACCGACCGTCTCGCCCGAGCGG 60
QY 61 CTCGTACGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCAGCGCGAAGGATGTC 120
DB 121 GGCATCGAGAGGCGGTGCGAGCGGTCTCCGCGCCCTGCTGGAGCAGCGCGAAGGATGTC 180
QY 121 GGCATCGAGAGGCGGTGCGAGCGGTCTCCGCGCCCTGCTGGAGCAGCGCGAAGGATGTC 180
DB 121 GGCATCGAGAGGCGGTGCGAGCGGTCTCCGCGCCCTGCTGGAGCAGCGCGAAGGATGTC 180
QY 181 GAGACCAAGGACGAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACCCAGATCGGC 240
DB 181 GAGACCAAGGACGAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACCCAGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGATGGAAGAAGTGGAGGCGTCTCGCTCGAAGCCCGTAC 300
DB 241 ATCTCGGCGTACTTGGCCACCGACATGAGCGGTATGAGGCGTCTCCGCGCGCGTAC 420

RESULT 36
ADV99180
ID ADV99180 standard; DNA; 420 BP.
XX
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QY 361 ATCTCGCGTACTTCCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
Db 361 ATCTCGCGTACTTCCGCCACGACATGAGCGTATGAGGCGTCTCGACGACCCGCTAC 420

RESULT 37
ADV99145
ID ADV99145 standard; DNA; 420 BP.
XX
AC ADV99145;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 25.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces coeruleorubidus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 25; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 83 A; 145 C; 136 G; 56 T; 0 U; 0 Other;
Query Match 90.9%; Score 381.6; DB 14; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTCGACGATACGACACCGCGGCTCTCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTCGACGATACGACACCGCGGCTCTCGCCAGGCG 60

QY 61 CTGTCAGCGAGGCGCTCGCGGTCGACGTCGCGGTCGACACCGCGGCTCTCGACGCG 120
Db 61 CTGTCAGCGAGGCGCTCGCGGTCGACGTCGCGGTCGACACCGCGGCTCTCGACGCG 120

QY 121 GGCATCAGAGAGGCGCTCGAGGCGCTCTCGCGGCGCTCTCGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCAGAGAGGCGCTCGAGGCGCTCTCGCGGCGCTCTCGAGCAGGCGAAGGATGTC 180

QY 181 GAGACCAAGGACGATGCTGCTCCACGGCTCTCCATCTCCCGCCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATGCTGCTCCACGGCTCTCCATCTCCCGCCCGACACCCAGATCGGC 240
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QY 241 GAGCTCATCCGAGGCGATGCAAGGTCCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300
Db 241 GAGCTCATCCGAGGCGCATGCAAGGTCCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300

QY 301 TCCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATCGCTTCCACAGGGCTAC 360
Db 301 TCCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATCGCTTCCACAGGGCTAC 360

QY 361 ATCTCGCGTACTTCCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
Db 361 ATCTCGCGTACTTCCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420

RESULT 38
ADV99149
ID ADV99149 standard; DNA; 420 BP.
XX
AC ADV99149;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 29.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces djakartensis.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 29; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 82 A; 148 C; 135 G; 55 T; 0 U; 0 Other;
Query Match 90.9%; Score 381.6; DB 14; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTCGACGATACGACACCGCGGCTCTCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTCGACGATACGACACCGCGGCTCTCGCCAGGCG 60

QY 61 CTGTCAGCGAGGCGCTCGCGGTCGACGTCGCGGTCGACACCGCGGCTCTCGACGCG 120
Db 61 CTGTCAGCGAGGCGCTCGCGGTCGACGTCGCGGTCGACACCGCGGCTCTCGACGCG 120
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Db 61 CTGGTCAAGAGGCGCTGCGCAAGCTGCGCGCGCGCGCGCAACCCGATGGCCCTGGAAGCGC 120
QY 121 GGATCATGAGAGGCGCTGAGGCGCGCTTCCGCGCGCGCTTCTGCGAGCAGGCGAGGATGTC 180
Db 121 GGTATCGAGCGCGCTGAGGCGCGCTTCCGCGCGCGCTTCTGCGAGCAGGCGAGGATGTC 180
QY 181 GAGACCAAGAGCAGATCGTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCGCGCGCGAGATCGGC 240
Db 181 GAGACCAAGAGCAGATCGTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCGCGCGCGAGATCGGC 240
QY 241 GAGCTCATCGCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 300
Db 241 GAGCTCATCGCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATGCGTTCCAGCAAGGCGCTAC 360
Db 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATGCGTTCCAGCAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 420
Db 361 ATCTCGGCGTACTTCCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 420

RESULT 39

ADV99141

ID ADV99141 standard; DNA; 420 BP.

AC ADV99141;

DT 24-MAR-2005 (first entry)

DE groEL2 gene fragment, SEQ ID 21.

XX Microorganism identification; microorganism detection; groEL2;

KW potato scab; gene; ds.

OS Streptomyces chattanoogensis.

XX US2004265873-A1.

XX 30-DEC-2004.

PF 15-APR-2004; 2004US-00824527.

XX 18-APR-2003; 2003KR-00024656.

PR 14-NOV-2003; 2003KR-00080580.

XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces species, useful in identifying the genus Streptomyces, and for isolating or purifying natural products using such microorganisms.

PS Claim 3; SEQ ID NO 21; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment derived from a potato scab pathogenic microorganism (ADV99163-ADV99181). CC Potato scab is a pathogenic disease caused by certain Streptomyces CC species. Primers ADV99121 and ADV99122 are useful in a method for CC identifying Streptomyces species, comprising amplifying groEL2 gene CC fragment of target strain, analyzing the nucleotide sequence of groEL2 CC gene fragment amplified, and comparing the nucleotide sequence obtained CC with that of groEL2 gene fragment of a reference strain.

SQ Sequence 420 BP; 81 A; 139 C; 139 G; 61 T; 0 U; 0 Other;

Query Match 90.9%; Score 381.6; DB 14; Length 420;

Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAGACGAGGAGCTGCGCGCTGACCGTACGACACCGCGACCGTCTTCCGCCAGGCG 60
Db 1 AAGAGACGAGGAGCTGCGCGCTGACCGTACGACACCGCGACCGTCTTCCGCCAGGCG 60
QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTGGTCCGCGAGGCGCTGCGCAACGTTGCGCGCGGTGCGCAACCCGATGGCTGAAGCGC 120
QY 121 GGCATCGAGAGGCGCTGAGGCGCGCTTCCGCGCGCGCTTCTGCGAGCAGGCGAGGATGTC 180
Db 121 GGTATCGAGAGGCGCTGAGTCCGCTTCCGCGCGCGCTTCTGCGAGCAGGCGAGGATGTC 180
QY 181 GAGACCAAGAGCAGATCGTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCGCGCGAGATCGGC 240
Db 181 GAGACCAAGAGCAGATCGTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCGCGCGAGATCGGC 240
QY 241 GAGCTCATCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 300
Db 241 GAGCTCATCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATGCGTTCCAGCAAGGCGCTAC 360
Db 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTATGCGTTCCAGCAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 420
Db 361 ATCTCGGCGTACTTCCGCGCGCGATGGAAGAGTTCGCGCAAGAGGCGCTCATCCGTCGAGGAG 420

RESULT 40

ADV99134

ID ADV99134 standard; DNA; 420 BP.

XX AC ADV99134;

XX 24-MAR-2005 (first entry)

XX groEL2 gene fragment, SEQ ID 14.

XX Microorganism identification; microorganism detection; groEL2;

KW potato scab; gene; ds.

XX Streptomyces argenteolus.

XX US2004265873-A1.

XX 30-DEC-2004.

XX 15-APR-2004; 2004US-00824527.

XX 18-APR-2003; 2003KR-00024656.

XX 14-NOV-2003; 2003KR-00080580.

XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces species, useful in identifying the genus Streptomyces, and for isolating or purifying natural products using such microorganisms.

PS Claim 3; SEQ ID NO 14; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment derived from a potato scab pathogenic microorganism (ADV99163-ADV99181). CC Potato scab is a pathogenic disease caused by certain Streptomyces

CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 83 A; 147 C; 137 G; 53 T; 0 U; 0 Other;

Query Match 90.58; Score 380; DB 14; Length 420;
Best Local Similarity 94.08; Pred. No. 3.2e-54;
Matches 395; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGATACGACACCGCGACCGTCTTCGCCAGGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGGTGACGATACGACACCGCGACCGTCTTCGCCAGGGCG 60

QY 61 CTGCTACGCGAGGCGCTTCGCAACGTCGCGCGGTGACCAACCGCGATGGCTCTCAAGCGC 120
DB 61 CTGCTACGCGAGGCGCTTCGCAACGTCGCGCGGTGACCAACCGCGATGGCTCTCAAGCGC 120

QY 121 GGCATCAGAAAGCGCGTTCGAGGCGCTTCGCGGCGCTTCGAGAGCGGCAAGATGTC 180
DB 121 GGTATCAGAAAGCGCGTTCGAGGCGCTTCGCGGCGCTTCGAGAGCGGCAAGATGTC 180

QY 181 GAGACCAAGGACGACGATCGCTTCACGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGACGACGATCGCTTCACGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240

QY 241 GAGCTCATCTCCGCGAGGCGATGGACAGGTTCGCAAGGAGCGCTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCTCCGCGAGGCGATGGACAGGTTCGCAAGGAGCGCTCATCACCGTCGAGGAG 300

QY 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
DB 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360

QY 361 ATCTCGCGCTACTTCGCCACCGACATGGAGCGATGGAGCGCTTCGACGACCGCGTAC 420
DB 361 ATCTCGCGCTACTTCGCCACCGACATGGAGCGATGGAGCGCTTCGACGACCGCGTAC 420

RESULT 41
ADV99171
ID ADV99171 standard; DNA; 420 BP.

XX AC ADV99171;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 51.

XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.

XX OS Streptomyces turgidiscabies.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX DR WPI; 2005-089568/10.

XX PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating

PT or purifying natural products using such microorganisms.

XX Claim 4; SEQ ID NO 51; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 420 BP; 83 A; 135 C; 147 G; 55 T; 0 U; 0 Other;

Query Match 90.1%; Score 378.4; DB 14; Length 420;
Best Local Similarity 93.8%; Pred. No. 6e-54;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGATACGACACCGCGACCGTCTTCGCCAGGGCG 60

DB 1 AAGAAGACGACGACGTCGCGCGGTGACGATACGACACCGCGACCGTCTTCGCCAGGGCG 60

QY 61 CTGCTACGCGAGGCGCTTCGCAACGTCGCGCGGTGACCAACCGCGATGGCTCTCAAGCGC 120

DB 61 CTGCTACGCGAGGCGCTTCGCAACGTCGCGCGGTGACCAACCGCGATGGCTCTCAAGCGC 120

QY 121 GGCATCAGAAAGCGCGTTCGAGGCGCTTCGCGGCGCTTCGAGAGCGGCAAGATGTC 180

DB 121 GGCATCAGAAAGCGCGTTCGAGGCGCTTCGCGGCGCTTCGAGAGCGGCAAGATGTC 180

QY 181 GAGACCAAGGACGACGATCGCTTCACGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240

DB 181 GAGACCAAGGACGACGATCGCTTCACGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240

QY 241 GAGCTCATCTCCGCGAGGCGATGGACAGGTTCGCAAGGAGCGCTCATCACCGTCGAGGAG 300

DB 241 GAGCTCATCTCCGCGAGGCGATGGACAGGTTCGCAAGGAGCGCTCATCACCGTCGAGGAG 300

QY 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360

DB 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360

QY 361 ATCTCGCGCTACTTCGCCACCGACATGGAGCGATGGAGCGCTTCGACGACCGCGTAC 420

DB 361 ATCTCGCGCTACTTCGCCACCGACATGGAGCGATGGAGCGCTTCGACGACCGCGTAC 420

RESULT 42

ADV99172

ID ADV99172 standard; DNA; 420 BP.

XX AC ADV99172;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 52.

XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.

XX OS Streptomyces turgidiscabies.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

```
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX PD WPI; 2005-089568/10.
XX PF New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PR species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 52; 34pp; English.
XX PS The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 83 A; 135 C; 147 G; 55 T; 0 U; 0 Other;

Query Match 90.1%; Score 378.4; DB 14; Length 420;
Best Local Similarity 93.8%; Pred. No. 6e-54;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 AAGACGCGGACGAGTCCCGGTACCGGTACGACCGGACCGGACCGGTCCTGCCCGGCGG 60
DB 1 AAGACGCGGACGAGTCCCGGTACCGGTACGACCGGACCGGACCGGTCCTGCCCGGCGG 60
QY 61 CTGCTACGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 180
DB 121 GGCAATCGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 180
QY 121 GGCAATCGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 180
DB 121 GGCAATCGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 180
QY 181 GAGACCAAGGAGGACGAGTCCGCTTCCACGCGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGGACGAGTCCGCTTCCACGCGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGGAGGCGGATGGAACAAGTGGCAAGGAGGCGTCAATCCCGTTCGAGGAG 300
DB 241 GAGCTCATCGCGGAGGCGGATGGAACAAGTGGCAAGGAGGCGTCAATCCCGTTCGAGGAG 300
QY 301 TCCAGACCTTCGCTTCGAGGCTGAGGCTACCCAGGGGTATGCGCTTCGACAAAGGGCTAC 360
DB 301 TCCAGACCTTCGCTTCGAGGCTGAGGCTACCCAGGGGTATGCGCTTCGACAAAGGGCTAC 360
QY 361 ATCTCGGGGTACTTCGCGACCGGACATGAGCGGATGAGGGGTGCTCGTTCGAGGAGCCCGTAC 420
DB 361 ATCTCGGGGTACTTCGCGACCGGACATGAGCGGATGAGGGGTGCTCGTTCGAGGAGCCCGTAC 420

RESULT 43
ADV99173
ID ADV99173 standard; DNA; 420 BP.
XX AC ADV99173;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 53.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces turgidiscabies.
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XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX PD WPI; 2005-089568/10.
XX PF New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PR species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 53; 34pp; English.
XX PS The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 83 A; 135 C; 147 G; 55 T; 0 U; 0 Other;

Query Match 90.1%; Score 378.4; DB 14; Length 420;
Best Local Similarity 93.8%; Pred. No. 6e-54;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 AAGACGCGGACGAGTCCCGGTACCGGTACGACCGGACCGGTCCTGCCCGGCGG 60
DB 1 AAGACGCGGACGAGTCCCGGTACCGGTACGACCGGACCGGTCCTGCCCGGCGG 60
QY 61 CTGCTACGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 120
DB 61 CTGCTACGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 120
QY 121 GGCAATCGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 180
DB 121 GGCAATCGAGAGCGGCTCGAGCGGCTCTCCGCGCGCTCTCGAGCGAGCGGCGAAGGATGTC 180
QY 181 GAGACCAAGGAGGACGAGTCCGCTTCCACGCGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGGACGAGTCCGCTTCCACGCGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGGAGGCGGATGGAACAAGTGGCAAGGAGGCGTCAATCCCGTTCGAGGAG 300
DB 241 GAGCTCATCGCGGAGGCGGATGGAACAAGTGGCAAGGAGGCGTCAATCCCGTTCGAGGAG 300
QY 301 TCCAGACCTTCGCTTCGAGGCTGAGGCTACCCAGGGGTATGCGCTTCGACAAAGGGCTAC 360
DB 301 TCCAGACCTTCGCTTCGAGGCTGAGGCTACCCAGGGGTATGCGCTTCGACAAAGGGCTAC 360
QY 361 ATCTCGGGGTACTTCGCGACCGGACATGAGCGGATGAGGGGTGCTCGTTCGAGGAGCCCGTAC 420
DB 361 ATCTCGGGGTACTTCGCGACCGGACATGAGCGGATGAGGGGTGCTCGTTCGAGGAGCCCGTAC 420

RESULT 44
ADV99174
ID ADV99174 standard; DNA; 420 BP.
XX AC ADV99174;
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XX 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 54.
XX Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
XX Streptomyces turgidiscabies.
XX US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX Claim 4; SEQ ID NO 54; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 83 A; 135 C; 147 G; 55 T; 0 U; 0 Other;
Query Match 90.1%; Score 378.4; DB 14; Length 420;
Best Local Similarity 93.8%; Pred. No. 6e-54;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGACCGACCGTCTTCGCCCGCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGACCGACCGTCTTCGCCCGCAGGCG 60
QY 61 CTCGTACGAGAGCGGCTTCGCAACGTCGCGCGCGTGCACCGGTCGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTTCGCAACGTCGCGCGCGTGCACCGGTCGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGCGGCTTCGCGGCGCGTCTCGGCGCGCTCTCGGCGCGCTCTCGGCGCGCTCTCGGCGCGC 180
DB 121 GGCATCGAGAAGCGGCTTCGCGGCGCGTCTCGGCGCGCTCTCGGCGCGCTCTCGGCGCGCTCTCGGCGCGC 180
QY 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
DB 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
QY 241 GAGCTCATCTCCGAGGCGGATGGACAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTC 300
DB 241 GAGCTCATCTCCGAGGCGGATGGACAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTC 300
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGGAGCTCACCGAGGGATGCGCTTCGACAGAGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGAGCTGGAGCTCACCGAGGGATGCGCTTCGACAGAGGCTAC 360
QY 361 ATCTCGCGCTACTTGGCCACCGACATGGAGCGGATGGAGGCGTCTCGCTTCGACGACCGCGTAC 420
DB 361 ATCTCGCGCTACTTGGCCACCGACATGGAGCGGATGGAGGCGTCTCGCTTCGACGACCGCGTAC 420
RESULT 45
ADV99170
ID ADV99170 standard; DNA; 420 BP.
XX ADV99170;
XX 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 50.
XX Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
XX Streptomyces acidiscabies.
XX US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX Claim 4; SEQ ID NO 50; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX Sequence 420 BP; 84 A; 141 C; 143 G; 52 T; 0 U; 0 Other;
Query Match 89.0%; Score 373.6; DB 14; Length 420;
Best Local Similarity 93.1%; Pred. No. 3.7e-53;
Matches 391; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGACCGACCGTCTTCGCCCGCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGACCGACCGTCTTCGCCCGCAGGCG 60
QY 61 CTCGTACGAGAGCGGCTTCGCGGCGCGTGCACCGGTCGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTTCGCGGCGCGTGCACCGGTCGCGGCGCGTCTTCGCCCGCAGGCG 120
QY 121 GGCATCGAGAAGCGGCTTCGAGGCGCGTCTTCGCGCGCGCTCTCGGCGCGCTCTCGGCGCGCTCTCGGCGCGC 180
DB 121 GGCATCGAGAAGCGGCTTCGAGGCGCGTCTTCGCGCGCGCTCTCGGCGCGCTCTCGGCGCGCTCTCGGCGCGC 180
QY 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
DB 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
QY 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
DB 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
QY 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
DB 181 GAGACCAAGGACGAGATCGCTTCACCGCTTCATCTCCCGCGCGACACCGATCGGC 240
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QY 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTTAC 420
DB 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTTAC 420

RESULT 46
ADV99176
ID ADV99176 standard; DNA; 420 BP.
XX
AC ADV99176;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 56.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces diastatochromogenes.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 4; SEQ ID NO 56; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 85 A; 142 C; 138 G; 55 T; 0 U; 0 Other;

Query Match 88.6%; Score 372; DB 14; Length 420;
Best Local Similarity 92.9%; Pred. No. 6.8e-53;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTACGACACCGGACCGTTCGCGCCGAGCG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGCTACGACACCGGACCGTTCGCGCCGAGCG 60
QY 61 CTCGTCACGCGAGGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGCATGCTTCAAGCGC 120
DB 61 CTGGGTCAAGGAAGGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGCATGCTTCAAGCGC 120
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QY 121 GGCATCGAAGGCGCGTCGAGGCCGTCCTCCGCGCCCTCTCGAGCAGCGGAGGATGTC 180
DB 121 GGCATCGAAGGCGCGTCGAGGCCGTCCTCCGCGCCCTCTCGAGCAGCGGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCGACGGCTTCATCTCGCGCCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCGACGGCTTCATCTCGCGCCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTTAC 420
DB 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTTAC 420
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RESULT 47

ADV99179
ID ADV99179 standard; DNA; 420 BP.

XX
AC ADV99179;

XX
DT 24-MAR-2005 (first entry)

XX
DE groEL2 gene fragment, SEQ ID 59.

XX
KW Microorganism identification; microorganism detection; groEL2;

XX
KW potato scab; gene; ds.

XX
OS Streptomyces scabiei.

XX
PN US2004265873-A1.

XX
PD 30-DEC-2004.

XX
PF 15-APR-2004; 2004US-00824527.

XX
PR 18-APR-2003; 2003KR-00024656.

XX
PR 14-NOV-2003; 2003KR-00080580.

XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX
WPI; 2005-089568/10.

XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces species, useful in identifying the genus Streptomyces, and for isolating or purifying natural products using such microorganisms.

XX
PS Claim 4; SEQ ID NO 59; 34pp; English.

XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment derived from a potato scab pathogenic microorganism (ADV99163-ADV99181). CC Potato scab is a pathogenic disease caused by certain Streptomyces species. Primers ADV99121 and ADV99122 are useful in a method for CC identifying Streptomyces species, comprising amplifying groEL2 gene CC fragment of target strain, analyzing the nucleotide sequence of groEL2 CC gene fragment amplified, and comparing the nucleotide sequence obtained CC with that of groEL2 gene fragment of a reference strain.

SQ Sequence 420 BP; 83 A; 142 C; 141 G; 54 T; 0 U; 0 Other;

Query Match 88.6%; Score 372; DB 14; Length 420;
Best Local Similarity 92.9%; Pred. No. 6.8e-53;

XX PS Claim 4; SEQ ID NO 44; 34pp; English.

XX CC The present invention relates to novel primers STGR0F1 (ADV99121) and

CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of

CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment

CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces

CC species. Primers ADV99121 and ADV99122 are useful in a method for

CC identifying Streptomyces species, comprising amplifying groEL2 gene

CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC gene fragment amplified, and comparing the nucleotide sequence obtained

CC with that of groEL2 gene fragment of a reference strain.

XX SQ Sequence 420 BP; 82 A; 142 C; 142 G; 54 T; 0 U; 0 Other;

Query Match 88.6%; Score 372; DB 14; Length 420;

Best Local Similarity 92.9%; Pred. No. 6.8e-53;

Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 AAGAACGACGACGACGCTCCGGTGACGGTACGACCAACCGATGGCTCTCAAGCGC 60

DB |||||

QY 1 AAGAACGACGACGACGCTCCGGTGACGGTACGACCAACCGATGGCTCTCAAGCGC 60

DB |||||

QY 61 CTCGTACGCGAGGGCTCGCAACGTCGCGCGCGTGCACCGATGGCTCTCAAGCGC 120

DB |||||

QY 61 CTGGTCCGCGAGGGCTCGCAACGTCGCGCGCGTGCACCGATGGCTCTCAAGCGC 120

DB |||||

QY 121 CGCATCGAGAGCGCTCGAGCGCGTCTCCGCGCGCTCGTGCAGCGAGGATGTC 180

DB |||||

QY 121 GGTATCGAGAGCGCTCGAGCGCGTCTCCGCGCGCTCGTGCAGCGAGGATGTC 180

DB |||||

QY 181 GAGACCAAGAGGAGATCGCTTCCAGCGCTCCATCTCCGCGCGGACACCCAGATCGGC 240

DB |||||

QY 181 GAGACCAAGAGGAGATCGCTTCCAGCGCTCCATCTCCGCGCGGACACCCAGATCGGC 240

DB |||||

QY 241 GAGCTCATCGCGAGCGATGACACAGTTCGCGAGGAGGCTCATCAAGCTCGAGGAG 300

DB |||||

QY 241 GAGCTCATCGCGAGCGATGACACAGTTCGCGAGGAGGCTCATCAAGCTCGAGGAG 300

DB |||||

QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGCTTCGACAGGGCTAC 360

DB |||||

QY 301 TCGAGACCTTCGCGCTTGAGCTTACCGAGGGATCGCTTCGACAGGGCTAC 360

DB |||||

QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGCTCGCTCGACACCCGTAC 420

DB |||||

QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGCTCGCTCGACACCCGTAC 420

DB |||||

RESULT 50

ADV99125

ID ADV99125 standard; DNA; 420 BP.

XX AC ADV99125;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 5.

XX KW Microorganism identification; microorganism detection; groEL2;

XX KW potato scab; gene; db.

XX OS Streptomyces alanosinicus.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX XX

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX DR WPI; 2005-089568/10.

XX PT New primer specifically amplifying groEL2 gene fragment of Streptomyces

XX PT species, useful in identifying the genus Streptomyces, and for isolating

XX PT or purifying natural products using such microorganisms.

XX PS Claim 3; SEQ ID NO 5; 34pp; English.

XX CC The present invention relates to novel primers STGR0F1 (ADV99121) and

CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of

CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment

CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces

CC species. Primers ADV99121 and ADV99122 are useful in a method for

CC identifying Streptomyces species, comprising amplifying groEL2 gene

CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC gene fragment amplified, and comparing the nucleotide sequence obtained

CC with that of groEL2 gene fragment of a reference strain.

XX SQ Sequence 420 BP; 86 A; 144 C; 137 G; 53 T; 0 U; 0 Other;

Query Match 88.2%; Score 370.4; DB 14; Length 420;

Best Local Similarity 92.6%; Pred. No. 1.3e-52;

Matches 389; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 AAGAACGACGACGACGCTCCGGTGACGGTACGACCAACCGATGGCTCTCGCCAGGCG 60

DB |||||

QY 1 AAGAACGACGACGACGCTCCGGTGACGGTACGACCAACCGATGGCTCTCGCCAGGCG 60

DB |||||

QY 61 CTCTGATCGAGAGGCGCTCGCAACGTCGCGCGCGTGCACCGATGGCTCTCAAGCGC 120

DB |||||

QY 61 CTGTCAGAGGAGGCGCTCGCAACGTCGCGCGCGTGCACCGATGGCTCTCAAGCGC 120

DB |||||

QY 121 GGCATCGAGAGGCGCTCGAGCGCGTCTCCGCGCGCTCGTGCAGCGAGGATGTC 180

DB |||||

QY 121 GGTATCGAGAGGCGCTCGAGCGCGTCTCCGCGCGCTCGTGCAGCGAGGATGTC 180

DB |||||

QY 181 GAGACCAAGAGGAGATCGCTTCCAGCGCTCCATCTCCGCGCGGACACCCAGATCGGC 240

DB |||||

QY 181 GAGACCAAGAGGAGATCGCTTCCAGCGCTCCATCTCCGCGCGGACACCCAGATCGGC 240

DB |||||

QY 241 GAGCTCATCGCGAGGCGATGACACAGTTCGCGAGGAGGCTCATCAAGCTCGAGGAG 300

DB |||||

QY 241 GAGCTCATCGCGAGGCGATGACACAGTTCGCGAGGAGGCTCATCAAGCTCGAGGAG 300

DB |||||

QY 301 TCCGAGACCTTCGCTTCGAGCTGAGCTCACCGAGGGTATCGCTTCGACAGGGCTAC 360

DB |||||

QY 301 AGCAACACCTTCGCTTCGAGCTTACCGAGGGATCGCTTCGACAGGGCTAC 360

DB |||||

QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGCTCGCTCGACACCCGTAC 420

DB |||||

QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGCTCGCTCGACACCCGTAC 420

DB |||||

RESULT 51

ADV99127

ID ADV99127 standard; DNA; 423 BP.

XX AC ADV99127;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 7.

XX KW Microorganism identification; microorganism detection; groEL2;

XX KW potato scab; gene; ds.

XX OS Streptomyces albofaciens.

XX XX

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PN US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 7; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX Sequence 423 BP; 82 A; 149 C; 138 G; 54 T; 0 U; 0 Other;
XX Query Match 88.1%; Score 370.2; DB 14; Length 423;
XX Best Local Similarity 93.9%; Pred. No. 1.4e-52;
XX Matches 397; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 1 AAGNAGACGACGACGTCGCGGTGACGGTACGACACCGCGACCGTCTCGCCCGAGGG 60
DB 1 AAGNAGACGACGACGTCGCGGTGACGGTACGACACCGCGACCGTCTCGCCCGAGGG 60
QY 61 CTGCT---ACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 117
DB 61 CTGCTACACGGGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 120
QY 118 CGCGGCATCGAGAAGCGCGTCGAGGCGCTCTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 177
DB 121 CGCGGTATCGAGAAGCGCGTCGAGGCGCTCTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 180
QY 178 GTGAGACCGAGGACGATCGCTTCCACCGCGCTCCATCTCCGCGCGCGGTGCCAACCGATG 237
DB 181 GTGAGACCGAGGACGATCGCTTCCACCGCGCTCCATCTCCGCGCGCGGTGCCAACCGATG 240
QY 238 GCGAGCTCATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGCTCATCCGCTCGAG 297
DB 241 GCGAGCTCATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGCTCATCCGCTCGAG 300
QY 298 GAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGGC 357
DB 301 GAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGGC 360
QY 358 TACATCTCGGCGTACTTCGCGCACCGACATGAGGCGGATGAGGGGTGCTTCGAGGACCG 417
DB 361 TACATCTCGGCGTACTTCGCGCACCGACATGAGGCGGATGAGGGGTGCTTCGAGGACCG 420
QY 418 TAC 420
DB 421 TAC 423
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RESULT 52
ADV99150

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ID ADV99150 standard; DNA; 423 BP.
XX ADV99150;
XX 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 30.
XX Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
XX Streptomyces erumpens.
XX OS US2004265873-A1.
XX PN 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 30; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX Sequence 423 BP; 84 A; 147 C; 137 G; 55 T; 0 U; 0 Other;
XX Query Match 87.8%; Score 368.6; DB 14; Length 423;
XX Best Local Similarity 93.6%; Pred. No. 2.5e-52;
XX Matches 396; Conservative 0; Mismatches 24; Indels 3; Gaps 1;
QY 1 AAGNAGACGACGACGTCGCGGTGACGGTACGACACCGCGACCGTCTCGCCCGAGGG 60
DB 1 AAGNAGACGACGACGTCGCGGTGACGGTACGACACCGCGACCGTCTCGCCCGAGGG 60
QY 61 CTGCT---ACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 117
DB 61 CTGCTACACGGGAGGCGCTTGCACACGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 120
QY 118 CGCGGCATCGAGAAGCGCGTCGAGGCGCTCTCGCGCGCGGTGCCAACCGATGGCGAAGGAT 177
DB 121 CGCGGTATCGAGAAGCGCGTCGAGGCGCTCTCGCGCGCGGTGCCAACCGATGGCGAAGGAT 180
QY 178 GTGAGACCGAGGACGATCGCTTCCACCGCGCTCCATCTCCGCGCGCGGTGCCAACCGATG 237
DB 181 GTGAGACCGAGGACGATCGCTTCCACCGCGCTCCATCTCCGCGCGCGGTGCCAACCGATG 240
QY 238 GCGAGCTCATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGCTCATCCGCTCGAG 297
DB 241 GCGAGCTCATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGCTCATCCGCTCGAG 300
QY 298 GAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGGC 357
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Db 301 GAGTCCAGACCTTCGGTCTGGAGCTGGAACTCACCAGGGGTATGCGCTTCGACAAAGGGC 360
QY 358 TACATCTCGCGCTACTTCGCCACCGCATGAGCGGATGAGGCGTTCGCTCGACGACCCG 417
Db 361 TACATCTCGCGCTACTTCGCCACCGCATGAGCGGATGAGGCGGCTCGACGACCCG 420
QY 418 TAC 420
Db 421 TAC 423

RESULT 53
ADV99124
ID ADV99124 standard; DNA; 420 BP.
XX
AC ADV99124;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 4.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces aculeolatus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 4; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 85 A; 145 C; 141 G; 49 T; 0 U; 0 Other;

Query Match 87.0%; Score 365.6; DB 14; Length 420;
Best Local Similarity 91.9%; Pred. No. 7.8e-52;
Matches 386; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCAGTCGCGCGTACCGGTACGACACCGGACCGGTCGCTCGCCAGCGC 60
Db 1 AAGAGACGAGCAGTCGCGCGTACCGGTACGACACCGGACCGGTCGCTCGCCAGGCC 60
QY 61 CTCGTACCGAGGGCGCTCGCAACTCGCGCGGTGCAACCCGATGCTCTCAAGCGC 120
Db 61 CTGTGTCAAGAGGGCGCTCGGNACGTGGCGCGCGCGCGCAACCCGATGCGCTGAGCGC 120
QY 121 GGCATCGAAGGCGGCTCGAGGCGCTCTCCGCGCGCTCTCGAGCAGGCGAAGGATGTC 180
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Db 121 GGCATCGAAGGCGGACCGAGGCGCTCTCCGCGCGCTCTCGAGCAGGCGCAAGGACGTG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGGATGGAACAAGGTGCGCAAGGAAGGCGTTCATCACCGTCCAGGAG 300
Db 241 GAGCTGATCGCGAGGCGGATGGAACAAGGTGCGCAAGGAAGGCGTTCATCACCGTCCAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGAGCTCACCAGGGGTATGCGCTTCGACAAAGGCGCTAC 360
Db 301 TCGCAGACCTTCGGGCTGAGCTTACCGAGGGCATGCGCTTCGACAAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTTCGAGACCGCTAC 420
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RESULT 54

ADV99153

ID ADV99153 standard; DNA; 420 BP.

XX AC ADV99153;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 33.

XX KW Microorganism identification; microorganism detection; groEL2;

XX KW potato scab; gene; ds.

XX OS Streptomyces griseochromogenes.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces species, useful in identifying the genus Streptomyces, and for isolating or purifying natural products using such microorganisms.

Claim 3; SEQ ID NO 33; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment derived from a potato scab pathogenic microorganism (ADV99163-ADV99181). Potato scab is a pathogenic disease caused by certain Streptomyces species. Primers ADV99121 and ADV99122 are useful in a method for identifying Streptomyces species, comprising amplifying groEL2 gene fragment of target strain, analyzing the nucleotide sequence of groEL2 gene fragment amplified, and comparing the nucleotide sequence obtained with that of groEL2 gene fragment of a reference strain.

SQ Sequence 420 BP; 86 A; 147 C; 136 G; 51 T; 0 U; 0 Other;

Query Match 86.3%; Score 362.4; DB 14; Length 420;

Best Local Similarity 91.4%; Pred. No. 2.6e-51;

Matches 384; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTACGACACCGACCGGCTTCTCGCCAGGCG 60
DB |||||
1 AAGAAGACGACGACGTCGCGGTGACGCTACGACACCGACCGGCTTCTCGCCAGGCG 60
QY 61 CTCGTAGCGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
DB |||||
61 CTGGTCAAGGAAGGCGCTCCGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAAGAGCGCTGCGAGGCGCTTCCGCGCGCTGCTGAGCAGGCGGAGGATGTC 180
DB |||||
121 GGTATCGAAGAGCGCTGCGAGGCGCTTCCGCGCGCTGCTGAGCAGGCGGAGGACGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 240
DB |||||
181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 240
QY 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGATGCGCAAGGATGCGCAAGGATGCG 300
DB |||||
241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGATGCGCAAGGATGCGCAAGGATGCG 300
QY 301 TCCGAGACCTTCGCTGAGGCTGAGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 360
DB |||||
301 AGCAACACCTTCGCTGAGGCTGAGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 360
QY 361 ATCTCGGCGTACTTTCGCGACCGACGATGAGCGGATGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCT 420
DB |||||
361 ATCTCGGCGTACTTTCGCGACCGACGATGAGCGGATGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCT 420

RESULT 55

ADV99159
ID ADV99159 standard; DNA; 423 BP.
XX
AC ADV99159;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 39.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces murinus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 39; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 423 BP; 86 A; 148 C; 134 G; 55 T; 0 U; 0 Other;

Query Match 86.2%; Score 362.2; DB 14; Length 423;
Best Local Similarity 92.7%; Pred. No. 2.9e-51;
Matches 392; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTACGACACCGACCGGCTTCTCGCCAGGCG 60
DB |||||
1 AAGAAGACGACGACGTCGCGGTGACGCTACGACACCGACCGGCTTCTCGCCAGGCG 60
QY 61 CTCGT---ACGCGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAG 117
DB |||||
61 CTGGTCAAGGAAGGCGCTTCCGCGCGCTGCGCAACCGGATGGCTCTCAAG 120
QY 118 CGCGGCTATCGAAGAGGCGCTTCCAGGCGCTTCCGCGCGCTTCCAGGCGCTTCCAGGCGCT 177
DB |||||
121 CGCGGCTATCGAAGAGGCGCTTCCAGGCGCTTCCGCGCGCTTCCAGGCGCTTCCAGGCGCT 180
QY 178 GTCGAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 237
DB |||||
181 GTCGAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 240
QY 238 GCGGAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGATGCGCAAGGATGCGCAAGGATGCG 297
DB |||||
241 GCGGAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGATGCGCAAGGATGCGCAAGGATGCG 300
QY 298 GAGTCCCGACACCTTCGCTGAGGCTGAGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 357
DB |||||
301 GAGGCAACACCTTCGCTGAGGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCT 360
QY 358 TACATCTCGCGTACTTTCGCGACCGACATGAGCGGATGAGCGGCTTCCAGGCGCTTCCAGGCGCT 417
DB |||||
361 TACATCTTCGCGTACTTTCGCGACCGACATGAGCGGATGAGCGGCTTCCAGGCGCTTCCAGGCGCT 420
QY 418 TAC 420
DB |||||
421 TAC 423

RESULT 56

ADV99130
ID ADV99130 standard; DNA; 420 BP.
XX
AC ADV99130;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 10.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces albus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces

PT species, useful in identifying the genus *Streptomyces*, and for isolating
XX or purifying natural products using such microorganisms.

PS Claim 3; SEQ ID NO 10; 34pp; English.

XX The present invention relates to novel primers STGR0F1 (ADV99121) and
XX STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC *Streptomyces* species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain *Streptomyces*
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying *Streptomyces* species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 420 BP; 83 A; 143 C; 139 G; 55 T; 0 U; 0 Other;

Query Match 85.9%; Score 360.8; DB 14; Length 420;
Best Local Similarity 91.2%; Pred. No. 4.9e-51;
Matches 383; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 AAGAACGACGACGACGTCGCGGTGACGCTACGACACCGCGACCGCTTCGCCCCAGGCG 60

DB 1 AAGAACGACGACGACGTCGCGGTGACGCTACGACACCGCGACCGCTTCGCCCCAGGCG 60

QY 61 CTGCTACGCGAGGCGCTGCGCAACGTCGCGCGCGTGCCAAACCGCATGCTCTCAAGCGC 120

DB 61 CTGCTACGCGAGGCGCTGCGCAACGTCGCGCGCGTGCCAAACCGCATGCTCTCAAGCGC 120

QY 121 GGCATCGAAGGCGCTGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180

DB 121 GGCATCGAAGGCGCTGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCACACCCAGATCGGC 240

DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCACACCCAGATCGGC 240

QY 241 GAGCTCATCGCGAGGCGATGGACAAAGGTGCGCAAGGAGGCGTCATCACCCGTCGAGGAG 300

DB 241 GAGCTCATCGCGAGGCGATGGACAAAGGTGCGCAAGGAGGCGTCATCACCCGTCGAGGAG 300

QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360

DB 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360

QY 361 ATCTCGGCGTACTTCCGACCGACATGGAGCGGATGGAGGCGTCGCTCGACACCGCTAC 420

DB 361 ATCTCGGCGTACTTCCGACCGACATGGAGCGGATGGAGGCGTCGCTCGACACCGCTAC 420

RESULT 57

ADV99132

ID ADV99132 standard; DNA; 420 BP.

XX

AC ADV99132;

XX 24-MAR-2005 (first entry)

XX groEL2 gene fragment, SEQ ID 12.

XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX *Streptomyces* cacaoti subsp. cacaoti.

OS US2004265873-A1.

PN 30-DEC-2004.

XX 15-APR-2004; 2004US-00824527.

XX 18-APR-2003; 2003KR-00024656.

PR 14-NOV-2003; 2003KR-00080580.

XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of *Streptomyces*
PT species, useful in identifying the genus *Streptomyces*, and for isolating
PT or purifying natural products using such microorganisms.

PS Claim 3; SEQ ID NO 12; 34pp; English.

XX The present invention relates to novel primers STGR0F1 (ADV99121) and
CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC *Streptomyces* species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain *Streptomyces*
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying *Streptomyces* species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX Sequence 420 BP; 83 A; 148 C; 138 G; 51 T; 0 U; 0 Other;

Query Match 85.5%; Score 359.2; DB 14; Length 420;

Best Local Similarity 91.0%; Pred. No. 8.9e-51;

Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 AAGAACGACGACGACGTCGCGGTGACGCTACGACACCGCGACCGCTTCGCCCCAGGCG 60

DB 1 AAGAACGACGACGACGTCGCGGTGACGCTACGACACCGCGACCGCTTCGCCCCAGGCG 60

QY 61 CTCGTACCGGAGGCGCTCGGCAACGTCGCGCGCGTGCCAAACCCGATGCTCTCAAGCGC 120

DB 61 CTCGTACCGGAGGCGCTCGGCAACGTCGCGCGCGTGCCAAACCCGATGCTCTCAAGCGC 120

QY 121 GGCATCGAAGGCGCTGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180

DB 121 GGCATCGAAGGCGCTGAGGCGCTCTCGGCGCCCTCTGAGGAGGCGCAAGGATGTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCACACCCAGATCGGC 240

DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCACACCCAGATCGGC 240

QY 241 GAGCTCATCGCGAGGCGATGGACAAAGGTGCGCAAGGAGGCGTCATCACCCGTCGAGGAG 300

DB 241 GAGCTCATCGCGAGGCGATGGACAAAGGTGCGCAAGGAGGCGTCATCACCCGTCGAGGAG 300

QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360

DB 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360

QY 361 ATCTCGGCGTACTTCCGACCGACATGGAGCGGATGGAGGCGTCGCTCGACACCGCTAC 420

DB 361 ATCTCGGCGTACTTCCGACCGACATGGAGCGGATGGAGGCGTCGCTCGACACCGCTAC 420

RESULT 58

ACF04295

ID ACF04295 standard; DNA; 604 BP.

XX

AC ACF04295;

XX 06-NOV-2003 (first entry)

XX M phlei hsp65 gene fragment.

XX Mycobacterium; hsp65; heat shock protein 65; identification;
KW tuberculosis; gene; ds.
XX

Db 361 ATCTCGTGTACTTCGCGACCGGACCGGAGCGTTCAGGAAGCGTCTCGAGGATCGGTAC 420

RESULT 60

ACC70275

ID ACC70275 standard; DNA; 1626 BP.

XX AC ACC70275;

XX 11-AUG-2003 (first entry)

XX Nucleotide sequence of the Rhodococcus equi GroEL2 protein.

XX GroEL protein; protein aggregation; protein folding; immune response;

XX antigen; pathogenic infection; gene; ss.

XX Rhodococcus equi.

XX Key

XX CDS 1

XX Location/Qualifiers

XX /*tag= a

XX /product= "GroEL2"

XX WO2003035676-A1.

XX 01-MAY-2003.

XX 25-OCT-2002; 2002WO-AU001460.

XX 26-OCT-2001; 2001AU-00008523.

XX (UYSA-) UNIV SOUTH AUSTRALIA.

XX (MEDV-) MEDVET SCI PTY LTD.

XX (RURA-) RURAL IND RES & DEV CORP.

XX Vanniasinkam T, Barton M, Heuzenroeder MW;

XX WPI; 2003-482030/45.

XX P-PSDB; ABR55530.

XX New GroEL protein, useful for preparing a composition for preventing or

XX treating pathogenic infections.

XX Disclosure; Fig 1; 77pp; English.

XX The present sequence encodes a GroEL protein. The groEL2 gene is highly

XX conserved between species, and the protein facilitates the correct

XX folding of various bacterial proteins as well as prevent the aggregation

XX of denatured proteins by an ATP-dependent mechanism. The specification

XX describes a chimeric protein, consisting of a GroEL protein which has a

XX modification or analogue comprising a surface exposed exogenous amino

XX acid sequence inserted to it. The exogenous amino acid sequence is

XX configured to elicit an immune response specifically reactive to the

XX antigenic determinant. The chimeric protein is useful for preparing a

XX composition for preventing or treating pathogenic infections

XX Sequence 1626 BP; 300 A; 544 C; 549 G; 233 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 76.4%; Score 320.8; DB 9; Length 1626;

XX Matches 358; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 AAGAGAGCGGAGCGTCCGCGTACGCGTACGCGACCGGACCGGTCCTCGCCCGGCG 60

Db 232 AAGAGAGCGGAGCGTCCGCGTACGCGTACGCGACCGGTCCTCGCCCGGCG 291

QY 61 CTCGTACCGGAGCGGCTCGCAACCGTCGCGCGCGTGCACACCGGATGGCTCTCAAGCGC 120

Db 292 CTCGTCCGCGAGGCGCTGGCAACCGTCGTCGCGCGCGCCACCGCTGGGTCTGAGCGC 351

QY 121 GGCATCGAGAGGCGCGTTCGAGCGCGTTCGCGCGCGCTTCGCGAGCGCGAAGGATGTC 180

Db 352 GGCATCGAGAGGCGCGTTCGAGCGCGTTCACCGCAAGCTGCTCGACACCGCCCAAGGAGGTC 411

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCGCGCGCGGACACCCAGATCGGC 240

Db 412 GAGACCAAGGAGCAGATCGCTCCACCGCGGGATCTCGCGGGGCGACTTCCACGATCGGC 471

QY 241 GAGCTCATCGCGAGGCGGATGGAACAAGGTTCGCAAGGAAAGGCGTTCATCACCGTCGAGGAG 300

Db 472 GAGCTCATCGCGAGGCGGATGGAACAAGGTTCGCAAGGAAAGGCGTTCATCACCGTCGAGGAG 531

QY 301 TCCGAGACCTTCGGTCTGGAGCTGAGCTCACCAGGGGTATGCGCTTCGACAGGGGCTAC 360

Db 532 TCGAACTCCTTCGGCTTCGAGCTCAGCTCACCAGGGGTATGCGCTTCGACAGGGGCTAC 591

QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGGAGGCGTTCGCTCGACGACCGGTAC 420

Db 592 ATCTCGGCGTACTTCGCCACCGACGCGCGGCGTTCAGGAAGGCGTTCCTCGAGGATCGGTAC 651

Search completed: April 1, 2006, 22:21:36
Job time : 855.578 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:06:31 ; Search time 5784.96 Seconds
(without alignments)
3396.840 Million cell updates/sec

Title: US-10-824-527-43

Perfect score: 420

Sequence: 1 aagaagacgagacgtgc.....cgtcgtcgacgaccgtac 420

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gsa1: *
10: gb_gsa2: *
11: gb_gsa3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	195.2	46.5	817	10	CG811365
2	185.6	44.2	652	8	DR606790
3	185.6	44.2	696	8	DR606213
4	185.6	44.2	918	8	DR649351
5	179	42.6	639	7	CO377844
6	173.6	41.3	690	6	CF712525
7	173.6	41.3	738	6	CF693874
8	173.6	41.3	741	6	CF718151
9	173.6	41.3	749	6	CF682602
10	173.6	41.3	752	6	CF693560
11	173.6	41.3	760	6	CF692108
12	173.6	41.3	763	6	CF676179
13	173.6	41.3	766	6	CF722454
14	173.6	41.3	767	6	CF710636
15	173.6	41.3	768	6	CF709888
16	173.6	41.3	773	6	CF701856
17	173.6	41.3	776	6	CF702480
18	173.6	41.3	778	6	CF681781
19	173.6	41.3	779	6	CF695095
20	173.6	41.3	790	6	CF694632
21	173.6	41.3	797	6	CF713816
22	173.6	41.3	801	6	CF703574

RESULT 1

CG811365/c 817 bp DNA linear GSS 13-NOV-2003
LOCUS PSAT60TR LargeInsertGenomicLibrary Fusarium virguliforme genomic
clone KMV5J24, genomic survey sequence.
DEFINITION CG811365.1 GI:38264839
ACCESSION CG811365
VERSION CG811365
KEYWORDS GSS.
SOURCE Fusarium virguliforme
ORGANISM Fusarium virguliforme
Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
Hypocnemycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 817)
AUTHORS Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J.,
Lightfoot, D. A. and Town, C. D.
TITLE End sequencing of BACs from a fingerprint physical map of the
causative agent of soybean sudden death syndrome, Fusarium
virguliforme
JOURNAL Unpublished (2003)
COMMENT Other GSSs: FSAAT60TF
Contact: Chris Town and K. Meksem
The Center of Excellence in Soybean Research, Teaching and
Outreach, Southern Illinois University at Carbondale and Plant
Genomics, The Institute for Genomic Research
Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415,
USA and 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 618 453 3103 and 301-838-3523
Fax: 618 453-7457 and 301-838-0208
Email: meksem@siu.edu; cdtown@tigr.org (URL:
http://Fusariumvirguliform.siu.edu)

ALIGNMENTS

23	173.6	41.3	801	6	CF709185
24	173.6	41.3	803	6	CF713651
25	173.6	41.3	804	6	CF711476
26	173.6	41.3	815	6	CF703324
27	173.6	41.3	820	6	CF699756
28	173.6	41.3	827	6	CF687348
29	173.6	41.3	831	6	CF713573
30	173.6	41.3	833	6	CF701087
31	173.6	41.3	834	6	CF696500
32	173.6	41.3	861	6	CF690854
33	173.6	41.3	869	6	CF699606
34	173.6	41.3	872	6	CF695217
35	173.6	41.3	874	6	CF719528
36	173.6	41.3	877	6	CF706367
37	173.6	41.3	878	6	CF682687
38	173.6	41.3	881	6	CF700757
39	173.6	41.3	891	6	CF696919
40	173.6	41.3	901	6	CF719458
41	173.6	41.3	910	6	CF716339
42	173.6	41.3	921	6	CF711999
43	173.2	41.2	716	6	CF716527
44	173.2	41.2	759	6	CF687310
45	173.2	41.2	794	6	CF679031
46	172	41.0	758	6	CF707648
47	172	41.0	796	6	CF697914
48	171.6	40.9	746	6	CF714926
49	171.2	40.8	752	7	CK446096
50	170.8	40.7	724	6	CF707221
51	170.8	40.7	731	6	CF704854
52	170.6	40.6	707	6	CF689741
53	170.6	40.6	778	6	CF691132
54	170.6	40.6	840	6	CF708616
55	168.8	40.2	799	6	CF711662
56	168.8	40.2	851	6	CF698612
57	165.8	39.5	653	7	CF843128
58	165	39.3	393	6	CF640823
59	162.6	38.7	698	8	CV899250
60	162.6	38.7	757	6	CF697565

Seq primer: CAGGAACACTATGACC
Class: BAC ends.

FEATURES

source
1. .817
Location/Qualifiers
/organism="Fusarium virguliforme"
/mol_type="genomic DNA"
/cultivar="Monticello"
/db_xref="taxon:232082"
/clone="KMV5J24"
/clone_lib="LargeInsertGenomicLibrary"
/notes="Organ: Hyphae; Vector: pINDIGOBAC5; A single spore derived culture was used. Hyphae were grown in an incubator for four days. Nuclei were isolated and embedded in agarose, restriction digested with Hind III. Large size DNA fragments were ligated in vector pINDIGOBAC5 and electro-transformed into DH10B cells."

ORIGIN

Query Match 46.5%; Score 195.2; DB 10; Length 817;
Best Local Similarity 68.5%; Pred. No. 1.5e-30;
Matches 285; Conservative 0; Mismatches 128; Indels 3; Gaps 1;
QY 4 AAGACGACGACGCTCGCGGTGACGATACGACCGACCGGCTTCTCGCCAGGGGCTC 63
DB 683 AAGACCAACGAGTTCGCGGTGACGATACGACCGGCACTGCTTCGCGCGGCATC 624
QY 64 GTACGGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGGGC 123
DB 623 TTCTCCGAGACCGTCAAGAACGTCGCGCGGTGCAACCCCATGACATTCGACGCGGT 564
QY 124 ATCGAGAGGCGCTCGAGGCGGCTCGCGCGGCTGTCGAGGAGGAGGATGTCGAG 183
DB 563 ATCAGGCTCGGTCGAGGCGGCTGTCGAGTTCCTCAGAAGAACAAAGCGGGACATACC 504
QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 503 ACCAGCGCGAGATCGCTCAGTTCGCGCACCATCTCCGCCAACGGTGAAGTTCATTTGGT 444
QY 241 GAGCTCATTCGCGAGGCGATGGAACAGGTTCGGAAGAACGGGTATCATCGCTCGAGGAG 300
DB 443 GAGATGATTGCCAACGCGATGGAAGGTTCGGAAGGAGGTGTCTCATCTGTCGAGGAG 384
QY 301 TCCGACGCTTCGCTTCGAGCTGAGCTCAGCGAGGATGCGCTTCGACGAGGCTAC 360
DB 383 GCGAAGACCGTCCAGGATGAGCTCGAGGTACCGAGGGATGCGATTCGACCGGTGCTTC 324
QY 361 ATCTCGGCGTACTTCGCGCACCGCATGAGCGGATGAGCGGTGCGCTTCGACGACCC 416
DB 323 GTCTCTCTCTACTTCATCACCGACACCAAGTCCAGAGGTTCGAGTTTGAGAACCC 268

RESULT 2
DR606790
LOCUS
DEFINITION EST996918 FvG Gibberella moniliformis cDNA clone FVGBQ50, mRNA
sequence.
ACCESSION DR606790
VERSION DR606790.1 GI:70681438
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis

REFERENCE 1 (bases 1 to 652)
AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Uterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.P., Town, C.D., and Whitelaw, C.A.

TITLE Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAUR
USDA

1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVGBQ50TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

source
1. .652
Location/Qualifiers
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVGBQ50"
/tissue_type="mycelia"
/clone_lib="FvG"
/note="Vector: pBlueScript II SK(+); Site: 1: EcoRI; Site 2: XhoI; anamorph: Fusarium verticillioides. Mycelia was collected after growth in liquid GYM medium for 96 hours. Cultures were vacuum filtered and the mycelial mats were frozen in liquid nitrogen, ground to a powder, and then added to Trizol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml Trizol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 44.2%; Score 185.6; DB 8; Length 652;
Best Local Similarity 67.1%; Pred. No. 1.5e-28;
Matches 279; Conservative 0; Mismatches 134; Indels 3; Gaps 1;
QY 4 AAGACGAGCAGCTCGCGGTGACGATACGACCGACCGGCTTCTCGCCAGGGGCTC 63
DB 98 AAGACCAACGAGTTCGCGGTGACGATACGACCGGCTTCTCGCGGTGCAATC 157
QY 64 GTACGGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGGGC 123
DB 158 TTCTCCGAGACCGTCAAGAACGTTGCGGTGCAACCTATGACCTCGCGCGGT 217
QY 124 ATCGAGAGGCGCTCGAGGCGGTCTCGGGGCGCTCTCGAGGAGGAGGATGTCGAG 183
DB 218 ATCAAGCTGCTGTTCGAGGCGGTGTCGAGTTCCTCAGAAGAACAAAGCGGTGATATACC 277
QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 278 ACCAGCGGTGAGATCGCTCAGTTCGCTCATCTCCGCCAACGGTATGTCACATCGGC 337
QY 241 GAGCTCATTCGCGAGGCGATGGAACAGGTTCGGAAGAACGGGTATCATCGCTCGAGGAG 300
DB 338 CAGATGATTGCCAACGCGCATGGAAGGTTCGGAAGGAGGTGTCTCATCTCACCTGCAAGGAG 397
QY 301 TCCGACGCTTCGCTTCGAGCTGAGCTCAGCGAGGATGCGCTTCGACAGGGCTAC 360
DB 398 GCGAAGACCGTTCGCGATGAGCTCGAGGTACCGAGGGATGCGATTCGACCGGTGCTTC 457
QY 361 ATCTCGGCGTACTTCGCGCACCGCATGAGCGGATGAGCGGTGCGCTTCGACGACCC 416
DB 458 GTCTCTCTCTACTTCATCACCGACACCAAGTCCAGAGGTTCGAGTTTGAGAACCC 513

RESULT 3

DR606213
LOCUS
DEFINITION EST996341 FvG Gibberella moniliformis cDNA clone FVGBJ59, mRNA
sequence.
ACCESSION DR606213
VERSION DR606213.1 GI:70680861
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
REFERENCE 1 (bases 1 to 696)
AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
 Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
 Unpublished (2005)
 Contact: Brown, D.W.
 USDA/ARS/NCAUR

TITLE
 JOURNAL
 COMMENT

USDA
 1815 N. University St, Peoria, IL 61604, USA
 Tel: 309 681 6230
 Fax: 309 681 6689
 Email: brown@ncaur.usda.gov
 TIGR sequence name: FVGBJ59TH
 Seq primer: AAT TAA CCC TCA CTA AAG GG.

FEATURES
 source

Location/Qualifiers
 1. .696
 /organism="Gibberella moniliformis"
 /mol_type="mRNA"
 /strain="m3125"
 /db_xref="taxon:117187"
 /clone="FVGBJ59"
 /tissue_type="mycelia"
 /clone_lib="FvG"
 /note="Vector: pBlueScript II SK(+), Site 1: EcoRI; Site 2: XhoI; anamorph: Fusarium verticillioides. Mycelia was collected after growth in liquid CYAM medium for 96 hours. Cultures were vacuum filtered and the mycelial mats were frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad, CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 44.2%; Score 185.6; DB 8; Length 696;
 Best Local Similarity 67.1%; Pred. No. 1.5e-28;
 Matches 279; Conservative 0; Mismatches 134; Indels 3; Gaps 1;
 QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTCTCGCCCGCGGCTC 63
 Db 96 AAGACCAACGAGGTGCGGTGACGGTACCGACCGGCTACCGTCTCGCCCGGCGATC 155
 QY 64 GTACCGGAGGCGCTCGGCAACGTCGCGCGGTGCAACCGGATGGCTCTCAAGCGGCG 123
 Db 156 TTCTCCGAGACCGTCAAGAACGTTGCGCGTGGCTGCAACCGCTATGACCTCGCGCGGT 215
 QY 124 ATCGAGAGGCGGTGAGGCGGTCTCGCGGCGCTGCTGGAGCGGCGAAGATGCGAG 183
 Db 216 ATCCAAAGCTGTGTGAGCGCGCTGCTGAGTTCTCCAGAGAACAAACGCGTATATACC 275
 QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCGCACACCGATCGGC 240
 Db 276 ACCAGCGTGAGATGCTCAGGTGCTACCATCTCGGCAACGGTGATGTCACATCGGC 335
 QY 241 GAGCTCATGCGGAGCGATGCAAGGTGCGCAAGGAGGCGTCATCACCGTCGAGGAG 300
 Db 336 CAGATGATGCGCAACCGCATGAGAAGGTGCGAAGGAGGCTGTCATCACCTGCAAGGAG 395
 QY 301 TCCGAGACCTTGGTCTGAGTGGAGTCAACCGGATGATGCGTTTCGACAGGGGTAC 360
 Db 396 GGAAGACCGTTGCGCGATGAGTTCGAGTCAACCGGATGATGCGATTCGACCGTGGCTTC 455
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTGCTCGAGGAGCC 416
 Db 456 GTCTCCCCCTACTTCATCCGACACCAAGTCCCAAGAGGTTCGAGTTTGAGAACCC 511

RESULT 4

DR649351
 LOCUS
 DEFINITION ES1039468 FvN Gibberella moniliformis cDNA clone FVNM52, mRNA
 sequence.
 accession
 DR649351

VERSION
 KEYWORDS
 SOURCE
 ORGANISM

DR649351.1 GI:70737826
 EST.
 Gibberella moniliformis
 Gibberella moniliformis
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE
 AUTHORS

1 (bases 1 to 918)
 Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
 Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
 Unpublished (2005)
 Contact: Brown, D.W.
 USDA/ARS/NCAUR

TITLE

JOURNAL
 COMMENT

USDA
 1815 N. University St, Peoria, IL 61604, USA
 Tel: 309 681 6230
 Fax: 309 681 6689
 Email: brown@ncaur.usda.gov
 TIGR sequence name: FVNM52TH
 Seq primer: AAT TAA CCC TCA CTA AAG GG.

FEATURES
 source

Location/Qualifiers
 1. .918
 /organism="Gibberella moniliformis"
 /mol_type="mRNA"
 /strain="m3125"
 /db_xref="taxon:117187"
 /clone="FVNM52"
 /tissue_type="mycelia"
 /clone_lib="FvN"
 /note="Vector: pBlueScript II SK(+), Site 1: EcoRI; Site 2: XhoI; anamorph: Fusarium verticillioides. Library was obtained from RNA derived from a corn meal medium culture of strain M-3125. These cultures were prepared by inoculating an autoclaved mixture of 25 g corn meal and 5 ml distilled water with 5 ml of water containing 5 x 10⁶ cfu. The inoculated medium was mixed thoroughly, distributed equally into two 100-mm plastic petri dishes, and incubated at room temperature for four or six days."

ORIGIN

Query Match 44.2%; Score 185.6; DB 8; Length 918;
 Best Local Similarity 67.1%; Pred. No. 1.5e-28;
 Matches 279; Conservative 0; Mismatches 134; Indels 3; Gaps 1;
 QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTCTCGCCCGCGGCTC 63
 Db 438 AAGACCAACGAGGTGCGGTGACGGTACCGACCGGCTACCGTCTCGCCCGGCGATC 497
 QY 64 GTACCGGAGGCGCTCGGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGGCG 123
 Db 498 TTCTCCGAGACCGTCAAGAACGTTGCGCGTGGCTGCAACCGCTATGAGACTCGCGCGGT 557
 QY 124 ATCGAGAGGCGGTGAGGCGGTCTCGCGGCGCTGCTGGAGCGGCGAAGATGTCGAG 183
 Db 558 ATCCAAAGCTGTGTGAGCGCGTCTCGAGTTCTCCAGAGAACAAACGCGTATATACC 617
 QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCGCACACCGATCGGC 240
 Db 618 ACCAGCGCTGAGATCGCTGAGTCAACCATCTCCCGCAACCGGTGATGTCACATCGGC 677
 QY 241 GAGCTCATCGCGAGGCGATGCAACGTCGCGGAGGAGGCGTCATCACCGTCGAGGAG 300
 Db 678 CAGATGATGCGCAACCGCATGAGAAGGTGCGAAGGAGGCTGTCATCACCTGCAAGGAG 737
 QY 301 TCCGAGACCTTGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGGGTAC 360
 Db 738 GGAAGACCGTTGCGGATGAGTTCAGGTCAACCGGAGGATGCGATTTCGACCGGTGCTTC 797
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGAGGATGAGGCGGTGCTCGAGGAGCC 416
 Db 798 GTCTCCCCCTACTTCATCCGACACCAAGTCCCAAGAGGTTCGAGTTTGAGAACCC 853

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RESULT 5
CO977844/c
LOCUS
DEFINITION
  CO977844 639 bp mRNA linear EST 11-FEB-2005
  BeZSPN11P12 BeZSPN Blastoclastiella emersonii cDNA clone BeZSPN11P12
  5' mRNA sequence.
ACCESSION
  CO977844
VERSION
  CO977844.1 GI:59296937
SOURCE
  EST.
ORGANISM
  Blastoclastiella emersonii
  Eukaryota; Fungi; Chytridiomycota; Blastocladiiales;
  Blastocladiaceae; Blastocladiella.
REFERENCE
  1 (bases 1 to 639)
  Ribichich, K.F., Salem-Izacc, S.M., Georg, R.C., Vencio, R.Z.N.,
  Navarro, L.D. and Gomes, S.L.
  Gene discovery and expression profile analysis through sequencing
  of expressed sequence tags from different developmental stages of
  the chytridiomycete Blastoclastiella emersonii
  Eukaryotic Cell 4 (2), 455-464 (2005)
  Contact: Gomes, Sueli Lopes
  Department of Biochemistry
  Institute of Chemistry, University of Sao Paulo
  Av. Prof. Lineu Prestes, 748, Sao Paulo, SP, 05508-900, BRASIL
  Tel: (55) 11-30913826
  Fax: (55) 11-30912186
  Email: sulgomes@ig.usp.br
PCR Primers
  FORWARD: T7 universal forward primer
  BACKWARD: SP6 universal reverse primer
  Plate: 11 row: F column: 12
  Seq primer: T7 universal forward primer
  High quality sequence stop: 639.
  Location/Qualifiers
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    /mol_type="mRNA"
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    /clone="BeZSPN11P12"
    /sex="Asexual"
    /dev_stage="Zoospore"
    /lab_host="E. coli DH5a cells (ampicillin resistant)"
    /clone_lib="BeZSPN"
    /notes="vector: pSPORT 1; Cloned unidirectionally, 5' end
    of the cDNA cloned into SalI / NotI site of pSPORT 1.
    Primer: Oligo (dT). Average insert size: 1 kb; Superscript
    Plasmid system -5' adaptor sequence: 5'CCACGGGTCG3' -3'
    adaptor sequence:
    5'GGCCGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT3'"

FEATURES
source
  1..639
  /organism="Blastoclastiella emersonii"
  /mol_type="mRNA"
  /strain="JEC21"
  /db_xref="taxon:40410"
  /clone_lib="CCAGO56"
  /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
  length, normalized library was prepared from a variety of
  conditions using RNA provided by Joseph Heitman and
  Jennifer Lodge"

ORIGIN
Query Match 42.6%; Score 179; DB 7; Length 639;
Best Local Similarity 65.9%; Pred. No. 3.6e-27;
Matches 276; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTCTCGCCGAGCG 60
DB 627 AACAAAGACCAACGAGGTGCGCGGTGACGGTACGACACACCGGACCGTCTCGCCGCGCC 568
QY 61 CTGTAGCGGAGGCGTTCGACAGCTGCGCGCGGTGCGACCGGATGGTCTCTAGCGC 120
DB 567 ATCTTCAACGAGGCGCTCAAGAACGTTGCGCGCGGTGCGAACCCGACGACCTCGCGCGC 508
QY 121 GGCAATCAGAAAGGCGGTGCGAGGCGGTCTCGCGCGCGTCTCGTGGAGCAGGCGAAGGATGTC 180
DB 507 GGTGTCAAGTGGCGGTGCGAGCGGTCTCAAGACCTCAAGAGAACCGCCGCGATGATC 448
QY 181 GAGACCAAGGACGACGATCGCTTCCACGGCTTCCATCTCCGC---CGCCGACACCCAGATC 237
DB 447 ACGTCGTCCGAGGAGGTGGCGGTGCGAGTCCGACCACTTTTCGGCCAAACGCGGACCGCACGTC 388
QY 238 GCGGAGCTCATCGCCGAGGCGGATGGACAGGTGCGGCAAGGAGCGTTCATCACCGTCGAG 297

```

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DB 387 GGCGCCCTGATCGCGAGGCCCATGAGAGGTTGGCAAGGAGGGGTTCATCAGCGTCCAG 328
QY 298 GAGTCCGACACCTTCGCTTGGAGCTGAGCTCACCAGGGGTATCGCTTCACAGGCGC 357
DB 327 GAGGCGAAGACCTCGAGGACGAGCTCCAGATCACCGAGGGGTATCGCTTTACCGCGGC 268
QY 358 TACATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTCGACGACCC 416
DB 267 TTCATCTCGCCCTACTTCATCCAGATGTCAAGGCCGACAGGTGAGTTCGAGAGCC 209

RESULT 6
CO9712525
LOCUS
DEFINITION
  CO9712525 690 bp mRNA linear EST 16-AUG-2004
  CCAGO56TR C.neoformans strain JEC21 Cryptococcus neoformans var.
  neoformans cDNA clone CCAGO56, mRNA sequence.
ACCESSION
  CO9712525
VERSION
  CO9712525.1 GI:41566684
KEYWORDS
  EST.
SOURCE
  Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
  var. neoformans)
  Cryptococcus neoformans var. neoformans
  Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
  Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
  Filobasidiella.
REFERENCE
  1 (bases 1 to 690)
  Loftus, B.
  End sequencing of clones from a Full length enriched, normalized
  JEC21 cDNA library
  Unpublished (2003)
  Other ESTs: CCAGO56TF
  Contact: Brendan Loftus
  The Institute for Genomic Research (TIGR; www.tigr.org)
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-3543
  Fax: 301-838-0208
  Email: bjloftus@tigr.org
  Seq primer: TR.
  Location/Qualifiers
    1..690
    /organism="Cryptococcus neoformans var. neoformans"
    /mol_type="mRNA"
    /strain="JEC21"
    /db_xref="taxon:40410"
    /clone_lib="CCAGO56"
    /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
    length, normalized library was prepared from a variety of
    conditions using RNA provided by Joseph Heitman and
    Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 690;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTCTCGCCGAGCGCTC 63
DB 270 AAGACCAACGACACTCGCGGTGACGGTACGACACCGGACCGTCTCGCCGCGGCGATC 329
QY 64 GTACGCGAGGCGTTCGCGCGGTGCGACCGTTCGCGGTCGCAACCCGATGCTCTCAAGCGCGC 123
DB 330 TACTCTGAGGGTGTGAAGACGTCGCTCGCGGTGCAACCCGATGACCTCTCGTGGAGGT 389
QY 124 ATCGAGAGGCGGTTCGAGGCGGTCTCGCGCGCTCTCGCGCGCTCTGAGCAGGCGAAGATGTCGAG 183
DB 390 GCCCAGAGGCTGTGCAAGGTTCTCGAGGTTCTTGTGTCGCAACAAAGAGGTATCACCC 449
QY 184 ACCAAGAGGACGATCGCTTCCACGGGCTTCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 450 ACCTCTGAGGAGATTGCCAGGTTCGCCATCCATCTCGCCCAACGCGGATACCCACGTCGCT 509

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QY 241 GAGCTCATCCGCGGATGACAGGTCGGCAAGGAGGCGCTCATCCGTCGAGGAG 300
 Db 510 GCATCATTCGCCAAGCCATGAGAGCGGTCCGCAAGGAGGCTCATCACTGTTAAGGAG 569
 QY 301 TCCAGACCTTCGCTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGCGTAC 360
 Db 570 GCGCGAACCATTCAGCAGGAGATTGAGATTACCGAGGGTATGCGCTTCGACCGAGGCTTC 629
 QY 361 ATCTCGGCTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGCTTCGACGACCGGTAC 420
 Db 630 ATCTCCCTTACCTCATCCGACACCAAGACGAGCGTGTGCGAGCTCGAGAGGCGCTTC 689

RESULT 7
 CF693874
 LOCUS CCADM43TR C.neofomans strain JEC21 mRNA linear EST 16-AUG-2004
 DEFINITION neofomans cDNA clone CCADM43, mRNA sequence.
 ACCESSION CF693874
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 738)

AUTHORS Loftus,B.

TITLE End sequencing of clones from a Full length enriched, normalized

JOURNAL JEC21 cDNA library

COMMENT Other ESTs: CCADM43TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR: www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1..738

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCADM43"

/clone_lib="C.neofomans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 738;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGCGGAGCGTCCGCGGTACCGGTACGACCGGACCGGTTCGCCCGAGCGGTC 63

Db 318 AAGCAACACGACTGCGCGGTACCGGTACCGACCGGCACTGCTCCGCCGAGCCATC 377

QY 64 GTACGCGAGGCGCTCGCAACCTGCGCGGTGCGCAACCGGATGCTCAAGCGCGGC 123

Db 378 TACTCTGAGGGTGTGAGAACGTGCTGCCGGCTGCAACCCCATGAGCTTCGTCGAGGT 437

QY 124 ATCGAAGGCGCTCGAGCGCTTCGCCGCGCTTCGTCGAGCGGCGAAGGATGTCGAG 183

Db 438 GCCCAGAGGCTGTGCAAGGCTTCGAGGTTCTTGCTGCCAACAAAGGTATACCC 497

QY 184 ACCAAGGAGCAGATCGCTTCACCGGCTTCATCTCCGC---CGCCGACACCGAGATCGGC 240

Db 498 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAAGCGGATACCCACGTCGGT 557

QY 241 GAGCTCATCCGCGGCGATGACAGGTCGGCAAGGAGGCGCTCATCCGTCGAGGAG 300
 Db 558 GCATCATTCGCCAAGCCATGAGAGCGGTCCGCAAGGAGGCTCATCACTGTTAAGGAG 617
 QY 301 TCCAGACCTTCGCTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGCGTAC 360
 Db 618 GCGCGAACCATTCAGCAGGAGATTGAGATTACCGAGGGTATGCGATTTCGACCGAGGCTTC 677
 QY 361 ATCTCGGCTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGCTTCGACGACCGGTAC 420
 Db 678 ATCTCCCTTACCTCATCCGACACCAAGACGAGCGTGTGCGAGCTCGAGAGGCGCTTC 737

RESULT 8
 CF718151

LOCUS CCAHZ70TR C.neofomans strain JEC21 mRNA linear EST 16-AUG-2004

DEFINITION neofomans cDNA clone CCAHZ70, mRNA sequence.

ACCESSION CF718151

VERSION

KEYWORDS

SOURCE

ORGANISM

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

REFERENCE 1 (bases 1 to 741)

AUTHORS Loftus,B.

TITLE End sequencing of clones from a Full length enriched, normalized

JOURNAL JEC21 cDNA library

COMMENT Other ESTs: CCAHZ70TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR: www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1..741

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAHZ70"

/clone_lib="C.neofomans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 741;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGCGGAGCGTCCGCGGTACCGGTACGACCGGACCGGTTCGCCCGAGCGGTC 63

Db 316 AAGACCAACGACACTGCGCGGTACCGGTACCGACCGGCACTGCTCCGCCGAGCCATC 375

QY 64 GTACGCGAGGCGCTCGCAACCTGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGC 123

Db 376 TACTCTGAGGGTGTGAGAACGTGCTGCCGGCTGCAACCCCATGAGCTTCGTCGAGGT 435

QY 124 ATCGAAGGCGCTCGAGGCGCTTCGCCGCGCTTCGTCGAGCGGCGAAGGATGTCGAG 183

Db 436 GCCCAGAGGCTGTGCAAGGCTTCGAGGTTCTTGCTGCCAACAAAGGTATATACC 495

QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTTCATCTCCGC---CGCCGACACCGAGATCGGC 240

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Db      496 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACAGCGCATACCCACGTCGGT 555
QY      241 GAGCTCATCGCCGAGCGATGACCAAGTCCGCAAGGAGCGCTCATCCGTCGAGGAG 300
Db      556 GCATCATTTCCCAAGCCATGGAGCGAGGTCCGCAAGGAGGTGTCTCATCTGTTAAGGAG 615
QY      301 TCCACGACCTTCGGTCTGGAGCTTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGGCTAC 360
Db      616 GCGCGAACCATTCACGACGAGATTGAGATTACCGAGGGTATGCGATTCCGACCGAGGCTTC 675
QY      361 ATCTCGGCGTACTTCGCGCACCGCATGGAGCGGATGGAGCGGTCGCTCGACGACCCGTCAC 420
Db      676 ATCTCCCTTACCTCATACCGACACCAAGAACGAGCGTGTGAGCTCGAGAGCCGCTTC 735

RESULT 9
LOCUS   CF682602              749 bp mRNA linear EST 16-AUG-2004
DEFINITION
        CCABP32TR C.neoformans strain JEC21 Cryptococcus neoformans var.
        neoformans cDNA clone CCABP32, mRNA sequence.
ACCESSION
        CF682602
VERSION
        CF682602.1 GI:41536761
KEYWORDS
        EST.
SOURCE
        Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
        var. neoformans)
ORGANISM
        Cryptococcus neoformans var. neoformans
        Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
        Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
        Filobasidiella.
REFERENCE
        1 (bases 1 to 749)
AUTHORS
        Loftus,B.
TITLE
        End sequencing of clones from a Full length enriched, normalized
        JEC21 cDNA library
JOURNAL
        Unpublished (2003)
COMMENT
        Other ESTs: CCABP32TF
        Contact: Brendan Loftus
        The Institute for Genomic Research (TIGR; www.tigr.org)
        9712 Medical Center Drive, Rockville, MD 20850, USA
        Tel: 301-838-3543
        Fax: 301-838-0208
        Email: bjloftus@tigr.org
        Seq primer: TR.

FEATURES
        source
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        /organism="Cryptococcus neoformans var. neoformans"
        /mol_type="mRNA"
        /strain="JEC21"
        /db_xref="taxon:40410"
        /clone="CCABP32"
        /clone_lib="C.neoformans strain JEC21"
        /note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full
        length, normalized library was prepared from a variety of
        conditions using RNA provided by Joseph Heitman and
        Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 749;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGCTTCGCGCCGAGCGCTC 63
Db      325 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGGCACTGTCTCGCCGAGCCATC 384
QY      64 GTACGCGAGGCGCTCGCGCAAGCTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGGC 123
Db      385 TACTCTGAGGGTGTGAAGAACGTCTGCGCGGTGCAACCCATCGACCTTCGTCGAGGT 444
QY      124 ATCGAGAGGCGGTGAGAGCGGCTCTCGCGCGCCCTGTCTGGAGAGCGGCGAAGGATGTGAG 183
Db      445 GCCCAGAAGGCTGTGCAAGGTCCTCGAGGTTCTTGCTGCAACAAAAGGTTATCACC 504
QY      184 ACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGC---CGCCGACCCAGATCGGC 240

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Db      505 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACAGCGCATACCCACGTCGGT 564
QY      241 GAGCTCATCGCCGAGCGATGACCAAGTCCGCAAGGAGCGGTCTCATCCGTCGAGGAG 300
Db      565 GCATCATTTCCCAAGCCATGGAGCGAGGTCCGCAAGGAGGTGTCTCATCTGTTAAGGAG 624
QY      301 TCCACGACCTTCGGTCTGGAGCTTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGGCTAC 360
Db      625 GCGCGAACCATTCACGACGAGATTGAGATTACCGAGGGTATGCGATTCCGACCGAGGCTTC 684
QY      361 ATCTCGGCGTACTTCGCGCACCGCATGGAGCGGATGGAGCGGTCGCTCGACGACCCGTCAC 420
Db      685 ATCTCCCTTACCTCATACCGACACCAAGAACCGAGCGTGTGAGCTCGAAGAGCCGCTTC 744

RESULT 10
LOCUS   CF693560              752 bp mRNA linear EST 16-AUG-2004
DEFINITION
        CCAGV54TR C.neoformans strain JEC21 Cryptococcus neoformans var.
        neoformans cDNA clone CCAGV54, mRNA sequence.
ACCESSION
        CF693560
VERSION
        CF693560.1 GI:41547719
KEYWORDS
        EST.
SOURCE
        Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
        var. neoformans)
ORGANISM
        Cryptococcus neoformans var. neoformans
        Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
        Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
        Filobasidiella.
REFERENCE
        1 (bases 1 to 752)
AUTHORS
        Loftus,B.
TITLE
        End sequencing of clones from a Full length enriched, normalized
        JEC21 cDNA library
JOURNAL
        Unpublished (2003)
COMMENT
        Other ESTs: CCAGV54TF
        Contact: Brendan Loftus
        The Institute for Genomic Research (TIGR; www.tigr.org)
        9712 Medical Center Drive, Rockville, MD 20850, USA
        Tel: 301-838-3543
        Fax: 301-838-0208
        Email: bjloftus@tigr.org
        Seq primer: TR.

FEATURES
        source
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        /organism="Cryptococcus neoformans var. neoformans"
        /mol_type="mRNA"
        /strain="JEC21"
        /db_xref="taxon:40410"
        /clone="CCAGV54"
        /clone_lib="C.neoformans strain JEC21"
        /note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full
        length, normalized library was prepared from a variety of
        conditions using RNA provided by Joseph Heitman and
        Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 752;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGCTTCGCGCCGAGCGCTC 63
Db      329 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGGCACTGTCTCGCCGAGCCATC 388
QY      64 GTACGCGAGGCGCTCGCGCAAGCTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGGC 123
Db      389 TACTCTGAGGGTGTGAAGAACGTCTGCGCGGTGCAACCCATCGACCTTCGTCGAGGT 448
QY      124 ATCGAGAGGCGGTGAGAGCGGCTCTCGCGCGCCCTGTCTGGAGAGCGGCGAAGGATGTGAG 183
Db      449 GCCCAGAAGGCTGTGCAAGGTCCTCGAGGTTCTTGCTGCCAACAAAAGGTTATCACC 508

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Db      445  GCCAGAGGCTGTGCACAGGCTCTCGAGGTTCTTGCTGCCAACAAGAGGTTATCACC 504
QY      184  ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db      505  ACCTCTGAGGAGATGCGCCAGGTCGCCACCATCTCCGCCAACCGCGATACCCACGTCGGT 564
QY      241  GAGCTCATCCCGAGGCGATGGACAGGTCGGAAGGAGGCGTCTATCAGCGTCGAGGAG 300
Db      565  GCATCATCTCCAGCCATGGAGAGGTCGGCAGAGGAGGTCATCACTGTTAAGGAG 624
QY      301  TCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
Db      625  GCGGACCATTCAGCAGCAGATTTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 684
QY      361  ATCTCGGCTACTTCGCCACCGATGGAGCGGATGGAGCGTCTCGACGACCGGTAC 420
Db      685  ATCTCCCTTACCTCATCACCAGCACCACCAAGACGAGCGTGTGAGCTCGAGAGGCCCTTC 744

RESULT 13
CF722454
LOCUS      766 bp      mRNA      linear      EST 16-AUG-2004
DEFINITION C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAE270, mRNA sequence.
ACCESSION CF722454
VERSION    1
KEYWORDS   EST.
SOURCE     Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM   Cryptococcus neoformans var. neoformans
            Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
REFERENCE  1 (bases 1 to 766)
AUTHORS   Loftus,B.
TITLE     End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL   Unpublished (2003)
COMMENT   Other_ESTs: CCAE270TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.
FEATURES   Location/Qualifiers
            source          1..766
            /organism="Cryptococcus neoformans var. neoformans"
            /mol_type="mRNA"
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            /db_xref="taxon:40410"
            /clone="CCA270"
            /clone_lib="C.neoformans strain JEC21"
            /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
            length, normalized library was prepared from a variety of
            conditions using RNA provided by Joseph Heitman and
            Jennifer Lodge"
ORIGIN
Query Match      41.3%; Score 173.6; DB 6; Length 766;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4  AAGACGAGCAGCTCGCGGTGACGATACGACCAACCGGACCGTTCTCGCCGAGCGCTC 63
Db      271  AAGACCAACGACACTCGCGGTGACGATACGACCAACCGGACCGTCTCGCCGAGCCATC 330
QY      64  GTACGAGGCGCTTCGCAACGTCGCGCGGTGCGCAACCGGATGGTCTCTCAAGCGCGC 123
Db      331  TACTCTGAGGGTGTGAAGAACGTCGCGCGGTGCGCAACCGGATGGTCTCTCGGAGGT 390
QY      124  ATCGAAGAGGCGCTCGAGGCGCTCTCCGCGCGCGCTCTCGGAGGAGGAGTGTGAG 183

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Db      391  GCCAGAGGCTGTGCACAGGCTCTCGAGGTTCTTGCTGCCAACAAGAGGTTATCACC 450
QY      184  ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db      451  ACCTCTGAGGAGATGCGCCAGGTCGCCACCATCTCCGCCAACCGCGATACCCACGTCGGT 510
QY      241  GAGCTCATCCCGAGGCGATGGACAGGTCGGAAGGAGGCGTCTATCAGCGTCGAGGAG 300
Db      511  GCATCATCTCCAGCCATGGAGAGGTCGGCAGAGGAGGTCATCACTGTTAAGGAG 570
QY      301  TCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
Db      571  GCGGACCATTCAGCAGCAGATTTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 630
QY      361  ATCTCGGCTACTTCGCCACCGATGGAGCGGATGGAGCGTCTCGACGACCGGTAC 420
Db      631  ATCTCCCTTACCTCATCACCAGCACCACCAAGACGAGCGTGTGAGCTCGAAGAGGCCCTTC 690

RESULT 14
CF710636
LOCUS      767 bp      mRNA      linear      EST 16-AUG-2004
DEFINITION C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAFC87, mRNA sequence.
ACCESSION CF710636
VERSION    1
KEYWORDS   EST.
SOURCE     Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM   Cryptococcus neoformans var. neoformans
            Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
REFERENCE  1 (bases 1 to 767)
AUTHORS   Loftus,B.
TITLE     End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL   Unpublished (2003)
COMMENT   Other_ESTs: CCAFC87TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.
FEATURES   Location/Qualifiers
            source          1..767
            /organism="Cryptococcus neoformans var. neoformans"
            /mol_type="mRNA"
            /strain="JEC21"
            /db_xref="taxon:40410"
            /clone="CCAFC87"
            /clone_lib="C.neoformans strain JEC21"
            /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
            length, normalized library was prepared from a variety of
            conditions using RNA provided by Joseph Heitman and
            Jennifer Lodge"
ORIGIN
Query Match      41.3%; Score 173.6; DB 6; Length 767;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4  AAGACGAGCAGCTCGCGGTGACGATACGACCAACCGGACCGTTCTCGCCGAGCGCTC 63
Db      331  AAGACCAACGACACTCGCGGTGACGATACGACCAACCGGACCGTCTCTCGCCGAGCCATC 390
QY      64  GTACGAGGCGCTTCGCAACGTCGCGCGGTGCGCAACCGGATGGTCTCTCAAGCGCGC 123
Db      391  TACTCTGAGGGTGTGAAGAACGTCGCGCGGTGCGCAACCGGATGGTCTCTCGGAGGT 450

```

QY 124 ATCGAAGGCCGTCGAGGCCGCTCTCGGGCCCTCTGCTGGAGCAGCGAAGGATGTCGAG 183
 Db 451 GCCCAGAGGCTGTGCGACAGGCTCTCGAGGTTCTTGTGTCACCAAAAAGGTTATCACC 510
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCG---CGCCGACACCCAGATCGGC 240
 Db 511 ACTCTGAGGAGATGCCCAGGTGCGACCATCTCCGCAACGGCATACCCACGTCGGT 570
 QY 241 GAGCTCATCGCCGAGGCGATGGACAAGGTGCGCAAGGAAGGCGTCTATCCCGTCGAGGAG 300
 Db 571 GCCATCATGCCCAGCCATGAGGAGGTCGGCAAGGAGGTCATCATCTGTTAAGGAG 630
 QY 301 TCCAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGCGTAC 360
 Db 631 GGCCGAACCATTCACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 690
 QY 361 ATCTCGGCGTACTTTCGACCGACATGAGCGGATGAGGCGTTCGCTTCGACGACCGCTAC 420
 Db 691 ATCTCCCTTACTCTCATCCGACACCAAGAACCGGTCGAGCTCGAAGAGCCCTTC 750

RESULT 15
 CF709688 768 bp mRNA linear EST 16-AUG-2004
 LOCUS
 DEFINITION
 CCAPP74TR C.neofomans strain JEC21 Cryptococcus neoformans var.
 CF709688
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 EST.
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 768)
 Loftus,B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 Unpublished (2003)
 Other ESTs: CCAPP74TO
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 source
 1..768
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
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 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 768;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
 QY 4 AAGACGAGCAGTCGCCGGTACGATACGACCAACCGGACCGTTCCTGCCCGAGCGCTC 63
 Db 325 AAGACCAACGACACTCGCGGTGACGATACCAACCGGACCTGTCTCTGCCCGAGCCATC 384
 QY 64 GTACGCGAGGCGCTCGGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGCGCGC 123
 Db 385 TACTCTGAGGGTGTGAAGAACGTCGTCGCGCTGCAACCCATGACCTCGTCGAGGT 444

QY 124 ATCGAAGGCCGTCGAGGCCGCTCTCGGGCCCTCTGCTGGAGCAGCGAAGGATGTCGAG 183
 Db 445 GCCCAGAGGCTGTGCGACAGGCTCTCGAGGTTCTTGTGTCACCAAAAAGGTTATCACC 504
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCG---CGCCGACACCCAGATCGGC 240
 Db 505 ACTCTGAGGAGATGCCCAGGTGCGCACCATCTCCGCAACGGCATACCCACGTCGGT 564
 QY 241 GAGCTCATCGCCGAGGCGATGACAAGGTGCGCAAGGAAGGCGTCTATCCCGTCGAGGAG 300
 Db 565 GCCATCATGCCCAGCCATGAGGAGGTCGGCAAGGAGGTCATCATCTGTTAAGGAG 624
 QY 301 TCCAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGCGTAC 360
 Db 625 GGCCGAACCATTCGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 684
 QY 361 ATCTCGGCGTACTTTCGACCGACATGAGCGGATGAGGCGTTCGCTTCGACGACCGCTAC 420
 Db 685 ATCTCCCTTACTCTCATCCGACACCAAGAACCGGTCGAGCTCGAAGAGCCCTTC 744

RESULT 16
 CF701856 773 bp mRNA linear EST 16-AUG-2004
 LOCUS
 DEFINITION
 CCAD54TR C.neofomans strain JEC21 Cryptococcus neoformans var.
 CF701856
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 EST.
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 773)
 Loftus,B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 Unpublished (2003)
 Other ESTs: CCAD54TP
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 Location/Qualifiers
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 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAD54"
 /clone_lib="C.neofomans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 773;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
 QY 4 AAGACGAGCAGTCGCCGGTACGATACGACCAACCGGACCGTTCCTGCCCGAGCGCTC 63
 Db 322 AAGACCAACGACACTCGCGGTGACGATACCAACCGGACCTGTCTCTGCCCGAGCCATC 381
 QY 64 GTACGCGAGGCGCTCGGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGCGCGC 123

Db 382 TACTCTGAGGCTGTGAAGAACGTCGCTGCGGCTGCACCCCATGACCTCCGTCGAGGT 441
 QY 124 ATCGAGAGCCGCTCGAGGCGCTCTCGGCGCCCTGCTGAGCAGCGGAGGATGTCGAG 193
 Db 442 GCCCAGAGGCTGTGCAAGAGTCTCGAGGTTCTTGCTGCCAACAAAAGAGTTATCACC 501
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 502 ACTCTGAGAGATGTCAGGCTGCGCACCATCTCCGCCAACCGGCGATACCCACGTCGGT 561
 QY 241 GAGCTCATCCCGAGGCGATGGAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
 Db 562 GCCATCATTCGCCAAGCATTGAGAGGTCGGCAAGGAGGTCATCATCTGTTAAGGAG 621
 QY 301 TCCGAGACCTTCGCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGTAC 360
 Db 622 GGCCGACCATTCGACGAGATGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 681
 QY 361 ATCTCGGCTACTTCCGCCCGCATGCGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 Db 682 ATCTCCCTTACCTCATCCGACACCCAGACGCGTCTCGAGCTCGAGAGCCCTTC 741

RESULT 17

CF702480
 LOCUS
 DEFINITION CAA550TR C.neoformans strain JEC21 Cryptococcus neoformans var.
 CF702480
 VERSION
 ACCESSION CF702480.1 GI:41556639
 EST.
 KEYWORDS
 SOURCE

ORGANISM
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 776)
 Loftus,B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 Unpublished (2003)
 Other ESTs: CCAA550TF
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 source
 1. .776
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAA550"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 776;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
 QY 4 AAGACGAGCAGCTGCGCGGTGACGGTACGACCAACCGGACCGTCTCGCCGAGCGCTC 63
 Db 323 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGGACCGTCTCGCCGAGCCATC 382
 QY 64 GTACGCGAGGCGCTGCGCAACGTCGCGCGGTGACCAACCGGATCTTCAGCGCGGC 123

Db 383 TACTCTGAGGCTGTGAAGAACGTCGCTGCGGCTGCACCCCATGACCTCCGTCGAGGT 442
 QY 124 ATCGAGAGCCGCTCGAGGCGCTCTCGGCGCCCTGCTGAGCAGCGGAGGATGTCGAG 193
 Db 443 GCCCAGAGGCTGTGCAAGAGTCTCGAGGTTCTTGCTGCCAACAAAAGAGTTATCACC 502
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 503 ACTCTGAGAGATGTCAGGCTGCGCACCATCTCCGCCAACCGGCGATACCCACGTCGGT 562
 QY 241 GAGCTCATCCCGAGGCGATGGAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
 Db 563 GCCATCATTCGCCAAGCATTGAGAGGTCGGCAAGGAGGTCATCATCTGTTAAGGAG 622
 QY 301 TCCGAGACCTTCGCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGTAC 360
 Db 623 GGCCGACCATTCGACGAGATGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 682
 QY 361 ATCTCGGCTACTTCCGCCCGCATGCGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 Db 683 ATCTCCCTTACCTCATCCGACACCCAGACGCGTCTCGAGCTCGAGAGCCCTTC 742

RESULT 18

CF681781
 LOCUS
 DEFINITION CAAH222FR C.neoformans strain JEC21 Cryptococcus neoformans var.
 CF681781
 VERSION
 ACCESSION CF681781.1 GI:41535940
 EST.
 KEYWORDS
 SOURCE

ORGANISM
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 778)
 Loftus,B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 Unpublished (2003)
 Other ESTs: CCAH222TF
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 source
 1. .778
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CAH222"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 778;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
 QY 4 AAGACGAGCAGCTGCGCGGTGACGGTACGACCAACCGGACCGTCTCGCCGAGCGCTC 63
 Db 287 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGGACCGTCTCGCCGAGCCATC 346

QY 64 GTACGAGGCGCTCGCAGCTCGCGCGCGTGCACACCCGATGCTCTCAAGCGCGC 123
 Db 347 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGCTGCACACCCATGACCTCCGTCAGGT 406
 QY 124 ATCGAGAGGCGCTCGAGGCGCTCGCGCGCGCTGCTGAGCAGCGGAGGATGCGAG 183
 Db 407 GCCAGAGGCTGTGCAAGGTCCTCGAGGTTCTGTCGCCAACAAAAGGTTATCACC 466
 QY 184 ACCAAGAGCAGATCGTTCCACGGCTTCATCTCCGC---GCGCGACACCCAGATCGGC 240
 Db 467 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAACAGCGGATATCCACGTCGT 526
 QY 241 GAGCTCATCGCCGAGGCTGACAGGTCGGCAAGAGGCGTCAACCGTCGAGGAG 300
 Db 527 GCCATCATTTGCCCAAGCCATGAGAGCGGTGCGCAAGGAGGGTGTCTATCTGTTAGGAG 586
 QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
 Db 587 GGCGAACCATTGACACGAGATTGAGATTACGAGGTTATGCGATTTCGACCGAGGCTTC 646
 QY 361 ATCTCGCGGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420
 Db 647 ATCTCCCTTACCTCATCCGACACCAAGACCGGTCGAGCTCGAGGTCGAGAGCCCTTC 706

RESULT 19
 CF695095 779 bp mRNA linear EST 16-AUG-2004
 LOCUS CCACS96TR C.neofomans strain JEC21 Cryptococcus neoformans var.
 DEFINITION
 neofomans cDNA clone CCACS96, mRNA sequence.
 ACCESSION CF695095
 VERSION
 KEYWORDS
 SOURCE

CRYPTOCOCCUS NEOFORMANS var. neoformans (Filobasidiella neoformans
 var. neoformans)
 ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 779)
 Loftus, B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 JOURNAL
 COMMENT
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 Location/Qualifiers
 1..779
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCACS96"
 /clone_lib="C.neofomans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 779;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCTCGCGGTGACCGTACGACACCGGACCGTCTCGCCGAGCGCTC 63
 Db 329 AAGACCAAGCACTCGCGGTGACCGTACGACACCGGACCGTCTCGCCGAGCCATC 388

QY 64 GTACGAGGCGCTCGCGCAACCTGCGCGCGTGCACACCCGATGCTCTCAAGCGCGC 123
 Db 389 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGCTGCACACCCATGACCTCCGTCAGGT 448
 QY 124 ATCGAGAGGCGCTGAGGCGCTCTCCGGCGCGCTCTGAGCAGCGGAGGATGTCGAG 183
 Db 449 GCCCAGAGGCTGTGCAAGGTCCTCGAGGTTCTGTCGCCAACAAAAGGTTATCACC 508
 QY 184 ACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGC---GCGCGACACCCAGATCGGC 240
 Db 509 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAACGGGATATCCACGTCGT 568
 QY 241 GAGCTCATCGCCGAGGCGATGACAAAGTTCGCAAGAGGCGTCAACCGTCGAGGAG 300
 Db 569 GCCATCATTTGCCCAAGCCATGAGAGCGGTGCGCAAGGAGGGTGTCTATCTGTTAGGAG 628
 QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
 Db 629 GGCGAACCATTGACACGAGATTGAGATTACGAGGTTATGCGATTTCGACCGAGGCTTC 688
 QY 361 ATCTCGCGGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420
 Db 689 ATCTCCCTTACCTCATCCGACACCAAGACCGGTCGAGCTCGAGGTCGAGAGCCCTTC 748

RESULT 20
 CF694632 790 bp mRNA linear EST 16-AUG-2004
 LOCUS CCAGK96TR C.neofomans strain JEC21 Cryptococcus neoformans var.
 DEFINITION
 neofomans cDNA clone CCAGK96, mRNA sequence.
 ACCESSION CF694632
 VERSION
 KEYWORDS
 SOURCE

CRYPTOCOCCUS NEOFORMANS var. neoformans (Filobasidiella neoformans
 var. neoformans)
 ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 790)
 Loftus, B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 JOURNAL
 COMMENT
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 Location/Qualifiers
 1..790
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAGK96"
 /clone_lib="C.neofomans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 790;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCTCGCGGTGACCGTACGACACCGGACCGTCTCGCCGAGCGCTC 63
 Db 325 AAGACCAAGCACTCGCGGTGACCGTACGACACCGGACCGTCTCGCCGAGCCATC 384

Qy	4	AAGA	CGGACG	ACGTCG	CGCGTG	ACGACG	CAACCG	CGACCG	GTTCCT	CGCCAG	CGGCTC	63
Db	237	AAGACCA	ACGACATC	GC	CGGTGA	CGGTAC	CAACAC	CGGCCA	CTGTCT	CGCCAG	GCCATC	296
Qy	64	GTA	CGCGAG	GGCCTG	CGGCMAC	CGTTCG	CGCGCG	CGGTGCCA	ACCCGATGG	CTCTCA	AGCGCGGC	123
Db	297	TACTCT	GAGGGTGT	GA	AAACGTCG	TC	CGCGGT	GCAACCC	CAATG	CACTCG	TCGAGGT	356
Qy	124	ATC	GAGAAG	GGCCGTCT	CGCGCG	CCCTCT	CGGAGC	AGCGG	CAAGATGT	CGAG		183
Db	357	GCC	CAGAAG	GGCTG	CGACMAG	GTCT	CGAGGTCT	TTGCTG	CCACAAA	AGGTTAT	CACC	416
Qy	184	ACC	AAGAGC	AGATCG	CTTCCAC	GGCCTT	CCATCT	CCGC	--CGCCG	CAACCCAG	ATCGCG	240
Db	417	ACCTCT	GAGGAGAT	GTG	CCAGTTCG	CCACCATCT	CGGCCA	ACGGCG	ATACCC	ACGTCG	GT	476
Qy	241	GAG	CTCATCG	CCGAGG	CGATNG	CA	AGTTCGGC	CAAGGA	GGGTCA	TACCGTC	CGAGNG	300
Db	477	GCC	ATCATTTG	CCCCAAG	CCATG	AGCGAG	GTTCGG	CAAGAGG	GGTGTCT	CACTGTTT	TAAGGAG	536
Qy	301	TCC	CAGACCTT	CGGTCT	GTGGAGCT	CGAGCT	CAACCG	AGGATATG	CGCTTC	GCACAAG	GGCTAC	360
Db	537	GGCCG	ACCATTTG	ACGACG	AGATTG	AGATTAC	CGGAGG	GTATG	CGATTG	CGACCG	AGGCTTC	596
Qy	361	ATCT	CGGCGTAT	CTTGC	CGACCG	CA	TGAGAG	CGGATG	GAGGCG	GTCCG	CTCGAC	420
Db	597	ATCT	CCCCCTT	ACCTCAT	CACCG	CAAC	CAAGAA	CCAGCG	GTTCG	AGCTCG	AGAAGGCC	656

RESULT 24	CF713651	CF713651	803 bp	linear	EST 16-AUG-2004
LOCUS	CF713651	CF713651			
DEFINITION	CCAH0505TR C. neoformans strain JEC21	CCAH0505TR C. neoformans strain JEC21			Cryptococcus neoformans var.
	neoformans	neoformans	CDNA clone CCAHP05,		mrna sequence.
ACCESSION	CF713651	CF713651			
VERSION	CF713651.1	CF713651.1			GI:41567810
KEYWORDS	EST.	EST.			

SOURCE	Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM	Cryptococcus neoformans var. neoformans Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
REFERENCE	1. (bases 1 to 803)
AUTHORS	Loftus, B.
TITLE	End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
JOURNAL	Unpublished (2003)
COMMENT	Other ESTs: CCAHP05TF Contact: Brendan Loftus The Institute for Genomic Research (TIGR; www.tigr.org) 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-3543 Fax: 301-838-0208 Email: bjloftus@tigr.org Seq primer: TR.

```

FEATURES             Location/Qualifiers
     1..803
         /organism="Cryptococcus neoformans var. neoformans"
         /mol_type="mRNA"
         /strain="JEC21"
         /db_xref="taxon:40410"
         /clone="CCAHF05"
         /clone_lib="C.neoformans strain JEC21"
         /note="Vector: pCMVSPORT6; Site: NotI EcoRV; The
length, normalized library was prepared from a vari
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

```

ORIGIN

Query Match	41.3%;	Score 173.6;	DB 6;	Length 803;
Best Local Similarity	65.0%;	Pred. No. 4.7e-26;		
Matches 273;	Conservative 0;	Mismatches 144;	Indels 3;	Gaps 1;

4	QAAGACGAGCAGCTGCGCGGTGACGGTACGACACACCGCGACCGTTCTCGCCCGACGGCGTC	63
265	AAGACCAACGACACTGCGCGGTGACGGTACCAACACCGCACTGCTCTCGCCCGAGGCCATC	324
64	GTACGCGAGGGCGTCGCAACGTCGCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGGC	123
325	TACTCTGAGGGTGTGAAGACGTGCTGCCCGGTGCAACCCATGACCTCTCGTCGAGGT	384
124	ATCGAGAAGGCGCTCGAGGGCGGTCTCGCGCGCCCTGCTGGAGCAGGCGAAGGATGTCCAG	183
385	GCCCAGAAGGCTGTCGACAAGGTCTCTGAGGTCTCTGCTGCCAACAAAAGGTTATCACC	444
184	ACCAAGAGCAGATCGCTTTCACGGCGCTTCATCTCCGC---CGCGACACCCAGATCGGC	240
445	ACCTCTGAGGAGATGTGCCAGTGCACCACCATCTCCGCCAACCGCGCATACCCACGTCGGT	504
241	GAGCTCATCGCCGAGGGCGATGGACAAAGTTCGGCAAGGAAGCGCTCATCACCGTCGAGAG	300
505	GCCATCATTGCCCAAGCCATGGAGAGGTTCGGCAAGGAGGGGTGTCTACTGTTTAAGAG	564
301	TCCCAGACCTTTCGGTCTGAGCTCGAGCTCAACCGAGGGTATGCGCTTCGACAAAGGGCTAC	360
565	GGCCGAACCATTGACGACGAGATTGAGATTACCGAGGGTATGCGATTCCGACCGAGGCTTC	624
361	ATCTCGGGTACTTTCGCCACCGACATGAGCGGGATGAGAGGGGTCTGCTCGACGCCGTAC	420
625	ATCTCCCTCTACTCTCATCACCAGACCAAGAACCAGCGGTGTCGAGCTCGAGAAGCCCTTC	684

RESULT	25
CF711476	
LOCUS	
DEFINITION	CF711476 804 bp mRNA linear EST 16-AUG-2004 CCAHX08TR C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAHX08, mRNA sequence.

ORIGIN	GenBank	EMBL	DDBJ
Query Match	41.3%	Score 173.6;	DB 6; Length 804;
Best Local Similarity	65.0%;	Pred. No. 4.7e-26;	
Matches 273; Conservative	0; Mismatches 144;	Indels 3; Gaps 1;	

Qy	4	AAGACGGACGAGCTCGCGGTGACGGTACGACACACCGGACCGTTCCTCGCCACGCGCTC	63
Db	333	AAGACCAACGACACTCGCGGTGACGGTACACACACCGCCACTGTCTCGCCGAGGCATC	392
Qy	64	GTACGCGAGGGCTGCGCAACGTCGCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGGC	123
Db	393	TACTCTGAGGGTGTGAAGAACGTCGTGCGGCTGCAACCCCATGACCTCCGTTCAGGT	452
Qy	124	ATCGAGAAGGCCGTTCGAGGCGGTCTCGGCGCCCTGCTGGAGCAGCGGAAGGATGTCGAG	183
Db	453	GCCACGAAGGCTGTCGACAAAGGTCTTCGAGGTCTTGTGTCCAACAAAAGGTTATCACC	512
Qy	184	ACCAAGGACGAGATCGTTCACGGGCTTCATCTCCGC---CGCGACACCCAGATCGGC	240
Db	513	ACCTCTGAGGAGATTGCCACGAGTTCGGCCACCATCTCGCCAAACGGCGATACCCACGTCGGT	572
Qy	241	GAGCTCATCCCGAGGCGATGGACAAGGTTCGGCAAGGAAGCGCTCATCACCGTCGAGGAG	300
Db	573	GCCATCATTTGCCACGCGATGGAGCAGGTTCGGCAAGGAGGGTGTCTACTGTTAAGGAG	632
Qy	301	TCCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC	360
Db	633	GGCCGAACCATTCGACGACGAGATTGAGATTACCGAGGGTATGCGATTTCGACCCGAGGCTTC	692
Qy	361	ATCTCGGCTACTTTCGCCACCGACATGGAGCGGATGGAGGCGTTCGTCGACGACCGGTAC	420
Db	693	ATCTCCCTTTACTCTCATACCGCACCAAGAACCCAGCGGTGTGAGCTTCGAGATGAGCCCTTC	752

RESULT	26
CF703324	
LOCUS	
DEFINITION	815 bp mRNA linear EST 16-AUG-2004 CCAUH57TR C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAHU57, mRNA sequence.

ORIGIN

Query Match	41.3%;	Score 173.6;	DB 6;	Length 815;
Best Local Similarity	65.0%;	Pred. No. 4.7e-26;		

Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGAGCGAGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 63
Db 321 AAGACCAACGACACTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 380
QY 64 GTACGCGAGGCGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 123
Db 381 TACTCTGAGGGGTGAGAAAGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 440
QY 124 ATCGAGAGGCGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 183
Db 441 GCCAGAGGCGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 500
QY 184 ACCAGAGGCGATCGCTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 240
Db 501 ACCTCTGAGGAGATTCGCCGAGTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 560
QY 241 GAGCTCATCGCGAGGCGATGACAAAGGTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 300
Db 561 GCCATCATTCGCCGAGGCGATGACAAAGGTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 620
QY 301 TCCGAGACCTCGGTCTGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 360
Db 621 GCGCGAACCATTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 680
QY 361 ATCTCGGCGTACTTCGCCGAGGCGATGAGCGGTTCGCGGTGACGGTACGACACCGCGCTC 420
Db 681 ATCTCCCTTACTCATCCGACGACGATGAGCGGTTCGCGGTGACGGTACGACACCGCGCTC 740

RESULT 27
CF699756 820 bp mRNA linear EST 16-AUG-2004
LOCUS CCA745STR C. neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCA745, mRNA sequence.
ACCESSION CF699756
VERSION CF699756.1 GI:41553915
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 820)
Loftus, B.
AUTHORS End sequencing of clones from a Full length enriched, normalized
TITLE JEC21 cDNA library
JOURNAL JEC21 CDNA library
COMMENT Other ESTs: CCA745TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR

FEATURES
1..820 Location/Qualifiers
mol_type="mRNA"
/organism="Cryptococcus neoformans var. neoformans"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCA745"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 820;

Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGAGCGAGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 63
Db 329 AAGACCAACGACACTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 388
QY 64 GTACGCGAGGCGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 123
Db 389 TACTCTGAGGGGTGAGAAAGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 448
QY 124 ATCGAGAGGCGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 183
Db 449 GCCAGAGGCGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 508
QY 184 ACCAGAGGCGATCGCTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 240
Db 509 ACCTCTGAGGAGATTCGCCGAGTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 568
QY 241 GAGCTCATCGCGAGGCGATGACAAAGGTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 300
Db 569 GCCATCATTCGCCGAGGCGATGACAAAGGTTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 628
QY 301 TCCGAGACCTCGGTCTGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 360
Db 629 GCGCGAACCATTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 688
QY 361 ATCTCGGCGTACTTCGCCGAGGCGATGAGCGGTTCGCGGTGACGGTACGACACCGCGCTC 420
Db 689 ATCTCCCTTACTCATCCGACGACGATGAGCGGTTCGCGGTGACGGTACGACACCGCGCTC 748

RESULT 28
CF687348 827 bp mRNA linear EST 16-AUG-2004
LOCUS CCA6060TR C. neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCA6060, mRNA sequence.
ACCESSION CF687348
VERSION CF687348.1 GI:41541507
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 827)
Loftus, B.
AUTHORS End sequencing of clones from a Full length enriched, normalized
TITLE JEC21 cDNA library
JOURNAL JEC21 CDNA library
COMMENT Other ESTs: CCA6060TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR

FEATURES
1..827 Location/Qualifiers
mol_type="mRNA"
/organism="Cryptococcus neoformans var. neoformans"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCA6060"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 827;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCGACGTCGCGGTGACGGTACGACCAACCGCGACCGTTCCTCGCCACGCGGCTC 63
 |||||
 Db 264 AAGACCAACGACACTGCGGTGAGGTACCAACCAACCGCCACTGTCTCGCCGAGCCATC 323
 |||||
 QY 64 GTACGGAGGGCCCTGCGCAACGTCGCGCGCGGTGCCAACCCGATGGCTTCTAAGCGCGGC 123
 |||||
 Db 324 TACTCTGAGGGGTGTGAAGAACGTCGTCGCGGTGCAACCCCAATGACCTTCGTCGAGGT 383
 |||||
 QY 124 ATCGAGAGGCGCTCGAGGCGCTCTCGGCGCCCTGCTGGAGCAGCGAAGGATGTCGAG 183
 |||||
 Db 384 GCCAGAAGGCTGTGACAAAGTCTCTCGAGGTTCTTGCTGCCAATAAAGGTTATCACC 443
 |||||
 QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 |||||
 Db 444 ACCTCTGAGGAGATTGCCAGGTGCGCCACCATCTCCGCCCAACGGCGATACCCACGTCGGT 503
 |||||
 QY 241 GAGCTATCGCCGAGGGATGGAACAAGTTCGGCAAGAGGGGTCTATCACCCTCGAGGAG 300
 |||||
 Db 504 GCCATCATTTGCCAAGCCATGAGGAGGTGCGCAAGGAGGGTGTCTATCTGTTAAGGAG 563
 |||||
 QY 301 TCCAGACCTTCGCTGAGGCTGGAGCTCACCGAGGTTATGCGTTTCGACAAAGGCTAC 360
 |||||
 Db 564 GGCGGAACCATTCAGACGAGATTGAGATTACGAGGGTATGCGATTGACCGAGGCTTC 623
 |||||
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGTCTCGACGACCCGTAC 420
 |||||
 Db 624 ATCTCCCTTACTCTATCATCCGACACCAAGACGAGGTGTCGAGCTCGAAGGCCCTTC 683
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RESULT 29

CF713573
 LOCUS
 DEFINITION CCF558TR C. neoformans strain JEC21 mRNA linear EST 16-AUG-2004
 neoformans cdna clone CCAF558, mRNA sequence.

CF713573
 VERSION
 KEYWORDS
 SOURCE EST.
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 831)
 AUTHORS Loftus, B.
 TITLE End sequencing of clones from a Full length enriched, normalized

JOURNAL JEC21 cdna library
 COMMENT Unpublished (2003)
 Other ESTs: CCAF558TO
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA

TEI: 301-838-3543
 Fax: 301-838-0208
 Email: bjlloftus@tigr.org
 Seq primer: TR.

FEATURES
 source Location/Qualifiers
 1..831
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAF558"

/clone_lib="C. neoformans strain JEC21"
 /note="Vector: pcMWsport6; Site_1: NotI_EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN
 Jennifer Lodge"

Query Match 41.3%; Score 173.6; DB 6; Length 831;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCGACGTCGCGGTGACGGTACGACCAACCGCGACCGTTCCTCGCCACGCGGCTC 63
 |||||
 Db 238 AAGACCAACGACACTGCGGTGACGGTACCAACCAACCGCCACTGTCTCGCCGAGCCATC 297
 |||||
 QY 64 GTACGGAGGGCCCTGCGCAACGTCGCGCGCGGTGCCAACCCGATGGCTTCTAAGCGCGGC 123
 |||||
 Db 298 TACTCTGAGGGGTGTGAAGAACGTCGTCGCGGTGCAACCCCAATGACCTTCGTCGAGGT 357
 |||||
 QY 124 ATCGAGAGGCGCTCGAGGCGCTCTCGGCGCCCTGCTGGAGCAGCGAAGGATGTCGAG 183
 |||||
 Db 358 GCCAGAAGGCTGTGACAAAGTCTCTCGAGGTTCTTGCTGCCAATAAAGGTTATCACC 417
 |||||
 QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 |||||
 Db 418 ACCTCTGAGGAGATTGCCAGGTGCGCCACCATCTCCGCCCAACGGCGATACCCACGTCGGT 477
 |||||
 QY 241 GAGCTATCGCCGAGGGATGGAACAAGTTCGGCAAGAGGGGTCTATCACCCTCGAGGAG 300
 |||||
 Db 478 GCCATCATTTGCCAAGCCATGAGGAGGTGCGCAAGGAGGGTGTCTATCTGTTAAGGAG 537
 |||||
 QY 301 TCCAGACCTTCGCTGAGGCTGGAGCTCACCGAGGTTATGCGTTTCGACAAAGGCTAC 360
 |||||
 Db 538 GGCGGAACCATTCAGACGAGATTGAGATTACGAGGGTATGCGATTGACCGAGGCTTC 597
 |||||
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGTCTCGACGACCCGTAC 420
 |||||
 Db 598 ATCTCCCTTACTCTATCATCCGACACCAAGACGAGGTGTCGAGCTCGAAGGCCCTTC 657
 |||||

RESULT 30

CF701087
 LOCUS

DEFINITION CCF506TR C. neoformans strain JEC21 mRNA linear EST 16-AUG-2004
 neoformans cdna clone CCAF506, mRNA sequence.

CF701087
 VERSION
 KEYWORDS
 SOURCE EST.
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 833)
 AUTHORS Loftus, B.
 TITLE End sequencing of clones from a Full length enriched, normalized

JOURNAL JEC21 cdna library
 COMMENT Unpublished (2003)
 Other ESTs: CCAF506TO
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA

TEI: 301-838-3543
 Fax: 301-838-0208
 Email: bjlloftus@tigr.org
 Seq primer: TR.

FEATURES
 source Location/Qualifiers
 1..833
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAF506"

/clone_lib="C. neoformans strain JEC21"
 /note="Vector: pcMWsport6; Site_1: NotI_EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN
 Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 833;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGGAGCGTCCCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 63
 DB 332 AAGACCAACGACACTCCCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 391
 QY 64 GTACGCGAGGCGCTCCGCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 123
 DB 392 TACTCTGAGGGTGTGAAGACGCTGCTGCGGTGACACCCACCTGACCTTCGTCAGGT 451
 QY 124 ATGAGAGGCGCTCGAGGCGCTCCGCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 183
 DB 452 GCCCAGAGGCTGTCGACAGGCTCCGAGGTTCTTGTGTCACAAACAAAAGGTTATCACC 511
 QY 184 ACCAAGGACGATCGCTTCCAGGCTCCATCTCCGCGACACCGGACCGTTCCTCCCGCAGGCGTC 240
 DB 512 ACCTCTGAGGAGATTCCCGAGGTCGACCATCTCCGCGACACCGGACCGTTCCTCCCGCAGGCGTC 571
 QY 241 GAGCTCATCCCGAGGCGTACGAGGTCGCGCAAGAGGCTCATCAACCGTTCGAGGAG 300
 DB 572 GCATCATTCGCAACCGATGAGCAGGTCGCGCAAGAGGCTCATCAACCGTTCGAGGAG 631
 QY 301 TCCAGACCTTCGCTGAGGCTGAGGCTACGCGAGGCTATCGCTTCGACAGGCGTAC 360
 DB 632 GCGCGAACCATTGACGACGAGATTGAGATTACCGAGGCTATCGGATTCGACGAGGCTTC 691
 QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCTCGCTCGACGACCGGTC 420
 DB 692 ATCTCCCTTACTCTCATCCGACACCAAGAGGCTGTCGAGCTCGAGAGGCGCTTC 751

RESULT 31

CF696500 834 bp mRNA linear EST 16-AUG-2004
 CCADB87TR C.neoformans strain JEC21 Cryptococcus neoformans var.
 CF696500
 CF696500.1 GI:41550659
 EST.

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

1 (bases 1 to 834)

Loftus, B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 Unpublished (2003)
 Other_ESTs: CCADB87F
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers
 1. .834
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCADB87"
 /clone_lib="C.neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site_1: NotI EcorV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and

FEATURES

source

Jennifer Lodge

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 834;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGGAGCGTCCCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 63
 DB 325 AAGACCAACGACACTCCCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 384
 QY 64 GTACGCGAGGCGCTCCGCGGTGACGCTACGACACCGGACCGTTCCTCCCGCAGGCGTC 123
 DB 385 TACTCTGAGGGTGTGAAGACGCTGCTGCGGTGACACCCACCTGACCTTCGTCAGGT 444
 QY 124 ATCGAAGAGGCGCTCGAGGCGCTTCGCGGCGCTGCTGGAGCAGCGAAGGATTCGAG 183
 DB 445 GCCCAGAGGCTGTGACACAGGCTCTCGAGGTTCTTGTGTCACAAAGGTTATCACC 504
 QY 184 ACCAAGGAGCAGATCGCTTCCACCGGCTTCATCTCCGCGACACCGGACCGTTCGCG 240
 DB 505 ACCTCTGAGGAGATTGCGCAGGTCGCCACCATCTCCGCGCAACCGGCGATACCCACGTCG 564
 QY 241 GAGCTCATCCCGAGGCGATGACACAGGTCGCGCAAGAGGCTCATCACGTCGAGGAG 300
 DB 565 GCCATCATTTGCCCAAGCCATGAGCAGGTCGCGCAAGAGGCTCATCATCTGTTAAGGAG 624
 QY 301 TCCCAGACCTTCGCTGAGGCTGAGGCTCACCGAGGCTATCGCTTCGACAAAGGCTAC 360
 DB 625 GCGCGAACCATTTGACGACGAGATTGAGATTACCGAGGCTATCGGATTCGACGAGGCTTC 684
 QY 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGGTC 420
 DB 685 ATCTCCCTTACTCTCATCCGACACCAAGAGGCTGTCGAGCTCGAGAGGCGCTTC 744

RESULT 32

CF690854

LOCUS

DEFINITION

neoformans cDNA clone CCAFI92, mRNA sequence.

ACCESSION

CF690854

VERSION

CF690854.1

KEYWORDS

EST.

SOURCE

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)

Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

1 (bases 1 to 861)

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other_ESTs: CCAFI92TO

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .861

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAF192"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site_1: NotI EcorV; The full
 length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN		Query Match	41.3%;	Score 173.6;	DB 6;	Length 861;
		Best Local Similarity	65.0%;	Pred. No. 4.7e-26;	Mismatches 144;	Indels 3;
		Matches 273;	Conservative	0;		
QY	4	AAGACGAGCAGCTGCGCGGTGACGTACGACACCGCGGCTTCTCGCCAGCGCTC	63			
Db	284	AAGACCAACGACACTGCGCGGTGACGTACGACACCGCGGCTTCTCGCCAGCGCTC	343			
QY	64	GTACGCGAGCGCTGCGCAACGTCGCGCGGTGCAACCCCGATGCTCTCAAGCGCGC	123			
Db	344	TACTCTGAGGGTGTGAAGACGTCGCGCGGTGCAACCCCGATGCTCTCGGTGAGGT	403			
QY	124	ATCGAAGGCGCGTTCGAGGCGCTTCTCGCGCGCTTCTCGAGCGAGGAGATGTCGAG	183			
Db	404	GCCGAGAAGCTGTGCAACAGGTCCTCGAGGTTCTTGTCTGCCAACAAGGTTATCACC	463			
QY	184	ACGAGGAGCAGATCGCTTCACGCGCTTCTCATCTCCGC---	240			
Db	464	ACCTCTGAGGAGATTCGCCAGGTTCGCCACCATCTCGCCCAACGCGGATACCCACGTCGT	523			
QY	241	GAGCTCATCGCGAGCGATGGCAAGTCTCGCAAGGAGGCTCATCACCGTCGAGGAG	300			
Db	524	GCCATCATTCGCCAGCCATGGAGCAGGTTCGCAAGGAGGTTCTCATCTGTTAAGGAG	583			
QY	301	TCCGAGACCTTCGCTCTGAGCTGGAGCTCACCGAGGGTATGCGTTTCGCAAGGGCTAC	360			
Db	584	GGCGAACCATTCGACGACGAGATTGAGATTACCGAGGGTATGCGATTCCGACCGAGGCTTC	643			
QY	361	ATCTCGCGCTACTTCGCCACGACATGAGCGGATGAGCGGCTGCTCGACGACCGCTAC	420			
Db	644	ATCTCCCTTACCTCATCACCGACCAACGACGCGTGTGAGCTTCGAGAGCGCCCTTC	703			

RESULT 33
CF699606
LOCUS
DEFINITION
CCAH574TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAH574, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
CF699606.1 GI:41553765
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS
TITLE
Loftus, B.
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library

JOURNAL
COMMENT
Unpublished (2003)
Other_ESTs: CCAH574TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.

FEATURES
source
1. .869
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAH574"
/clone_lib="C.neoformans strain JEC21"
/note="vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full

length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN		Query Match	41.3%;	Score 173.6;	DB 6;	Length 869;
		Best Local Similarity	65.0%;	Pred. No. 4.7e-26;	Mismatches 144;	Indels 3;
		Matches 273;	Conservative	0;		
QY	4	AAGACGAGCAGCTGCGCGGTGACGTACGACACCGCGGCTTCTCGCCAGCGCTC	63			
Db	325	AAGACCAACGACACTGCGCGGTGACGTACGACACCGCGGCTTCTCGCCAGCGCTC	384			
QY	64	GTACGCGAGCGCTGCGCAACGTCGCGCGGTGCAACCCCGATGCTCTCAAGCGCGC	123			
Db	385	TACTCTGAGGGTGTGAAGACGTCGCGCGGTGCAACCCCGATGCTCTCGGTGAGGT	444			
QY	124	ATCGAAGGCGCGTTCGAGGCGCTTCTCGCGCGCTTCTCGAGCGAGGAGATGTCGAG	183			
Db	445	GCCGAGAAGCTGTGCAACAGGTCCTCGAGGTTCTTGTCTGCCAACAAGGTTATCACC	504			
QY	184	ACGAGGAGCAGATCGCTTCACGCGCTTCTCATCTCCGC---	240			
Db	505	ACCTCTGAGGAGATTCGCCAGGTTCGCCACCATCTCGCCCAACGCGGATACCCACGTCGT	564			
QY	241	GAGCTCATCGCGAGCGATGGCAAGTCTCGCAAGGAGGCTCATCACCGTCGAGGAG	300			
Db	565	GCCATCATTCGCCAGCCATGGAGCAGGTTCGCAAGGAGGTTCTCATCTGTTAAGGAG	624			
QY	301	TCCGAGACCTTCGCTCTGAGCTGGAGCTCACCGAGGGTATGCGTTTCGCAAGGGCTAC	360			
Db	625	GGCGAACCATTCGACGACGAGATTGAGATTACCGAGGGTATGCGATTCCGACCGAGGCTTC	684			
QY	361	ATCTCGCGCTACTTCGCCACGACATGAGCGGATGAGCGGCTGCTCGACGACCGCTAC	420			
Db	685	ATCTCCCTTACCTCATCACCGACCAACGACGCGTGTGAGCTTCGAGAGCGCCCTTC	744			

RESULT 34
CF695217
LOCUS
DEFINITION
CCAFB71TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAFB71, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
CF695217.1 GI:41549376
EST.

ORGANISM
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

REFERENCE
AUTHORS
TITLE
Loftus, B.
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library

JOURNAL
COMMENT
Unpublished (2003)
Other_ESTs: CCAFB71TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.

FEATURES
source
1. .872
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAFB71"
/clone_lib="C.neoformans strain JEC21"

/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site_1: NotI, EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 877;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGCTCGCGGTACGCTACGACACCGACCGCTTCTCGCCAGCGGCTC 63
|||||
DB 298 AAGACCAACGACACTGCGGTGACGTACCAACACCGCCACTGTCTCGCCGAGCATC 357
|||||
QY 64 GTACGCGAGGCGCTTCGCAACGCTCGCGCGGTGCCAACCGCATGGCTCTCAAGCGCGGC 123
|||||
DB 358 TACTCTGAGGGGTGTGAAGAACGTCGCTCGCGGCTGCAACCCCATGACCTTCGTCGAGGT 417
|||||
QY 124 ATCGAAGAGCGCTCGAGGCGCTCTCGCGCGCTGCTGGAGCAGCGGAGGATGTCGAG 183
|||||
DB 418 GCCCAGAAGGCTGTGCAAGGTCCTCGAGGTTCTTGCTGCCAACAAAAGGTTATCACC 477
|||||
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
|||||
DB 478 ACCTCTGAGGAGATTGCCAGGTGCCACCATCTCCGCCAACCGCGATACCCACGTCGT 537
|||||
QY 241 GAGCTCATTCGCGAGGCGGTGACGACGAGTGGCGAAGGAGGCGTTCATCAGCTCGAGGAG 300
|||||
DB 538 GCCATCATTTGCCAAGCATGAGCAGGTGCGCAAGGAGGTTGTTCATCACTGTTAAGGAG 597
|||||
QY 301 TCCGAGACCTTCGCTGAGGCTGAGCTCACGAGGATGCGCTTCGACAGGCGCTAC 360
|||||
DB 598 GGCCGAACCATTTGACGACGAGATTGAGATTACGAGGTTATCGAATTCGACCGAGGCTTC 657
|||||
QY 361 ATCTCGCGGTACTTTCGCCACCGCATGGAGCGGATGAGGCGTTCGTCGACGACCCGCTAC 420
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DB 658 ATCTCCCTTACCTCATCAGCAGCACCAAGACAGCGGTGTCGAGCTCGAGAGCCCTTC 717
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RESULT 37
CF682687 878 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION CCA161TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAC161, mRNA sequence.

ACCESSION
VERSION CF682687.1 GI:41536846
KEYWORDS
SOURCE EST.

ORGANISM
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS 1 (bases 1 to 878)
Loftus, B.
TITLE End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAC161TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.

FEATURES
source Location/Qualifiers
1..878
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"

/clone="CCAC161"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site_1: NotI, EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 878;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGCTCGCGGTACGCTACGACACCGACCGCTTCTCGCCAGCGGCTC 63
|||||
DB 322 AAGACCAACGACACTGCGGTGACGTACCAACACCGCCACTGTCTCGCCGAGCATC 381
|||||
QY 64 GTACGCGAGGCGCTTCGCAACGCTCGCGCGGTGCCAACCGCATGGCTCTCAAGCGCGGC 123
|||||
DB 382 TACTCTGAGGGGTGTGAAGAACGTCGCTCGCGGCTGCAACCCCATGACCTTCGTCGAGGT 441
|||||
QY 124 ATCGAAGAGCGCTCGAGGCGCTCTCGCGCGCTGCTGGAGCAGCGGAGGATGTCGAG 183
|||||
DB 442 GCCCAGAAGGCTGTGCAAGGTCCTCGAGGTTCTTGCTGCCAACAAAAGGTTATCACC 501
|||||
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
|||||
DB 502 ACCTCTGAGGAGATTGCCAGGTGCCACCATCTCCGCCAACCGCGATACCCACGTCGT 561
|||||
QY 241 GAGCTCATTCGCGAGGCGGTGACGACGAGTGGCGAAGGAGGCGTTCATCAGCTCGAGGAG 300
|||||
DB 562 GCCATCATTTGCCAAGCATGAGCAGGTGCGCAAGGAGGTTGTTCATCACTGTTAAGGAG 621
|||||
QY 301 TCCGAGACCTTCGCTGAGGCTGAGCTCACGAGGATGCGCTTCGACAGGCGCTAC 360
|||||
DB 622 GGCCGAACCATTTGACGACGAGATTGAGATTACGAGGTTATCGAATTCGACCGAGGCTTC 681
|||||
QY 361 ATCTCGCGGTACTTTCGCCACCGCATGGAGCGGATGAGGCGTTCGTCGACGACCCGCTAC 420
|||||
DB 682 ATCTCCCTTACCTCATCAGCAGCACCAAGACAGCGGTGTCGAGCTCGAGAGCCCTTC 741
|||||

RESULT 38
CF700757 881 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION CCA150TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCA150, mRNA sequence.

ACCESSION
VERSION CF700757
KEYWORDS
SOURCE EST.

ORGANISM
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS 1 (bases 1 to 881)
Loftus, B.
TITLE End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCA150TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.

FEATURES
source Location/Qualifiers
1..881
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"

/db xref="taxon:40410"
/clone="CAH150"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 881;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGAGCAGCTGCGCGGTGACGGTACGACCAACCGGCGGCTTCGCGCCAGGCGCTC 63
DB 34 AAGACCAACGACACTGCGGTGACGGTACGACCAACCGGCGGCTTCGCGCCAGGCGCTC 93
QY 64 GTACGGAGGCGCTGCGCAAGCTGCGCGCGGTCGCAACCGGATGCTTCAAGCGCGC 123
DB 94 TACTCTGAGGGTGTGAAGAACGTCGCTGCGCGGTCGCAACCGGATGCTTCAAGCGCGC 153
QY 124 ATCGAGAGGCGCTGCGAGGCGCTTCGCGCGGCTGCTGAGCAGCGGAGGATGCGAG 183
DB 154 GCCCAGAGGCTGTGACGAGGCTCTCGAGGTTCTTCTGCTGCCAACAAGGTTATCACC 213
QY 184 ACCAAGAGCAGATGCTTCCAGGCTTCATCTCCG---CGCCGACACCGAGATCGGC 240
DB 214 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCGCGCAACCGGCGATACCCACGTCGT 273
QY 241 GAGCTCATGCCGAGCGGTGACAGAGTGGCAAGGAGGCGTTCATCCGTCGAGGAG 300
DB 274 GCATCATTGCCCAAGCCATGAGGAGGTCGCAAGGAGGTCATCATCTGTTAAGGAG 333
QY 301 TCCGAGACCTTCGCTGAGCTGAGCTCACCGAGGTCATGCGTTCCAGAGGCTAC 360
DB 334 GCGCGAACCATTCACGACGAGTTGAGATTACCGAGGTCATGCGTTCCAGGCTTC 393
QY 361 ATCTCGGCTACTTCGCGCACCGACATGAGCGGATGAGGCGCTGCTTCGACGACCGGTAC 420
DB 394 ATCTCCCTTACCTCATCCGACACCAAGAACCGGTCGAGCTCGAGAGGCGCTTC 453

RESULT 39

CF696919 891 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION
CF696919 C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCACL52, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

CF696919.1 GI:41551078
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 891)
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCACL52T0
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES

source

1..891
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"

/strain="JEC21"
/db xref="taxon:40410"
/clone="CCACL52"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 891;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGAGCAGCTGCGCGGTGACGGTACGACCAACCGGCGGCTTCGCGCCAGGCGCTC 63
DB 273 AAGACCAACGACACTGCGGTGACGGTACGACCAACCGGCGGCTTCGCGCCAGGCGCTC 332
QY 64 GTACGGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGGATGCTTCAAGCGCGC 123
DB 333 TACTCTGAGGGTGTGAAGAACGTCGCTGCGCGGTCGCAACCGGATGCTTCAAGCGCGC 392
QY 124 ATCGAGAGGCGCTGAGGCGCTTCGCGCGGCTGCTGAGCAGCGGAGGATGCGAG 183
DB 393 GCCCAGAGGCGCTGAGCAGGCTTCGAGGTTCTTGTGCTGCCAACAAGGTTATCACC 452
QY 184 ACCAAGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGAGATCGGC 240
DB 453 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCGCGCAACCGGCGATACCCACGTCGT 512
QY 241 GAGCTCATGCCGAGCGGATGACAAAGTTCGCAAGGAGGCGTCATCAACCGTCGAGGAG 300
DB 513 GCATCATTTGCCCAAGCCATGAGCAGGTCGCAAGGAGGTCATCATCTGTTAAGGAG 572
QY 301 TCCGAGACTTCGCTGAGCTGAGCTCACCGAGGTCATGCGTTCCAGAGGCTAC 360
DB 573 GCGCGAACCATTCACGACGAGATTGAGATTACCGAGGTCATGCGTTCCAGGCTTC 632
QY 361 ATCTCGGCTACTTCGCGCACCGACATGAGCGGATGAGGCGCTGCTTCGACGACCGGTAC 420
DB 633 ATCTCCCTTACCTCATCCGACACCAAGAACCGGTCGAGCTCGAGAGGCGCTTC 692

RESULT 40

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..901

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

Seq primer: TR.

Location/Qualifiers

1..901

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

Seq primer: TR.

Location/Qualifiers

1..901

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

Seq primer: TR.

Location/Qualifiers

1..901

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

Seq primer: TR.

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/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="CCAER16"
/clone_lib="C.neoformans strain JEC21"
/notes="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 901;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGACGATCGCGGTGACGATACGACCAACCGGACCGTTCTTCGCCAGGCGCTC 63
Db 325 AAGACCAACGACACTGCGCGGTGACGATACGACCAACCGGACCGTTCTTCGCCAGGCGCTC 384
QY 64 GTACGCGAGGCGCTGCGCAAGCTGCGCGGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123
Db 385 TACTCTGAGGCGTGAAGAACGTCGCTGCGCGGTGCGCAACCGGATGGCTCTTCGAGGT 444
QY 124 ATCAGAGAGGCGCTGCGAGCGGCTCTCGCGCGGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 183
Db 445 GCCAGAGGCGTTCGACAGGTCCTCGAGGTTCTTGTCTGCCAACAAGAGTTATCACC 504
QY 184 ACCAAGGAGCAGATCGCTTCCAGCGGCTTCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db 505 ACCTCTGAGGAGATTGCCAGGTGCGCAACCATCTCCGCAACCGGATACCCACGTCGGT 564
QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGGCAAGGCGTCATCAGCGTCGAGGAG 300
Db 565 GCCATCATTTGCCAAGCGATGGAGCGGTGCGCAAGGCGGTGTCATCTGTTAAGGAG 624
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCAGGATGATCGCTTTCGACCAAGGCGTAC 360
Db 625 GGCGAACCATTGACGAGGATTTGAGATTACCGAGGATGCGATTGCGACCGGCTTC 684
QY 361 ATCTCGGCGTACTTTCGACCGACATGAGCGGATGAGGCGGTGCTCGACGACCGCTAC 420
Db 685 ATCTCCCTTACCTCATCACCAGCAACCAAGAACGAGCGGTGTCGAGCTCGAAGAGCCCTTC 744

RESULT 41
CF716339 910 bp mRNA linear EST 16-AUG-2004
LOCUS CCAER16TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCAER16, mRNA sequence.
ACCESSION CF716339.1 GI:41570498
VERSION EST.
KEYWORDS Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
SOURCE var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 910)
AUTHORS Loftus, B.
TITLE End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAER16TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1. .910

FEATURES
source
1. .910

/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="CCADQ25"
/clone_lib="C.neoformans strain JEC21"
/notes="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 901;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGACGATCGCGGTGACGATACGACCAACCGGACCGTTCTTCGCCAGGCGCTC 63
Db 325 AAGACCAACGACACTGCGCGGTGACGATACGACCAACCGGACCGTTCTTCGCCAGGCGCTC 384
QY 64 GTACGCGAGGCGCTGCGCAAGCTGCGCGGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123
Db 385 TACTCTGAGGCGTGAAGAACGTCGCTGCGCGGTGCGCAACCGGATGGCTCTTCGAGGT 444
QY 124 ATCAGAGAGGCGCTGCGAGCGGCTCTCGCGCGGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 183
Db 445 GCCAGAGGCGTTCGACAGGTCCTCGAGGTTCTTGTCTGCCAACAAGAGTTATCACC 504
QY 184 ACCAAGGAGCAGATCGCTTCCAGCGGCTTCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db 505 ACCTCTGAGGAGATTGCCAGGTGCGCAACCATCTCCGCAACCGGATACCCACGTCGGT 564
QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGGCAAGGCGTCATCAGCGTCGAGGAG 300
Db 565 GCCATCATTTGCCAAGCGATGGAGCGGTGCGCAAGGCGGTGTCATCTGTTAAGGAG 624
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCAGGATGATCGCTTTCGACCAAGGCGTAC 360
Db 625 GGCGAACCATTGACGAGGATTTGAGATTACCGAGGATGCGATTGCGACCGGCTTC 684
QY 361 ATCTCGGCGTACTTTCGACCGACATGAGCGGATGAGGCGGTGCTCGACGACCGCTAC 420
Db 685 ATCTCCCTTACCTCATCACCAGCAACCAAGAACGAGCGGTGTCGAGCTCGAAGAGCCCTTC 744

RESULT 42
CF711999 921 bp mRNA linear EST 16-AUG-2004
LOCUS CCAC030TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCAC030, mRNA sequence.
ACCESSION CF711999
VERSION CF711999.1 GI:41566158
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
ORGANISM var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 921)
AUTHORS Loftus, B.
TITLE End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAC030TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1. .910

FEATURES
source
1. .910
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source 1. .921
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/note="vector: pCMVSPORT6; Site 1: NotI EcorV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 921;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGAGGTACGACACCGCGGATCTTCGCGCCGAGCGCTC 63
Db 322 AAGACCAACGACACTGCGGTGAGGTACGACACCGCGGATCTTCGCGCCGAGCCATC 381
QY 64 GTACGCGAGGCGCTCGCGGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGC 123
Db 382 TACTCTGAGGGTGTGAAGACGTGCTGCGGTGCGCAACCGGATGCTCTCAAGCGCGC 441
QY 124 ATCGAAGCGCGTTCGAGCGCGTCTCGCGCGCGTCTCGCGCGCGGTGCGCAACCGGATGCTCGAG 183
Db 442 GCCCAGAAGCGTTCGACAGAGTCTCGAGGTCTTCGCGCGCGGTGCGCAACCGGATGCTCAACC 501
QY 184 ACCAAGGACGATCGTTCACGCGCTCCATCTCGC---CGCGACACCGGATCGGC 240
Db 502 ACCTCTGAGGAGATGCGCGAGTTCGCGCGCGGTGCGCAACCGGATGCTCAACC 551
QY 241 GAGCTCATCGCGAGCGGTGCGCAAGTTCGCGCAAGGCGTTCATCCGTCGAGGAG 300
Db 562 GCATCATGTCGCGACGATGAGCGGTGCGCGAGGAGGTGCTCATCTGTAAGGAG 621
QY 301 TCCGACGCTTCGCTGAGCTGAGCTCACGAGGTATGCGTTCGACAGGCGCTAC 360
Db 622 GCGCGAACCATTGACGACGAGATTGAGATTACCGGGGTATGCGATTGCGACGAGCTTC 681
QY 361 ATCTCGGCTACTTCGCGCGGATGAGCGGATGAGCGGTGCTTCGACGACCGTAC 420
Db 682 ATCTCCCTTACCTCATCGCGACACCAAGACCGGTGTCGAGTTCGAGAGCGCTTC 741

RESULT 43
CF716527
LOCUS
DEFINITION
CF716527 C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAGN89, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
CF716527.1 GI:41570686
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
Loftus, B.
1 (bases 1 to 716)
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCAGN89TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES
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/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
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/note="vector: pCMVSPORT6; Site 1: NotI EcorV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.2%; Score 173.2; DB 6; Length 716;
Best Local Similarity 65.1%; Pred. No. 5.7e-26;
Matches 272; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGAGGTACGACACCGCGGATCTTCGCGCCGAGCGCTC 63
Db 298 AAGACCAACGACACTGCGGTGAGGTACGACACCGCGGATCTTCGCGCCGAGCCATC 357
QY 64 GTACGCGAGGCGCTCGCGGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGC 123
Db 358 TACTCTGAGGGTGTGAAGAACGTGCTGCGCGGTGCGCAACCGGATGCTCTCAAGCGCT 417
QY 124 ATCGAAGCGCGTTCGAGCGCGTCTCGCGCGCGTCTCGCGCGCGGTGCGCAACCGGATGCTCGAG 183
Db 418 GCCCAGAAGCGTTCGACAGGTCTCGAGGTCTTCGCGCGGTGCGCAACCGGATGCTCAACC 477
QY 184 ACCAAGGACGATCGTTCACGCGCTCCATCTCGC---CGCGACACCGGATCGGC 240
Db 478 ACCTCTGAGGAGATTGCCCGAGTTCGCCCATCTTCGCCCAACCGGATGCTCAACC 537
QY 241 GAGCTCATCGCGAGCGGTGCGCAAGTTCGCGCAAGGAGGTGCTCATCCGTCGAGGAG 300
Db 538 GCATCATGTCGCGACGATGAGCGGTGCGCGAGGAGGTGCTCATCTGTTAAGGAG 597
QY 301 TCCGACGCTTCGCTGAGCTGAGCTCACGAGGTATGCGTTCGACAGGCGCTAC 360
Db 598 GCGCGAACCATTGACGACGAGATTGAGATTACCGGGGTATGCGATTGCGACGAGCTTC 657
QY 361 ATCTCGGCTACTTCGCGCGGATGAGCGGATGAGCGGTGCTTCGACGACCGCTAC 418
Db 658 ATCTCCCTTACCTCATCGCGACACCAAGACCGGTGTCGAGTTCGAGAGCGCT 715

RESULT 44
CF687310
LOCUS
DEFINITION
CF687310 C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAA141, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
CF687310.1 GI:41541469
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
Loftus, B.
1 (bases 1 to 759)
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

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FEATURES
source
  Location/Qualifiers
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      /mol_type="mRNA"
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      /clone_lib="C.neoformans strain JEC21"
      /note="Vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      41.2%; Score 173.2; DB 6; Length 759;
Best Local Similarity 65.1%; Pred. No. 5.7e-26;
Matches 272; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCGTCGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 63
Db 332 AAGACCAACGACACTGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 391
QY 64 GTACGCGAGGCGCTGCGCAAGTTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
Db 392 TACTCTGAGGGTGTGAAGACGTGCGTCCGGCTGCAACCCATGGACCTCGGTGAGGT 451
QY 124 ATCAGAGAGCGGTGCGAGCGGTCTCCGGCGCCCTGCTGGAGCGGCGAAGGATGTCGAG 183
Db 452 GCCCAGAGGCTGCGACAGGTCTCTCGAGGTCTTGTGCTGCAACAAAGAGGTATCACC 511
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGATCGGC 240
Db 512 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCGAAGCGGATACCCAGTGGT 571
QY 241 GAGCTCATTCGCGAGGCGATGACAGGTGCGCAAGGAGGCGTCAACCGTTCGAGGAG 300
Db 572 GCCATCATTCGCGAGGCGATGAGCAGGTGCGCAAGGAGGCGTCAACCGTTCGAGGAG 631
QY 301 TCCAGACCTTCGCTGAGGCTGAGCTACCGAGGATGCGCTTCGACAGGCGTAC 360
Db 632 GGCCGAACCATTCGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTC 691
QY 361 ATCTCGGCGTACTTCGCCACCGATGAGCGGATGAGGCGTCTCGACGACCCGT 418
Db 692 ATCTCCCTTACCTCATCACCAGACCAAGAACAGCGTGTGAGCTCGAGAGCCCTT 749

RESULT 45
CF679031
LOCUS
DEFINITION
  CCAC445TR C.neoformans strain JEC21 Cryptococcus neoformans var.
  neoformans cDNA clone CCAC445, mRNA sequence.
ACCESSION
  CF679031
VERSION
  CF679031.1 GI:41533190
KEYWORDS
  EST.
SOURCE
  Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
  var. neoformans)
ORGANISM
  Cryptococcus neoformans var. neoformans
  Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
  Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
  Filobasidiella.
REFERENCE
  1 (bases 1 to 794)
  Loftus,B.
  End sequencing of clones from a Full length enriched, normalized
  JEC21 cDNA library
  Unpublished (2003)
  Other_ESTs: CCAC445TF
  Contact: Brendan Loftus
  The Institute for Genomic Research (TIGR; www.tigr.org)
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-3543
  Fax: 301-838-0208
  Email: bjloftus@tigr.org

FEATURES
source
  Location/Qualifiers
    1..794
      /organism="Cryptococcus neoformans var. neoformans"
      /mol_type="mRNA"
      /strain="JEC21"
      /db_xref="taxon:40410"
      /clone="CCAC445"
      /clone_lib="C.neoformans strain JEC21"
      /note="Vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      41.2%; Score 173.2; DB 6; Length 794;
Best Local Similarity 65.1%; Pred. No. 5.7e-26;
Matches 272; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCGTCGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 63
Db 322 AAGACCAACGACACTGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 381
QY 64 GTACGCGAGGCGCTGCGCAAGTTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
Db 382 TACTCTGAGGGTGTGAAGACGTGCGTCCGGCTGCAACCCATGGACCTCGGTGAGGT 441
QY 124 ATCAGAGAGCGGTGCGAGCGGTCTCCGGCGCCCTGCTGGAGCGGCGAAGGATGTCGAG 183
Db 442 GCCCAGAGGCTGCGACAGGTCTCTCGAGGTCTTGTGCTGCAACAAAGAGGTATCACC 501
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGATCGGC 240
Db 502 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCGAAGCGGATACCCAGTGGT 561
QY 241 GAGCTCATTCGCGAGGCGATGGAAGTTCGCAAGGAGGCGTCAACCGTTCGAGGAG 300
Db 562 GCCATCATTCGCCAAGCATGGAGCGGTGCGCAAGGAGGCGTCAACCGTTCGAGGAG 621
QY 301 TCCAGACCTTCGCTGAGGCTGAGCTACCGAGGATGCGCTTCGACAGGCGTAC 360
Db 622 GGCCGAACCATTCGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTC 681
QY 361 ATCTCGGCGTACTTCGCCACCGATGAGCGGATGAGGCGTCTCGACGACCCGT 418
Db 682 ATCTCCCTTACCTCATCACCAGACCAAGAACAGCGTGTGAGCTCGAGAGCCCTT 739

RESULT 46
CF707648
LOCUS
DEFINITION
  CCAC864TR C.neoformans strain JEC21 Cryptococcus neoformans var.
  neoformans cDNA clone CCAC864, mRNA sequence.
ACCESSION
  CF707648
VERSION
  CF707648.1 GI:41561807
KEYWORDS
  EST.
SOURCE
  Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
  var. neoformans)
ORGANISM
  Cryptococcus neoformans var. neoformans
  Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
  Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
  Filobasidiella.
REFERENCE
  1 (bases 1 to 758)
  Loftus,B.
  End sequencing of clones from a Full length enriched, normalized
  JEC21 cDNA library
  Unpublished (2003)
  Other_ESTs: CCAC864TF
  Contact: Brendan Loftus
  The Institute for Genomic Research (TIGR; www.tigr.org)
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-3543
  Fax: 301-838-0208
```


Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TK.

FEATURES

source
 1. 746
 /organism="Cryptococcus neoformans var. neoformans"
 /strain="JEC21"
 /mol_type="mRNA"
 /db_xref="taxon:40410"
 /clone="CCAHF79"
 /clone_lib="C neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 40.9%; Score 171.6; DB 6; Length 746;
 Best Local Similarity 65.4%; Pred. No. 1.2e-25;
 Matches 268; Conservative 0; Mismatches 139; Indels 3; Gaps 1;
 QY 4 AAGACGACGACGTCGCGGTGACGATACGACCGACCGCGTTCCTCGCCAGGCGCTC 63
 DB 333 AAGACCAACGACACTGCGGTGACGATACCAACCGCCACTGTCTCGCCGAGCCATC 392
 QY 64 GTACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
 DB 393 TACTCTGAGGTGTGAAGAACGTCGCGCGGTGCAACCCATCGATGCGCGAGGT 452
 QY 124 ATCAGAGGCGGTGCGAGGCGCTCGCGCGCGCTGCTGGAGGCGAGGATGTCGAG 183
 DB 453 GCCCAGAGGCTGTGCGAAGCTCTCGAGGTTCTTGTGCGCAAAAGGTTATCACC 512
 QY 184 ACCAAGGACGACATCGCTTCCACGCGCTTCCATCTCCGC---CGCCGACACCCAGATCGC 240
 DB 513 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCAAGCGGATACCCAGTCGT 572
 QY 241 GAGCTATCGCGGAGGATGGAACAAGTTCGGGAAGAGGCGTCATCAGCGTCGAGGAG 300
 DB 573 GCCATCATTTGCCAAGCATGGAGCGGTGCGCAAGGAGGTTGTCATCACTGTTAAGGAG 632
 QY 301 TCCAGACCTTGGTGTGAGCTGAGCTACCGAGGATGCGCTTCGACCAAGGCGTAC 360
 DB 633 GGCGCAACATTGACGACGATGAGATTACCGAGGATGCGATTCGACCGAGGCTTC 692
 QY 361 ATCTCGGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGTCTGA 410
 DB 693 ATCTCCCTTACCTCATCACCACACCAAGAACGAGCGTGTGAGCTCGA 742

RESULT 49

CK446096
 LOCUS
 DEFINITION pncs914ad05.SP6 Aspergillus nidulans negative subtraction hybridization polysaccharide related cDNA plasmid library
 Emericella nidulans cDNA clone pncs914ad05 5', mRNA sequence.
 CK446096
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Emericella nidulans (anamorph: Aspergillus nidulans)
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
 REFERENCE Ray, A., Macwana, S., Ayoubi, P., Hall, L. T., Prade, R. and Mort, A. J.
 AUTHORS (bases 1 to 752)
 TITLE Negative subtraction hybridization: An efficient method to isolate large numbers of condition-specific cDNAs
 JOURNAL BMC Genomics 5 (1), 22 (2004)
 PUBMED 15050035
 COMMENT Contact: Patricia Ayoubi
 Department of Biochemistry and Molecular Biology
 Oklahoma State University

248 Noble Research Center, Stillwater OK, 74078
 Tel: 405-744-6209
 Fax: 405-744-7799
 Email: ayoubi@okstate.edu

PCR Primers

FORWARD: SP6
 BACKWARD: T7
 Insert Length: 1 Std Error: 0.00
 Seq primer: SP6.

FEATURES

source
 1. 752
 /organism="Emericella nidulans"
 /mol_type="mRNA"
 /strain="FGSC C26"
 /db_xref="taxon:162425"
 /clone="pncs914ad05"
 /tissue_type="vegetative mycelia"
 /lab_host="E. coli"
 /clone_lib="Aspergillus nidulans negative subtraction hybridization polysaccharide related cDNA plasmid library"
 /note="Vector: pCMVSPORT6.0; Site 1: EcoRI; Site 2: HindIII; 5' end of cDNA cloned near EcoRI site of pCMVSPORT6.0 and 3' end cloned near HindIII site of pCMVSPORT6.0. Average length of insert is 1.49 kb"

ORIGIN

Query Match 40.8%; Score 171.2; DB 7; Length 752;
 Best Local Similarity 64.9%; Pred. No. 1.5e-25;
 Matches 270; Conservative 0; Mismatches 143; Indels 3; Gaps 1;
 QY 4 AAGACGACGACGTCGCGGTGACGATACGACCGACCGCGTTCCTCGCCAGGCGCTC 63
 DB 99 AAGACCAACGACACTGCTGTGACGATACCAACCGCTACCGTTCTCGCCGCGCTATC 158
 QY 64 GTACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
 DB 159 TTTTCCGAGACCGCTTAAGAACGTTGTGTGCTGCGGTGCAACCCCATGGATCTGCGCCGCGT 218
 QY 124 ATCGAGAGGCGCTCGAGGCGCTCGCGCGCGCTGCTGGAGCAGGAGGATGTCGAG 183
 DB 219 ATCCAGGCTGCTGTGAAGCGCTGTGCTGCTACCTCCAGCAGAACAGCGTGTATCTACT 278
 QY 184 ACCAAGGACGACATCGCTTCCAGCGCTCCATCTCCGC---CGCCGACACCCAGATCGC 240
 DB 279 ACTGAGAGGAGATTGCTGTGCTGCTACCATCTCTGCTAACGCTGACACCCAGTTGGC 338
 QY 241 GAGCTATCCCGAGGCGATGGAACAAGTTCGGAAGAGGCGTCATCAGCGTCGAGGAG 300
 DB 339 AAGCTTATCTCCACTGCTGAGCGCGCTGCTGAAGGCGCGCTTATCACTGTCAAGGAG 398
 QY 301 TCCAGACCTTCTGCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGCTAC 360
 DB 399 GGCAAGACCTTGAAGGACGAGCTTGAAGTTACTGAGGATGCGCTTCGACCGTGGTTAC 458
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCC 416
 DB 459 ACCTCCCTTACTTCAATACGACTGCGCGCGCCAGGCCCTTCAAGCTCGAGAGGCC 514

RESULT 50

CF707221
 LOCUS
 DEFINITION CCAH138TR C. neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAH138, mRNA sequence.
 CF707221
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

```
REFERENCE 1 (bases 1 to 724)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a Full length enriched, normalized
JOURNAL JEC21 cDNA library
COMMENT Unpublished (2003)
Other ESTs: CCAH138TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
FEATURES
source 1..724
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="CCA138"
/clone_lib="C.neoformans strain JEC21"
/notes="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"
ORIGIN
Query Match 40.7%; Score 170.8; DB 6; Length 724;
Best Local Similarity 66.7%; Pred. No. 1.8e-25;
Matches 260; Conservative 0; Mismatches 127; Indels 3; Gaps 1;
QY 4 AAGACGAGGAGCGTCCGGTGACGAGTACGACACCGCGGACCGTCTTCGCCCGGCGCTC 63
DB 325 AAGACCAACGACACTGCGGTGACGAGTACCAACCGCCACTGTCTCGCCCGGAGCATC 384
QY 64 GTACGGGAGGCGCTGCGAACGTCGCGCGCGCTCTCGAGCAGCGAGGATGTCGAG 123
DB 385 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGTGCAACCCCACTGACCTTCGAGGT 444
QY 124 ATCGAGAGCGCGCTGAGCGCGCTCTCGCGCGCTCTCGAGCAGCGAGGATGTCGAG 183
DB 445 GCCCAGAGCGCTGCGACGAGTCTCGAGGTCTTCGCGCAACAAAGGTATCACC 504
QY 184 ACCAAGAGGAGATCGCTTCCAGCGCTCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 505 ACCTCTGAGGAGATGCGCAGGTGCGCACCATCTCGCCCAACGGCGATACCCAGTCGT 564
QY 241 GAGCTCATCGCGAGCGGATGGAAGAGTGGGCAAGAGGCGTCTATCAACGTCGAGGAG 300
DB 565 GCCATCATTTGCCCAAGCCATGGAGCAGGTGCGCAAGGAGGTGTCTATCATCTGTAAGGAG 624
QY 301 TCCGACACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGCAAGGCGCTAC 360
DB 625 GGCCGAACCATTCAGCAGGATTTAGATTACCGGGTATGCGATTTCGACCGAGGCTTC 684
QY 361 ATCTCGCGGTACTTTCGCCACCGACATGGAG 390
DB 685 ATCTCCCTTACCTCATACCGACCAAG 714
RESULT 51
CF704854 731 bp mRNA linear EST 16-AUG-2004
LOCUS CCAH737TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCAH737, mRNA sequence.
ACCESSION CF704854
VERSION CF704854.1 GI:41559013
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

REFERENCE 1 (bases 1 to 731)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a Full length enriched, normalized
JOURNAL JEC21 cDNA library
COMMENT Unpublished (2003)
Other ESTs: CCAH737TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
FEATURES
source 1..731
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="CCA737"
/clone_lib="C.neoformans strain JEC21"
/notes="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"
ORIGIN
Query Match 40.7%; Score 170.8; DB 6; Length 731;
Best Local Similarity 66.7%; Pred. No. 1.8e-25;
Matches 260; Conservative 0; Mismatches 127; Indels 3; Gaps 1;
QY 4 AAGACGAGGAGCGTCCGGTGACGAGTACGACACCGCGGACCGTCTTCGCCCGGCGCTC 63
DB 333 AAGACCAACGACACTGCGGTGACGAGTACCAACCGCCACTGTCTTCGCCCGGAGCATC 392
QY 64 GTACGAGGAGGCGCTGCGAACGTCGCGCGCGCTCTCAAGCGCGGC 123
DB 393 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGTGCAACCCCACTGACCTTCGAGGT 452
QY 124 ATCGAGAGGCGCTGAGCGCGCTCTCGCGCGCTCTCGAGCAGCGAGGATGTCGAG 183
DB 453 GCCCAGAGGCGTTCGACAGGTCTCGAGGTCTTCGCGCAACAAAGGTATCACC 512
QY 184 ACCAAGGAGCAGATCGCTTCCAGCGCTCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 513 ACCTCTGAGGAGATGCGCAGGTGCGCAGCTCTCGCCCAACGGCGATACCCACGTCGT 572
QY 241 GAGCTCATCGCGAGCGGATGGAAGGTGCGCAAGGAGGCGTCTATCAACGTCGAGGAG 300
DB 573 GCCATCATTTGCCCAAGCCATGGAGCAGGTGCGCAAGGAGGTGTCTATCATCTGTAAGGAG 632
QY 301 TCCGACACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGCAAGGCGCTAC 360
DB 633 GGCCGAACCATTCAGCAGGATTTAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 692
QY 361 ATCTCGCGGTACTTTCGCCACCGACATGGAG 390
DB 693 ATCTCCCTTACCTCATACCGACCAAG 722
RESULT 52
CF689741 707 bp mRNA linear EST 16-AUG-2004
LOCUS CCAH737TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCAH737, mRNA sequence.
ACCESSION CF689741
VERSION CF689741.1 GI:41543900
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
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Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

1 (bases 1 to 707)

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjlloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. 707

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clones="CCACS77"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

1 (bases 1 to 778)

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAA740TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjlloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. 778

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clones="CCAA740"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

RESULT 54

CF708616

LOCUS

DEFINITION

CCAB155TR C.neoformans strain JEC21 Cryptococcus neoformans var.

neoformans cDNA clone CCA155, mRNA sequence.

ACCESSION

CF708616

VERSION

CF708616.1

GI:41562775

EST.

KEYWORDS

SOURCE

ORGANISM

Query Match 40.6%; Score 170.6; DB 6; Length 778;

Best Local Similarity 67.0%; Pred. No. 2e-25;

Matches 258; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Loftus, B.
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCABI55TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES
source

1. .840
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCABI55"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 40.6%; Score 170.6; DB 6; Length 840;
Best Local Similarity 67.0%; Pred. No. 2e-25;
Matches 258; Conservative 0; Mismatches 124; Indels 3; Gaps 1;
QY 4 AAGACGACGACGTCGCGGTGACGTACGACACCGCGACCGTCTTCGCCCGAGGGCGTC 63
DB 329 AAGACCAACGACACTGCGCGGTGACGTACGACACCGCGACCGTCTTCGCCCGAGCCATC 388
QY 64 GTACGCGAGGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGCATGCTCTCAAGCGCGGC 123
DB 389 TACTCTGAGGGTGTGAAGAAGCTGCTGCGCGGTGCAACCCCATGACCTCGTCGAGGT 448
QY 124 ATGAGAAGCGCTGAGGCGGCTCTCGCGCGCTCTCGGCGCGCTCTCGGAGCGCGAAGATGCGAG 183
DB 449 GCCCAGAAGCGCTGCGCAAGGTCTCGAGGTTCTTGCTGCCAACAAAAAGGTATCACC 508
QY 184 ACCAAGGACGATCCGTTCCAGCGCTCCATCTCCGC---CGCGACACCCAGATCGGC 240
DB 509 ACCTCTGAGGAGATGCCAGGTCGCGACATCTCCGCAACGCGCGATACCCACGTCGCT 568
QY 241 GAGCTCATCGCGAGCGGATGGAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
DB 569 GCATCATTTGCCAAGCCATGAGCAGGTGCGCAAGGAGGTTTCATCACTGTTAAGGAG 628
QY 301 TCCAGACCTTGGTCTGGAGTGGAGCTCACGAGGGTATGCGTTTCGACAAAGGCTAC 360
DB 629 GGCCGAACCAATTGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGCTTC 688
QY 361 ATCTCGGCGTACTTTCGCCACCGACA 385
DB 689 ATCTCCCTTACTCATACCGACA 713

RESULT 55

CF711662
LOCUS
DEFINITION
CF711662
ACCESSION
VERSION
KEYWORDS
SOURCE
CF711662 799 bp mRNA linear EST 16-AUG-2004
CCAFR33TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAFR33, mRNA sequence.
CF711662
CF711662.1 GI:41565821
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)

ORGANISM

Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Loftus, B.
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCAFR33TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES
source

1. .799
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAFR33"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 40.2%; Score 168.8; DB 6; Length 799;
Best Local Similarity 64.3%; Pred. No. 4.7e-25;
Matches 270; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
QY 4 AAGACGACGACGTCGCGGTGACGTACGACACCGCGACCGTCTTCGCCCGAGGGCGTC 63
DB 323 AAGACCAACGACACTGCGCGGTGACGTACGACACCGCGACCGTCTTCGCCCGAGCCATC 382
QY 64 GTACGCGAGGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGCATGCTCTCAAGCGCGGC 123
DB 383 TACTCTGAGGGTGTGAAGAAGCTGCTGCGCGGTGCAACCCCATGACCTCGTCGAGGT 442
QY 124 ATCGAGAAGCGCGTCGAGCGCGCTCTTCGCCGCGCTCTGCGAGCAGCGAAGATGTCGAG 183
DB 443 GCCCAGAAGGCTGTCGACAGGTCTCTCGAGGTTCTTGCTGCCAACAAAAAGTTATCACC 502
QY 184 ACCAAGGACGATCGCTTCCAGCGCTTCATCTCCGC---CGCGACACCCAGATCGGC 240
DB 503 ACCTCTGAGGAGATTGCCAGGTGCGCCACCATCTCCGCAACGCGGATACCCACGTCGCT 562
QY 241 GAGCTCATCGCGAGCGGATGGAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
DB 563 GCATCATTTGCCAAGCCATGAGCAGGTGCGCAAGGAGGTTTCATCACTGTTAAGGAG 622
QY 301 TCCAGACCTTGGTCTGGAGTGGAGCTCACGAGGGTATGCGTTTCGACAAAGGCTAC 360
DB 623 GGCCGAACCAATTGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAAGCTTC 682
QY 361 ATCTCGGCGTACTTTCGCCACCGACAATGAGCGGATGAGGCGTCTTCGACGACCGCTAC 420
DB 683 ATCTCCCTTACTCATCAGCAGCAACCAAGACCGCGTGTGCGAGCTCGAGAAGCGCTTC 742

RESULT 56

CF698612
LOCUS
DEFINITION
CF698612
ACCESSION
VERSION
KEYWORDS
SOURCE
CF698612 851 bp mRNA linear EST 16-AUG-2004
CCAGN42TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAGN42, mRNA sequence.
CF698612
CF698612.1 GI:41552771
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)

var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 851)
AUTHORS Loftus, B.
TITLE End sequencing of clones from a full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAGN42TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.
FEATURES Location/Qualifiers
source
1..851
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAGN42"
/clone_lib="C.neoformans strain JEC21"
/notes="vector: pcwvSport6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"
ORIGIN
Query Match 40.2%; Score 168.8; DB 6; Length 851;
Best Local Similarity 64.8%; Pred. No. 4.7e-25;
Matches 267; Conservative 0; Mismatches 142; Indels 3; Gaps 1;
Qy 12 CGAGCTCGCGGTGACGTTGACGACCGGACCGTCTCGCCGAGCGCTCGTACGCGA 71
Db 1 CGACACTGCGGTGACGTTGACGACCGGACCGTCTCGCCGAGCCATCTACTCTGA 60
Qy 72 GGGCTCTCGCAACGCTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGCTCGAGAA 131
Db 61 GGGTGTGAAGACGTCGTCGCGGCTGCAACCGGATGGCTCTCGTGGTGGCCAGAA 120
Qy 132 GCGCGTCTGAGCGCTCTCGCGCGGCTCTGAGAGCGGCGGAGATGTCGAGACCAAGGA 191
Db 121 GGGTGTGCAAGGTCCTCGAGGTTCTTGTGTCGCAACAAAGAGGTTATCAACCACTCTGA 180
Qy 192 GCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGCGAGCTCAT 248
Db 181 GGAGATTGCCAGTTCGACCATCTCGCCACCGCGGATACCCAGCTGGTGCCATCAT 240
Qy 249 CGCCGAGCGGATGCAAGGTTCGCAAGGAGGCGTTCATCACCGTCGAGGAGTCCCGAGAC 308
Db 241 TGCCCAAGCATGAGCAGGTTCGCAAGGAGGCGTTCATCATCTTTAAGGAGGCGCGAAC 300
Qy 309 CTTGCGTCTGAGCTGAGGCTCACCGAGGATATCGGCTTCGCAAGGAGGCTATCTCGGC 368
Db 301 CATTTGACGACGAGATTGAGATTACCGAGGATTCGAGTTTCGACCGAGGCTTCATCTCCCC 360
Qy 369 GTACTTCGCCACCGATGAGCGGATGAGGCGTTCGTCGACCGACCCGTAC 420
Db 361 TTACTCTATCACCGACCAAGAACCGGTGTGCGAGCTCGAAGGCCCTTC 412
RESULT 57
LOCUS CF843128 653 bp mRNA linear EST 30-OCT-2003
DEFINITION pSHB023x117f USDA-IPAFS:Expression of Phytophthora sojae genes
during infection and propagation_SHB Phytophthora sojae cDNA clone
SHB023N17 5, mRNA sequence.
ACCESSION CF843128
VERSION CF843128.1 GI:38058782

EST.
Phytophthora sojae
Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1 (bases 1 to 653)
AUTHORS Tyler, B.
TITLE Tyler, B. Not Published
JOURNAL Unpublished (2003)
COMMENT Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyley@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 023 row: N column: 17
Seq primer: BK reverse primer
High quality sequence stop: 653.
FEATURES Location/Qualifiers
source
1..653
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="SHB023N17"
/tissue="mycelium"
/cell_line="P6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="USDA-IPAFS:Expression of Phytophthora sojae
genes during infection and propagation_SHB"
/notes="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN
Query Match 39.5%; Score 165.8; DB 7; Length 653;
Best Local Similarity 64.0%; Pred. No. 2e-24;
Matches 267; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
Qy 7 ACGGAGCGCTCGCGGTGACGTTGACGACCGGACCGTCTCGCCGAGCGCTCGTA 66
Db 144 ACCAAGCGCGCGGTGACGCGCACCGTTCGCGCCACCGTGTGACGCGCGCATCTTC 203
Qy 67 CGGAGGCGCTCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGCGCATC 126
Db 204 AGCGAGGCGCTGCAAGTTCGCGCGGTCGCGGATGAAACCCACGACCTCGCCCGGGATC 263
Qy 127 GAGAAGGCGCTCGAGGCGGCTCTCGCGCGCTCTCGGAGCAGGCGAAGGATGTCGAGAC 186
Db 264 CAGATGGCGGTGACCGACCGTCTGAGAGCGGCTGCGAGAGCTGTCGAGGAGCGTGGCGAC 323
Qy 187 AAGGAGCAGATCGCTTCCACGCGCTTCATCTCCGC---CGCCGACACCGAGATCGGCGAG 243
Db 324 AAGGAGAAGGTGCGCCAGGTGGCGCACCATCTCGGCGCAACTCGGAGACGAGATCGGCAAC 383
Qy 244 CTATCGCCGAGCGGATGGAAGTTCGCAAGGAGCGCTCATCACCTCGAGGAGTCC 303
Db 384 CTATCGACGACCGCATGGAAGCGGTGGGGGCGTTCATCACGGTTCGAGAGCGGC 443
Qy 304 CAGACCTTCGCTGAGAGCTGAGAGCTCACCGAGGATGCGCTTCGCAAGGAGGCTATCATC 363
Db 444 AAGACGCTGTACAACGAGCTAGAGGTGGTTCGAGGCGATGAAGTTCGACCGCGCTTCATC 503
Qy 364 TCGCGGTACTTCGCGCACCGGATGGAAGCGGATGAGGCGGTCTGTCGACGACCGGTAC 420
Db 504 TCGCCCTTACTTCGTCACCGGACCAAGACCCAGAGCTGCGAGATGGAAGACCCCTAC 560
RESULT 58
LOCUS CF640823 393 bp mRNA linear EST 02-OCT-2003
DEFINITION D32_A12 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

sequence.
CF640823
CF640823.1 GI:37406706
EST.
Ustilago maydis
Ustilago maydis
Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
1 (bases 1 to 393)
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
14761795
Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: beaville@utms.utoronto.ca
Plate: UTM-UM-D126/7-032-UTM row: 12 column: A
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 393.
Location/Qualifiers
1..393
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."

FEATURES
sourceCV899250
LOCUS
DEFINITIONACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISMREFERENCE
AUTHORS

TITLE

JOURNAL
PUBMED
COMMENTFEATURES
source

ORIGIN

Query Match 39.3%; Score 165; DB 6; Length 393;
Best Local Similarity 66.4%; Pred. No. 2.9e-24;
Matches 253; Conservative 0; Mismatches 125; Indels 3; Gaps 1;
QY 13 GAGTCGCCGCGTACGAGTACGACACCGCGACCGTTCGCGCCAGCGCTCGTAGCGGAG 72
DB 12 GAGTCGCCGCGTACGAGTACGACACCGCGACCTGTTCTGCGCGTGCATCTACGCGGAG 71
QY 73 GGCCTGCGCAAGTGCCTGCCGCGGTGCGCAACCGATGGCTCTCAAGCGCGGATCGAGAG 132
DB 72 GGTGTCAAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
QY 133 GCGTTCGAGCGCTGCTGCGCGCGCTGCTGCGAGCGGCGAAGGATGTCGAGACCAAGGAG 192
DB 132 GGTGTGAGCGCGTCTATCAAGTTCCTCGAGACCAACAGCGTGTGTACACCTTCTGCGC 191
QY 193 CAGATGCTTCCACGCGCTCTCATCTCCGC ---CGCGCACACCGAGATCGCGGAGTCTATC 249
DB 192 GAGATGCGCCAGTGCACCATCTCAGCCACCGCGGCGGACGAGTGTGCGTCACTCATC 251
QY 250 GCGGAGCGGATGAGCAGGTGCGGAGGAGGCGTTCATCCCGTGAAGGATGCCAGACC 309
DB 252 GCCACCGCCATGAGAGGTTGGCAGGAGGAGTGTCTATCTGTCTCAAGGAGGAGGAGAGC 311
QY 310 TTGCGTCTGAGCTGAGGCTCACCGAGGATGCGCTTCGACAGGCTTACATCTCGCGG 369
DB 312 CTCGAGAGCAGATCGAGATCACCGAGGCGATGCGCTTCGACCGTGGTGTACATCTCGCT 371
QY 370 TACTTCGCCACCGACATGAG 390
DB 372 TACTTCATCCCGACGTCAAG 392

RESULT 59

CV899250
PB021E9 mycelium, sporulating growth Phytophthora infestans cDNA,
mRNA sequence.
CV899250
CV899250.1 GI:58088748
EST.
Phytophthora infestans (potato late blight agent)
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 698)
Randall, T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C.,
Kelkar, H., Fong, A.M., Gates, K., Roberts, S., Yazkan, E., Gaffney, T.,
Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, E.,
Windass, J., Binder, A., Birch, P.R.J., Gisl, U., Govers, F., Gow, N.A.,
Mauch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S.,
Lam, S.T. and Judelson, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi
Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
1..698
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069"
/db_xref="taxon:4787"
/sex="M"
/clone_lib="mycelium, sporulating growth"
/note="Vector: pSPORT1"

ORIGIN

Query Match 38.7%; Score 162.6; DB 8; Length 698;
Best Local Similarity 63.5%; Pred. No. 9.1e-24;
Matches 265; Conservative 0; Mismatches 149; Indels 3; Gaps 1;
QY 7 ACGGACGAGTCCGCGGTGACGTACGACACCGCGCGTTCGCGCCAGCGGCTCGTA 66
DB 111 ACCACGACGCGCGGTGACGCGCACCGTCCGCGCGTTCGCGCGGCTTC 170
QY 67 CGCGAGGCGCTGCGCAAGTCCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGCTC 126
DB 171 AGCGAGGCTGCAAGTCCGCGCGGTGCGCGCATGACCCCGACCTGCGCGCGGCTC 230
QY 127 GAGAGGCGCTGCGAGCGGTCTTCGCGCGCTTCGCGAGCGGCGAAGATGTCGAGACC 186
DB 231 CAATGCGCGTGGACCGACGTGCGAGCGGTCTCGAAGAGCTGTCGATGAGCGTGGCCGAC 290
QY 187 AAGGACGAGTCCGCTTCACCGCGCTTCATCTCCGC ---CGCGCACACCGAGTCCGCGG 243
DB 291 AAGGAGAGGTTGGCGCGGTGCGCGCATCTCGCGCAACTCGGAGACGAGATCGGCAAC 350
QY 244 CTCATCGCGGAGGCGATGAGCAAGTCCGCAAGGAGGCGTTCATCCCGTTCGAGAGTCC 303
DB 351 CTCATCGTACGCGCATGAGCGGTGCGCGAGGCGGTGATCAGCGTTCGAGATGGC 410
QY 304 CAGACCTTCGCTGCGAGCTCAGCTCACCGAGGATGTCGCTTCGACAAAGGCTTACATC 363
DB 411 AAGACGCTGTACAACGAGCTGAGGTGCTCGAGGCGATGAAGTTTCGACCGCGGCTTATC 470
QY 364 TCGGCGTACTTTCGCGCGGATGAGGCGGTTCGCTCGACGACCGCTAC 420
DB 471 TCGCCCTACTTTCGTCACGAGCAATAAGACCGACCGTGTGCGAGATGGAGAACCCGTAC 527

RESULT 60

CF697565 757 bp mRNA linear EST 16-AUG-2004
LOCUS CCABM02TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCABM02, mRNA sequence.
ACCESSION CF697565
VERSION CF697565.1 GI:41551724
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)

ORGANISM

Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

1 (bases 1 to 757)

AUTHORS

Loftus, B.

TITLE

End sequencing of clones from a Full length enriched, normalized

JOURNAL

JEC21 cDNA library

COMMENT

Unpublished (2003)
Other ESTs: CCABM02TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES

source

1..757
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCABM02"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 38.7%; Score 162.6; DB 6; Length 757;
Best Local Similarity 64.8%; Pred. No. 9.1e-24; Indels 4; Gaps 2;
Matches 273; Conservative 0; Mismatches 144;
QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGACCGTTCCTCGCCGAGCGCTC 63
DB 328 AAGACCAACGACACTGCGGTGACGGTACCAACCGCCACTCTCTCGCCGAGCCATC 387
QY 64 GTACGCGAGGCGCTCGCGCAACGTCGCGGTGCGCAACCGCATGGCTCTCAAGCGCGGC 123
DB 388 TACTCTGAGGGTGTGAAGAACGTCGCTCGCGGTGCAACCCCATGACCTCCGTCGAGGT 447
QY 124 ATCGAGAGGCGCTCGAGCGCTCTCGCGCGCTCTGGAGCGGCGAGGATGTCGAG 183
DB 448 GCCCAGAGGCTGTGACAGGCTCTCGAGGTCTTGCTGCCAACAAGGTTATCACC 507
QY 184 ACC-AAGGACGAGATCGCTTCCAGCGCTCCATCTCCGC---CGCCGACACCCAGATCGG 239
DB 508 ACCTTCTGAGGAGATTGCCAGGTTCGCCACCATCTCCGCCAACCGCGATACCCAGCTCGG 567
QY 240 CGAGCTCATCCCGAGGCGATGGAACAAGTTCGGCAAGAGCGCTCATCCGTCGAGGA 299
DB 568 TGCCATCATTCGCCAAGCATGAGAGCGGTTCGGCAAGAGGGGTGTCTACTGTTAAGGA 627
QY 300 GTCCAGACCTTCGCTCTGGAGCTGGAGCTCACCGAGGTATGCGTTCGACAGGGCTA 359
DB 628 GGGCCGACCACTTACACGACAGGATTTAGATTACCGAGGGTATCGGATTCGACCGAGGCTT 687
QY 360 CATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGTTCGACGACCGTA 419
DB 688 CATCTCCCTTACCTCATCACCGACACCAAGAACCGAGCGTCTCGAGCTCGAGAGCCCTT 747

QY 420 C 420

DB 748 C 748

Search completed: April 2, 2006, 00:09:41
Job time : 5790.96 secs

;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/095,855
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/705,347
;; FILING DATE: 29-AUG-1996
;; APPLICATION NUMBER: 08/873,970
;; FILING DATE: 12-JUN-1997
;; APPLICATION NUMBER: 08/997,362
;; FILING DATE: 23-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sleath, Janet
;; REGISTRATION NUMBER: 37,007
;; REFERENCE/DOCKET NUMBER: 11000.1002c3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-269-0565
;; TELEFAX: 206-269-0563
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1569 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; US-09-095-855-113

Query Match 73.3%; Score 308; DB 3; Length 1569;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCCAGGG 60
Db 232 AAGAGACGAGCGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCTCAGGCT 291

QY 61 CTCGTACGAGGGCGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCCAGGG 120
Db 292 CTGGTTCGAGAGGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCTCAGGCT 351

QY 121 GGCATCGAGAGCGCGTTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCCAGGG 180
Db 352 GGCATCGAGAGCGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCTCAGGCT 411

QY 181 GAGACCAAGGAGCGATCGCTTCACGCGCTTCATCTCCGCGCGGCGACACCGAGATCGGC 240
Db 412 GAGACCAAGGAGCGATTCCTGCGCACCGCGCGGCTTCGCGCGGCGGACACCGAGATCGGC 471

QY 241 GAGCTCATCGCGAGCGGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCATCCGTCGAGGAG 300
Db 472 GAGCTCATCGCGAGCGGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCATCCGTCGAGGAG 531

QY 301 TCCGAGACCTTCGCTCGGAGCTGAGCTCACGAGGGGTATCGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGCGCTCGAGCTCACGAGGGGTATCGCTTCGACAAAGGGCTAC 591

QY 361 ATCTCGGCGTACTTCGCGCGGCTTCGCGGTGACGCGGATGAGGGGCTTCGTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGCGCGGCTTCGCGGTGACGCGGATGAGGGGCTTCGTCGAGGATCCCTAC 651

RESULT 4
US-09-324-542-113
; Sequence 113, Application US/09324542

;; Patent No. 6328978
;; GENERAL INFORMATION:
;; APPLICANT: Watson, James D.
;; APPLICANT: Tan, Paul L. J.
;; APPLICANT: Prestidge, Ross
;; TITLE OF INVENTION: Methods and Compounds for the Treatment
;; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
;; FILE REFERENCE: 11000.1007c1
;; CURRENT APPLICATION NUMBER: US/09/324,542
;; CURRENT FILING DATE: 1999-06-02
;; EARLIER APPLICATION NUMBER: US 08/997,080
;; EARLIER FILING DATE: 1997-12-23
;; NUMBER OF SEQ ID NOS: 194
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 113
;; LENGTH: 1569
;; TYPE: DNA
;; ORGANISM: Mycobacterium vaccae
;; US-09-324-542-113

Query Match 73.3%; Score 308; DB 3; Length 1569;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCCAGGG 60
Db 232 AAGAGACGAGCGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCTCAGGCT 291

QY 61 CTCGTACGAGGGCGCTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCCAGGG 120
Db 292 CTGGTTCGAGAGGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCTCAGGCT 351

QY 121 GGCATCGAGAGCGCGTTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCCAGGG 180
Db 352 GGCATCGAGAGGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCGCGCTCAGGCT 411

QY 181 GAGACCAAGGAGCGATCGCTTCACGCGCTTCATCTCCGCGCGGCGACACCGAGATCGGC 240
Db 412 GAGACCAAGGAGCGATTCCTGCGCACCGCGCGGCTTCGCGCGGCGGACACCGAGATCGGC 471

QY 241 GAGCTCATCGCGAGCGGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCATCCGTCGAGGAG 300
Db 472 GAGCTCATCGCGAGCGGCTTCGCGGTGACGCGTACGACACCGCGCGGCTTCATCCGTCGAGGAG 531

QY 301 TCCGAGACCTTCGCTCGGAGCTGAGCTCACGAGGGGTATCGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGCGCTCGAGCTCACGAGGGGTATCGCTTCGACAAAGGGCTAC 591

QY 361 ATCTCGGCGTACTTCGCGCGGCTTCGCGGTGACGCGGATGAGGGGCTTCGTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGCGCGGCTTCGCGGTGACGCGGATGAGGGGCTTCGTCGAGGATCCCTAC 651

RESULT 5
US-09-205-426-113
; Sequence 113, Application US/09205426
; Patent No. 6406704
;; GENERAL INFORMATION:
;; APPLICANT: Watson, James D.
;; APPLICANT: Tan, Paul L. J.
;; TITLE OF INVENTION: Compounds and Methods for Treatment and
;; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
;; FILE REFERENCE: 11000.1002c4
;; CURRENT APPLICATION NUMBER: US/09/205,426
;; CURRENT FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: 09/095,855
;; EARLIER FILING DATE: 1998-06-11
;; EARLIER APPLICATION NUMBER: 08/997,362
;; EARLIER FILING DATE: 1997-12-23
;; EARLIER APPLICATION NUMBER: 08/873,970
;; EARLIER FILING DATE: 1997-06-12
;; EARLIER APPLICATION NUMBER: 08/705,347
;; EARLIER FILING DATE: 1996-08-29

; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-113

Query Match 73.3%; Score 308; DB 3; Length 1569;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCG 60
DB 232 AAGAAGACGACGACGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 291
QY 61 CTGCTAGCGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCG 120
DB 292 CTGCTAGCGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 351
QY 121 GGATCGAGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 180
DB 352 GGATCGAGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 411
QY 181 GAGACCAAGGAGGAGTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT 240
DB 412 GAGACCAAGGAGGAGTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT 471
QY 241 GAGTCTATCGCGAGGCGTACGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 300
DB 472 GAGTCTATCGCGAGGCGTACGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 531
QY 301 TCCGAGACCTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 360
DB 532 TCGAAGACCTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 591
QY 361 ATCTCGGCTTACTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 420
DB 592 ATCTCGGCTTACTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 651

RESULT 6
US-08-997-080-159
; Sequence 159, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-080-159

Query Match 73.3%; Score 308; DB 2; Length 1626;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCG 60
DB 232 AAGAAGACGACGACGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 291
QY 61 CTGCTAGCGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCG 120
DB 292 CTGCTAGCGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 351
QY 121 GGATCGAGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 180
DB 352 GGATCGAGAGGCGCTCGCGGTCAGGTACGACACCGCGGCTTCTCGCCAGGCGT 411
QY 181 GAGACCAAGGAGGAGTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT 240
DB 412 GAGACCAAGGAGGAGTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT 471
QY 241 GAGTCTATCGCGAGGCGTACGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 300
DB 472 GAGTCTATCGCGAGGCGTACGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 531
QY 301 TCCGAGACCTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 360
DB 532 TCGAAGACCTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 591
QY 361 ATCTCGGCTTACTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 420
DB 592 ATCTCGGCTTACTTCGCTCGAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGTGCGGCAAGGT 651

RESULT 7
US-08-997-362-159
; Sequence 159, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362

APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007C1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 159
LENGTH: 1626
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-324-542-159

Query Match 73.3%; Score 308; DB 3; Length 1626;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGCAGCAGCAGCTCGCGGTGACGGTACGACACCCGCGACCGTCTCGCCCGAGGCG 60
DB 232 AAGAAGCAGCAGCAGCTCGCGGTGACGGTACGACACCCGCGACCGTCTCGCCCGAGGCG 291
QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGCGC 120
DB 292 CTGGTTCCGAGAGGCTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGCGT 351
QY 121 GGATCGAGAAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGGCGGAGGATGTC 180
DB 352 GGATCGAGAAGCGCTTCGAGGCGCTTCGAGGCGCTTCGAGGCGGAGGATGTC 411
QY 181 GAGACCAAGCAGCAGATCGCTTCGAGGCGCTTCGAGGCGGAGGATGTC 240
DB 412 GAGACCAAGCAGCAGATCGCTTCGAGGCGCTTCGAGGCGGAGGATGTC 471
QY 241 GAGCTCATCGCGAGGCGATGCGCAAGGTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGGCGATGCGCAAGGTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 531
QY 301 TCCGACACCTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 360
DB 532 TCGACACCTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 591
QY 361 ATCTCGCGTACTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 420
DB 592 ATCTCGCGTACTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 651

RESULT 10

US-09-205-426-159
Sequence 159, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002C4
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 159

LENGTH: 1626
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-205-426-159
Query Match 73.3%; Score 308; DB 3; Length 1626;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGCAGCAGCAGCTCGCGGTGACGGTACGACACCCGCGACCGTCTCGCCCGAGGCG 60
DB 232 AAGAAGCAGCAGCAGCTCGCGGTGACGGTACGACACCCGCGACCGTCTCGCCCGAGGCG 291
QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGCGC 120
DB 292 CTGGTTCCGAGAGGCTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGCGT 351
QY 121 GGATCGAGAAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGGCGGAGGATGTC 180
DB 352 GGATCGAGAAGCGCTTCGAGGCGCTTCGAGGCGCTTCGAGGCGGAGGATGTC 411
QY 181 GAGACCAAGCAGCAGATCGCTTCGAGGCGCTTCGAGGCGGAGGATGTC 240
DB 412 GAGACCAAGCAGCAGATCGCTTCGAGGCGCTTCGAGGCGGAGGATGTC 471
QY 241 GAGCTCATCGCGAGGCGATGCGCAAGGTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGGCGATGCGCAAGGTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 531
QY 301 TCCGACACCTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 360
DB 532 TCGACACCTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 591
QY 361 ATCTCGCGTACTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 420
DB 592 ATCTCGCGTACTTCGCGCTCGAGCTCGAGCTCACCAGGCGTATCGCTTCGACAGGCGTAC 651

RESULT 11

US-08-997-080-115
Sequence 115, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
MEDICATED SKIN DISORDERS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563

TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
US-08-997-080-115

Query Match 72.8%; Score 305.6; DB 2; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGTAACACCGGACCGTTCGCCCGGAGG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACGTAACACCGGACCGTTCGCCCGGAGG 291
QY 61 CTCGTACGAGGCGCTCGGCAACGTCGCGCGGCTGCGCAACCGGATGCTCAAGCG 120
DB 292 CTGTTTCGGAAGGCGCTCGGCAACGTCGCGCGGCTGCGCAACCGGATGCTCAAGCG 351
QY 121 GGCATCGAGAGCGCGTCTCGCGCGCTGCTCGGCGGCTGCGCAACCGGATGCTCAAGCG 180
DB 352 GGCATCGAGAGCGCGTCTCGCGCGCTGCTCGGCGGCTGCGCAACCGGATGCTCAAGCG 411
QY 181 GAGACCAAGGAGCAGATCTTCAGCGGCTTCATCTCCGCGCGGATTCGCGCGGAGG 240
DB 412 GAGACCAAGGAGCAGATCTTCAGCGGCTTCATCTCCGCGCGGATTCGCGCGGAGG 471
QY 241 GAGTCATCGGAGGCGTATGACAGGTCGCGAGGAGGCGTATCATCCGTCGAGGAG 300
DB 472 GAGTCATCGGAGGCGTATGACAGGTCGCGAGGAGGCGTATCATCCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGCTCGGAGCTGCGAGGCTCACGAGGCTATCGCTTCGACAGGCTAC 360
DB 532 TCGAACACCTTCGCTCGGAGCTGCGAGGCTCACGAGGCTATCGCTTCGACAGGCTAC 591
QY 361 ATCTCGGGTACTTTCGCCACCGATGAGCGGATGAGGCGCTCGCTCGACGACCC 416
DB 592 ATCTCGGGTACTTTCGCCACCGATGAGCGGATGAGGCGCTCGCTCGACGACCC 647

RESULT 12
US-08-997-362-115
; Sequence 115, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 1100.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
US-08-997-362-115

Query Match 72.8%; Score 305.6; DB 2; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGTAACACCGGACCGTTCGCCCGGAGG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACGTAACACCGGACCGTTCGCCCGGAGG 291
QY 61 CTCGTACGAGGCGCTCGGCAACGTCGCGCGGCTGCGCAACCGGATGCTCAAGCG 120
DB 292 CTGTTTCGGAAGGCGCTCGGCAACGTCGCGCGGCTGCGCAACCGGATGCTCAAGCG 351
QY 121 GGCATCGAGAGCGCGTCTCGCGCGCTGCTCGGCGGCTGCGCAACCGGATGCTCAAGCG 180
DB 352 GGCATCGAGAGCGCGTCTCGCGCGCTGCTCGGCGGCTGCGCAACCGGATGCTCAAGCG 411
QY 181 GAGACCAAGGAGCAGATCTTCAGCGGCTTCATCTCCGCGCGGATTCGCGCGGAGG 240
DB 412 GAGACCAAGGAGCAGATCTTCAGCGGCTTCATCTCCGCGCGGATTCGCGCGGAGG 471
QY 241 GAGTCATCGGAGGCGTATGACAGGTCGCGAGGAGGCGTATCATCCGTCGAGGAG 300
DB 472 GAGTCATCGGAGGCGTATGACAGGTCGCGAGGAGGCGTATCATCCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGCTCGGAGCTGCGAGGCTCACGAGGCTATCGCTTCGACAGGCTAC 360
DB 532 TCGAACACCTTCGCTCGGAGCTGCGAGGCTCACGAGGCTATCGCTTCGACAGGCTAC 591
QY 361 ATCTCGGGTACTTTCGCCACCGATGAGCGGATGAGGCGCTCGCTCGACGACCC 416
DB 592 ATCTCGGGTACTTTCGCCACCGATGAGCGGATGAGGCGCTCGCTCGACGACCC 647

RESULT 13
US-09-095-855-115
; Sequence 115, Application US/09095855
; Patent No. 616093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT AND DIAGNOSIS OF Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

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;
;
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
; US-09-095-855-115

Query Match 72.8%; Score 305.6; DB 3; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGCGAGCAGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 60
Db 232 AAGAAGCGAGCAGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 291
QY 61 CTGCTACGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
Db 292 CTGCTACGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 351
QY 121 GGATCGAGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 180
Db 352 GGATCGAGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 411
QY 181 GAGACCAAGAGCAGATCGCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 240
Db 412 GAGACCAAGAGCAGATCGCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 471
QY 241 GAGCTCATCGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 300
Db 472 GAGCTCATCGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 531
QY 301 TCCAGACACCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 360
Db 532 TCGAACACCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 591
QY 361 ATCTCGGCTACTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 416
Db 592 ATCTCGGCTACTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 647

RESULT 15
US-09-205-426-115
; Sequence 115, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115

;
;
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
; US-09-095-855-115

Query Match 72.8%; Score 305.6; DB 3; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGCGAGCAGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 60
Db 232 AAGAAGCGAGCAGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 291
QY 61 CTGCTACGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
Db 292 CTGCTACGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 351
QY 121 GGATCGAGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 180
Db 352 GGATCGAGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 411
QY 181 GAGACCAAGAGCAGATCGCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 240
Db 412 GAGACCAAGAGCAGATCGCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 471
QY 241 GAGCTCATCGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 300
Db 472 GAGCTCATCGCGAGGCGCTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 531
QY 301 TCCAGACACCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 360
Db 532 TCGAACACCTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 591
QY 361 ATCTCGGCTACTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 416
Db 592 ATCTCGGCTACTTCGCGGTGACGGTACGACACCGCGGTCGCAACCGGATGGCTCTCAAGCGC 647

RESULT 14
US-09-324-542-115
; Sequence 115, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
```

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; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-115

Query Match          72.8%; Score 305.6; DB 3; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGGTACGACACACCGCGACCGTTCGCGCCAGGCG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACGGGTACGACACACCGCGACCGTTCGCTCAGGCT 291
QY 61 CTGCTACGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGC 120
DB 292 CTGCTACGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGCTCGCGCTCAAGCGT 351
QY 121 GGCATCGAGAGCGCTCGAGGCGTCTCGGCGCGCTTCGCGCGCGCTTCGAGAGCGAGTATC 180
DB 352 GGCATCGAGAGCGCTCGAGGCGTCTCGGCGCGCTTCGCGCGCGCTTCGAGAGCGAGTATC 411
QY 181 GAGACCAAGGAGCAGATCGTTCACCGGCTTCACCGGCTTCGCGCGCGCTTCGAGAGCGAGTATC 240
DB 412 GAGACCAAGGAGCAGATCGTTCACCGGCTTCGCGCGCGCTTCGAGAGCGAGTATC 471
QY 241 GAGCTCATCGCGAGCGGATGCAAGGTTCGCGCAAGGAGGCGTTCATCACCGTTCGAGGAG 300
DB 1090 GACCTCATCGCGAGCGGATGCAAGGTTCGCGCAAGGAGGCGTTCATCACCGTTCGAGGAG 1149
QY 301 TCCGAGACCTTCGCTCGAGCTGAGGCTCACCGAGGCTATCGGCTTCGAGAGGCTATC 360
DB 1150 TCCGAGACCTTCGCTCGAGCTGAGGCTCACCGAGGCTATCGGCTTCGAGAGGCTATC 1209
QY 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGGTATC 420
DB 1210 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGGCGTTCGTCGAGAGCGGCTATC 1269

RESULT 17
US-09-613-303-3
; Sequence 3, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-09-613-303-3

Query Match          69.9%; Score 293.6; DB 3; Length 1623;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGGTACGACACCGCGACCGTTCGCGCCAGGCG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACGGGTACGACACCGCGACCGTTCGCGCCAGGCG 291
QY 61 CTGCTACGAGGCGCTTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGGCTTCGAGGCG 120
DB 292 TTGGTTTCGAGGCGCTTCGCGCAACGTCGCGCGGTGCGCAACCGCGCTTCGAGGCG 351
QY 121 GGCATCGAGAGGCGCTCGAGGCGTTCGCGCGCGCTTCGCGCGCGCTTCGAGAGCGAGTATC 180
DB 352 GGCATCGAGAGGCGCTCGAGAGGCTTCGCGCGCGCTTCGAGAGCGAGTATC 411
QY 181 GAGACCAAGGAGCAGATCGTTCACCGGCTTCATCTCGCGCGCGACACCGAGTTCGCGC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCGCGCTTCGCGCGCGTTCGCGCGGTTCGAGTTCATCGT 471
QY 241 GAGCTCATCGCGAGGCGATGCAAGGTTCGCGCAAGGAGGCGTTCATCACCGTTCGAGGAG 300
DB 472 GACCTCATCGCGAGGCGATGCAAGGTTCGCGCAAGGAGGCGTTCATCACCGTTCGAGGAG 531

Query Match          70.3%; Score 295.2; DB 3; Length 2241;
Best Local Similarity 81.4%; Pred. No. 3.5e-48;
Matches 342; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGGTACGACACCGCGACCGTTCGCGCCAGGCG 60
DB 850 AAGAAGACGAGCAGCTCGCGGTGACGGGTACGACACCGCGACCGTTCGCGCCAGGCG 909
QY 61 CTGCTACGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGGCTTCGAGGCGC 120
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QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGTTCCGACAGGGCTAC 360
Db 532 TCCAAACACCTTTGGCTGCGAGCTCGAGCTCACCGAGGGTATGCGTTCCGACAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGGCCACCGACGATGGAGCGGTGCGTCTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGGTACCGACCGGAGCGGTGCGTCTCGAGGACCGCTAC 651

RESULT 18
US-10-267-311-3
; Sequence 3, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 69.9%; Score 293.6; DB 3; Length 1623;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGAAGCAGCAGCTCGCGGTGACGGTACGACACCGGACCGGCTTCGCGCCAGGCG 60
Db 232 AAGAAGCAGCAGCTCGCGGTGACGGTACGACACCGGACCGGCTTCGCGCCAGGCG 291
QY 61 CTGCTACGAGGCGCTCGCAACAGCTCGCGCGGTCGCCAACCGGATGGCTCTCAAGCGC 120
Db 292 TTGGTTTCGCGAGGCGCTCGCGCAACAGCTCGCGCGGTCGCCAACCGGCTCTCAAGCGC 351
QY 121 GGATTCGAGAGGCGCTCGAGGCGCTTCACCGGCTTCATCTCCGCGCGGACACCGAGATGTC 180
Db 352 GGATTCGAGAGGCGCTTCGAGGCGCTTCACCGGCTTCATCTCCGCGCGGACACCGAGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCACCGGCTTCATCTCCGCGCGGACACCGAGATGTC 240
Db 412 GAGACCAAGGAGCAGATTCGGGCCACCGGAGCGATTCGGCGGGTGACAGTCCATCGGT 471
QY 241 GAGCTCATCTCGCGAGGCGATGGCAAGGTCGGCAAGGAGCGCTCATCCCGTCGAGGAG 300
Db 472 GAGCTCATCTCGCGAGGCGATGGCAAGGTCGGCAAGGAGCGCTCATCCCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGTTTCGACAGGGGCTAC 360
Db 532 TCCAAACACCTTTGGCTGCGAGCTCGAGCTCACCGAGGGTATGCGTTTCGACAGGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGGCCACCGACGATGGAGCGGTGCGTCTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGGTACCGACCGGAGCGGTGCGTCTCGAGGACCGCTAC 651

RESULT 19

US-09-712-363-23
; Sequence 23, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 69.9%; Score 293.6; DB 3; Length 1623;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGAAGCAGCAGCTCGCGGTGACGGTACGACACCGGACCGGCTTCGCGCCAGGCG 60
Db 232 AAGAAGCAGCAGCTCGCGGTGACGGTACGACACCGGACCGGCTTCGCGCCAGGCG 291
QY 61 CTGCTACGAGGCGCTTCGCGCAACAGCTCGCGCGGTCGCCAACCGGATGGCTCTCAAGCGC 120
Db 292 TTGGTTTCGCGAGGCGCTTCGCGCAACAGCTCGCGCGGTCGCCAACCGGCTCTCAAGCGC 351
QY 121 GGATTCGAGAGGCGCTTCGAGGCGCTTCACCGGCTTCATCTCCGCGCGGACACCGAGATGTC 180
Db 352 GGATTCGAGAGGCGCTTCGAGGCGCTTCACCGGCTTCATCTCCGCGCGGACACCGAGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCACCGGCTTCATCTCCGCGCGGACACCGAGATGTC 240
Db 412 GAGACCAAGGAGCAGATTCGGGCCACCGGAGCGATTCGGCGGGTGACAGTCCATCGGT 471
QY 241 GAGCTCATCTCGCGAGGCGATGGCAAGGTCGGCAAGGAGCGCTCATCCCGTCGAGGAG 300
Db 472 GAGCTCATCTCGCGAGGCGATGGCAAGGTCGGCAAGGAGCGCTCATCCCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGTTTCGACAGGGGCTAC 360
Db 532 TCCAAACACCTTTGGCTGCGAGCTCGAGCTCACCGAGGGTATGCGTTTCGACAGGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGGCCACCGACGATGGAGCGGTGCGTCTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGGTACCGACCGGAGCGGTGCGTCTCGAGGACCGCTAC 651

RESULT 20
US-09-613-303-16

Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAGACGAGACGTCGCGGTGACGGTACGACACCGGACCGTTCTCGCCAGGCG 60
Db |||||
556 AAGAGACCGATGATGATGCGCGGTGACGGACACCGACCGGACCGTCTCGCCAGGCG 615
Qy 61 CTGCTACGCGAGGCGCTCGCAAGTCCGCGCGCGGTGCCAACCGATGGCTCTCAAGCGC 120
Db |||||
616 TTGGTTCCGAGGCGCTCGCAAGTCCGCGCGCGGTGCCAACCGTCTCGGTCTCAACGC 675
Qy 121 GGATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCGCTTCTGGAGCAGGCGAAGATGTC 180
Db |||||
676 GGATCGAAGGCGCTCGAGAGGTCAACGAGACCTGTCTCAAGGCGCGCAAGGAGTTC 735
Qy 181 GAGACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db |||||
736 GAGACCAAGGACGATGCGCGGTGACGGACCGATTTCCGCGCGGTGACCAAGTCCATCGGT 795
Qy 241 GAGCTCATCGCGAGGCGATGGACAAGTCCGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 300
Db |||||
796 GACCTGATCGCGAGGCGATGGACAAGTGGGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 855
Qy 301 TCCGACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 360
Db |||||
856 TCCACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 915
Qy 361 ATCTCGCGGTACTTCGCGACCGACGATGAGCGGATGAGCGGTGCTCGACGACCGGTAC 420
Db |||||
916 ATCTCGGGGTACTTCGTGACCGACCGAGCGTCAAGGCGGTGCTCGAGGAGACCCCTAC 975

RESULT 23
US-10-267-311-28
; Sequence 28, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Chu, N. Randall
; APPLICANT: Siegel, Marvin
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-267-311-28

Query Match 69.9%; Score 293.6; DB 3; Length 1947;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAGACGAGACGTCGCGGTGACGGTACGACACCGGACCGTTCTCGCCAGGCG 60
Db |||||
556 AAGAGACCGATGATGATGCGCGGTGACGGACACCGACCGGACCGTCTCGCCAGGCG 615
Qy 61 CTGCTACGCGAGGCGCTCGCAAGTCCGCGCGCGGTGCCAACCGATGGCTCTCAAGCGC 120
Db |||||
616 TTGGTTCCGAGGCGCTCGCAAGTCCGCGCGCGGTGCCAACCGTCTCGGTCTCAACGC 675
Qy 121 GGATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCGCTTCTGGAGCAGGCGAAGATGTC 180
Db |||||
676 GGATCGAAGGCGCTCGAGAGGTCAACGAGACCTGTCTCAAGGCGCGCAAGGAGTTC 735
Qy 181 GAGACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db |||||
736 GAGACCAAGGACGATGCGCGGTGACGGACCGATTTCCGCGCGGTGACCAAGTCCATCGGT 795
Qy 241 GAGCTCATCGCGAGGCGATGGACAAGTCCGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 300
Db |||||
796 GACCTGATCGCGAGGCGATGGACAAGTGGGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 855
Qy 301 TCCGACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 360
Db |||||
856 TCCACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 915
Qy 361 ATCTCGCGGTACTTCGCGACCGACGATGAGCGGATGAGCGGTGCTCGACGACCGGTAC 420
Db |||||
916 ATCTCGGGGTACTTCGTGACCGACCGAGCGTCAAGGCGGTGCTCGAGGAGACCCCTAC 975

Qy 121 GGATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCGCTTCTCGAGCAGGCGAAGATGTC 180
Db |||||
676 GGATCGAAGGCGCTCGAGAGGTCAACGAGACCTGTCTCAAGGCGCGCAAGGAGTTC 735
Qy 181 GAGACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db |||||
736 GAGACCAAGGACGATGCGCGGTGACGGACCGATTTCCGCGCGGTGACCAAGTCCATCGGT 795
Qy 241 GAGCTCATCGCGAGGCGATGGACAAGTCCGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 300
Db |||||
796 GACCTGATCGCGAGGCGATGGACAAGTGGGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 855
Qy 301 TCCGACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 360
Db |||||
856 TCCACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 915
Qy 361 ATCTCGCGGTACTTCGCGACCGACGATGAGCGGATGAGCGGTGCTCGACGACCGGTAC 420
Db |||||
916 ATCTCGGGGTACTTCGTGACCGACCGAGCGTCAAGGCGGTGCTCGAGGAGACCCCTAC 975

RESULT 24
US-10-068-059-9
; Sequence 9, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match 69.9%; Score 293.6; DB 3; Length 2073;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAGACGAGACGTCGCGGTGACGGTACGACACCGGACCGTTCTCGCCAGGCG 60
Db |||||
682 AAGAGACCGATGATGATGCGCGGTGACGGACACCGACCGGACCGTCTCGCCAGGCG 741
Qy 61 CTGCTACGCGAGGCGCTCGCAAGTCCGCGCGGTGCCAACCGATGGCTCTCAAGCGC 120
Db |||||
742 TTGGTTCCGAGGCGCTCGCGCAACCGTCCGCGCGCGGTGACCAAGTCTCGGTCTCAACGC 801
Qy 121 GGATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCGCTTCTGGAGCAGGCGAAGATGTC 180
Db |||||
802 GGATCGAAGGCGCTCGAGAGGTCAACGAGACCTGTCTCAAGGCGCGCAAGGAGTTC 861
Qy 181 GAGACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db |||||
862 GAGACCAAGGACGATGCGCGGTGACGGACCGATTTCCGCGCGGTGACCAAGTCTCGGT 921
Qy 241 GAGCTCATCGCGAGGCGATGGACAAGTCCGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 300
Db |||||
922 GACCTGATCGCGAGGCGATGGACAAGTGGGCAAGGCGGTGACAGGAGGCGTCAACCGTCGAGGAG 981
Qy 301 TCCGACACCTTTCGCTCGAGCTGAGCTCAACGAGGCTATGCGCTTTCGACAAGGGCTAC 360
Db |||||


```
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGAGCGTACGACACACCGGACCGTTCGCGCCAGGCG 60
Db 292 AAGAAGACGACGATGACGTCGCGGTGACGCGACCAACGACGCGCCACCGTCTGCGCCAGGCG 351
QY 61 CTCGTACGAGGAGGCTGCGCAACGCTGCGCGCGGTCGCAACCGCATGCGTCTCAAGCGC 120
Db 352 TTGGTTCGCGAGGCGCTGCGCAACGTCGCGCGCGCGCCCAACCCGCTCGGTCTCAACGCG 411
QY 121 GGCATCGAAGAGCGCGTTCGAGGCGCGTCTCGCGCGCGCTCTGCTCGAGCAGGCGCAAGGATGTC 180
Db 412 GGCATCGAAGAGCGCGTTCGAGGAGGTCAACGAGACCTGCTCAAGGGCGCCAGGAGGTC 471
QY 181 GAGACCAAGAGAGAGATGCTTCACGCGCTTCATCTCCGCGCGGACACCCAGATCGGC 240
Db 472 GAGACCAAGAGAGAGATGCTCGGCGCACCGCAGCGATTTTCGCGCGGTGACCACTCCATCGGT 531
QY 241 GAGCTCATCGCGAGCGGCGATGACAGGTTCGCGAGGAGGCGTCAATCACCGTCGAGGAG 300
Db 532 GACCTGATCGCGAGGCGGATGACAGGTGGGCAACGAGGCGGTCAATCACCGTCGAGGAG 591
QY 301 TCCAGACCTTCGCTTCGAGCTGAGCTCACCGAGGGTATCGGCTTCGACCAAGGGCTAC 360
Db 592 TCCACACCTTTGGGCTGCGAGCTCGAGCTCACCGAGGGTATCGGCTTCGACCAAGGGCTAC 651
QY 361 ATCTCGCGTACTTCGCTCCACCGACATGAGCGGATGGAGCGTTCGCTCGACGACCGGTAC 420
Db 652 ATCTCGGGTACTTCGTCGACCGAGCGTCAGGAGGCGTCTCTGAGGAGCCCTTAC 711

RESULT 29
US-08-955-565A-3
; Sequence 3, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
; APPLICANT: Malkovsky, Miroslav
; APPLICANT: Wells, Andrew
; TITLE OF INVENTION: Immune Response Enhancer Therapy
; FILE REFERENCE: WARF-02625
; CURRENT APPLICATION NUMBER: US/08/955,565A
; CURRENT FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 4380
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-08-955-565A-3

Query Match      69.9%; Score 293.6; DB 3; Length 4380;
Best Local Similarity 81.2%; Pred. No. 7.3e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCGACCAACCGGACCGTTCGCGCCAGGCG 60
Db 483 AAGAAGACGATGACGTCGCGGTGACGCGACCAACCGGACCGTTCGCGCCAGGCG 542
QY 61 CTCGTACGAGGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCGCATGCGTCTCAAGCGC 120
Db 543 TTGGTTCGCGAGGCGCTGCGCAACGTCGCGCGCGCGCCCAACCCGCTCGGTCTCAACGCG 602
QY 121 GGCATCGAAGAGCGCGTTCGAGGCGCGTCTCGCGCGCGCTCTGCTCGAGCAGGCGCAAGGATGTC 180
Db 603 GGCATCGAAGAGCGCGTTCGAGGAGGTCAACGAGACCTGCTCAAGGGCGCCAGGAGGTC 662
QY 181 GAGACCAAGAGAGAGATGCTTCACGCGCTTCATCTCCGCGCGGACACCCAGATCGGC 240
Db 663 GAGACCAAGAGAGAGATGCTCGGCGCACCGCAGCGATTTTCGCGCGGTGACCACTCCATCGGT 722
QY 241 GAGCTCATCGCGAGGCGGATGACAGGTTCGCGAAGGAGGCGTCAATCACCGTCGAGGAG 300
Db 723 GACCTGATCGCGAGGCGGATGACAGGTGGGCAACGAGGCGGTCAATCACCGTCGAGGAG 782
QY 301 TCCAGACCTTCGCTTCGAGCTGAGCTCACCGAGGGTATCGGCTTCGACCAAGGGCTAC 360
Db 783 TCCACACCTTTGGGCTGCGAGCTCGAGCTCACCGAGGGTATCGGCTTCGACCAAGGGCTAC 842

; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGAGCGTACGACACACCGGACCGTTCGCGCCAGGCG 60
Db 292 AAGAAGACGACGATGACGTCGCGGTGAGCGTACGACACACCGGACCGTTCGCGCCAGGCG 351
QY 61 CTCGTACGAGGAGGCGCTGCGCAACGTCGCGCGCGGTCGCAACCGCATGCGTCTCAAGCGC 120
Db 352 TTGGTTCGCGAGGCGCTTCCGCAACGTCGCGCGCGCGCCCAACCCGCTCGGTCTCAACGCG 411
QY 121 GGCATCGAAGAGCGCGTTCGAGGCGCGTCTCGCGCGCGCTCTGCTCGAGCAGGCGCAAGGATGTC 180
Db 412 GGCATCGAAGAGCGCGTTCGAGGAGGTCAACGAGACCTGCTCAAGGGCGCCAGGAGGTC 471
QY 181 GAGACCAAGAGAGAGATGCTTCACGCGCTTCATCTCCGCGCGGACACCCAGATCGGC 240
Db 472 GAGACCAAGAGAGAGATGCTCGGCGCACCGCAGCGATTTTCGCGCGGTGACCACTCCATCGGT 531
QY 241 GAGCTCATCGCGAGGCGGATGACAGGTTCGCGAAGGAGGCGTCAATCACCGTCGAGGAG 300
Db 532 GACCTGATCGCGAGGCGGATGACAGGTGGGCAACGAGGCGGTCAATCACCGTCGAGGAG 591
QY 301 TCCAGACCTTCGCTTCGAGCTGAGCTCACCGAGGGTATCGGCTTCGACCAAGGGCTAC 360
Db 592 TCCACACCTTTGGGCTGCGAGCTCGAGCTCACCGAGGGTATCGGCTTCGACCAAGGGCTAC 651
QY 361 ATCTCGCGTACTTCGCTCCACCGACATGAGCGGATGAGCGTTCGCTCGACGACCGGTAC 420
Db 652 ATCTCGGGTACTTCGTCGACCGAGCGTCAGGAGGCGTCTCTGAGGAGCCCTTAC 711

RESULT 28
US-10-267-311-20
; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGAGCGTACGACACACCGGACCGTTCGCGCCAGGCG 60
```


CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1320
US-08-461-775-8

Query Match 64.2%; Score 269.8; DB 2; Length 1320;
Best Local Similarity 77.9%; Pred. No. 2.6e-43;
Matches 325; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4 AAGACGACGACGTCGCGCGGTGACGATACGACACCGACCGGCTTCTCGCCCGAGGGCTC 63
DB 235 AAGACCAACGACATCGCGGTGACGACACCGACCGGCTTCTCGCCCGAGGGCTG 294
QY 64 GTACGAGGCGCTCGCGACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGC 123
DB 295 GTCCGCGAGGCGCTCGCGACGTCGCGCGGTGCGCGCGGTCTCCCGCGCGCGCTTGAAGAAGGC 354
QY 124 ATGAGAAGCGCGTCGAGGCGCTCTCCGCGCGGTCTCGAGCAGCGGAGGATGTCGAG 183
DB 355 ATCGACGCGCGGTGCGCGCGGTCTCGCGCGGTCTCGACACCGCGCGCGGATCGAC 414
QY 184 ACCAAGGAGCAGATCGCTTCCAGGCGCTTCCGCGCGGTGCGACACCGACGATCGCGAG 243
DB 415 GACAGTCCGACATCGCGCGGTGCGCGCGGTCTCGCGCGGTGCGACACCGAGGATCGCGAG 474
QY 304 CAGACCTTCGCTCGGACGTCGAGGCTTCCGCGCGGTGCGCGCGGTGCGACACCGAGGCTACATC 363
DB 535 AACACCTTCGCTCGGACGTCGAGGCTTCCGCGCGGTGCGCGCGGTGCGACACCGAGGCTACCTG 594
QY 364 TCGCGCTACTTCGCGACCGACATGAGGCGGTGCGCGCGGTGCGCGCGGTGCGACACCGAGGCTAC 420
DB 595 TCCCGGTACTGTCGACCGACGAGGCGGTGCGCGCGGTGCGCGCGGTGCGACACCGAGGCTAC 651

RESULT 33

US-09-031-606-8
Sequence 8, Application US/09031606
Patent No. 6153404
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1320
US-09-031-606-8

Query Match 64.2%; Score 269.8; DB 3; Length 1320;
Best Local Similarity 77.9%; Pred. No. 2.6e-43;
Matches 325; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4 AAGACGACGACGTCGCGCGGTGACGATACGACACCGACCGGCTTCTCGCCCGAGGGCTC 63
DB 235 AAGACCAACGACATCGCGGTGACGACACCGACCGGCTTCTCGCCCGAGGGCTG 294
QY 64 GTACGAGGCGCTCGCGACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGC 123
DB 295 GTCCGCGAGGCGCTCGCGACGTCGCGCGGTGCGCGCGGTCTCCCGCGCGCGCTTGAAGAAGGC 354
QY 124 ATGAGAAGCGCGTCGAGGCGCTCTCCGCGCGGTCTCGAGCAGCGGAGGATGTCGAG 183
DB 355 ATCGACGCGCGGTGCGCGCGGTCTCGCGCGGTCTCGACACCGCGCGCGGATCGAC 414
QY 184 ACCAAGGAGCAGATCGCTTCCAGGCGCTTCCGCGCGGTGCGACACCGACGATCGCGAG 243
DB 415 GACAGTCCGACATCGCGCGGTGCGCGCGGTCTCGCGCGGTGCGACACCGAGGATCGCGAG 474
QY 304 CAGACCTTCGCTCGGACGTCGAGGCTTCCGCGCGGTGCGCGCGGTGCGACACCGAGGCTACATC 363
DB 535 AACACCTTCGCTCGGACGTCGAGGCTTCCGCGCGGTGCGCGCGGTGCGACACCGAGGCTACCTG 594
QY 364 TCGCGCTACTTCGCGACCGACATGAGGCGGTGCGCGCGGTGCGCGCGGTGCGACACCGAGGCTAC 420
DB 595 TCCCGGTACTGTCGACCGACGAGGCGGTGCGCGCGGTGCGCGCGGTGCGACACCGAGGCTAC 651

RESULT 34

US-08-461-775-10
Sequence 10, Application US/08461775
Patent No. 5858773
GENERAL INFORMATION:

APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,775
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-08-461-775-10

Query Match 64.2%; Score 269.8; DB 2; Length 1620;
Best Local Similarity 77.9%; Pred. No. 2.6e-43;
Matches 325; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4 AAGACGACGACGTGCGCGGTGACGGTACGACCGGACCGGACCGGTTCTCGCCCGCGCTC 63
DB 235 AAGACCAACGACATCGCGGTGAGGSCACCAACCGGACCGTGTGCGCCGAGGGCTG 294

QY 64 GTACGGAGGGCTGCGGCAAGTGGCGCGGTGCGGACCGGATGCTCTCAAGCGGCG 123
DB 295 GTCCGCGAGGGCTGCGCAAGTGGCGCGGTGCGGCGCGCTCCCGCGCGCTCGAAGGAGG 354

QY 124 ATCGAGAGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGG 183
DB 355 ATCGAGCGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGG 414

QY 184 ACCAAGAGGACGATCGCTTCCAGCGGTCTCCAGCGGTATGCGGTTCGACAGGGGTACATC 363
DB 535 AACACCTTCGGTGTGACCTGGACTTCACCGAGGGGATGGCTTCGACAGGGGTACCTG 594

QY 364 TCGCGGTACTTCGCCACCGACATGAGCGGATGAGGGGTGCTCGACGACCGCTAC 420
DB 595 TCCCGGTACATGGTACCGGACCGGAGGATGAGGGGTGCTCGACGACCGCTAC 651

RESULT 35
US-09-031-606-10
Sequence 10, Application US/09031606
Patent No. 6153404
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-09-031-606-10

Query Match 64.2%; Score 269.8; DB 3; Length 1620;
Best Local Similarity 77.9%; Pred. No. 2.6e-43;
Matches 325; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4 AAGACGACGACGTGCGCGGTGACGGTACGACCGGACCGGACCGGTTCTCGCCCGCGCTC 63
DB 235 AAGACCAACGACATCGCGGTGAGGSCACCAACCGGACCGTGTGCGCCGAGGGCTG 294

QY 64 GTACGGAGGGCTGCGGCAAGTGGCGCGGTGCGGACCGGATGCTCTCAAGCGGCG 123
DB 295 GTCCGCGAGGGCTGCGCAAGTGGCGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGG 354

QY 124 ATCGAGAGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGG 183
DB 355 ATCGAGCGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTGCGG 414

QY 184 ACCAAGAGGACGATCGCTTCCAGCGGTCTCCAGCGGTATGCGGTTCGACAGGGGTAC 243

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Db 415 GACAAGTCCGACATCGCGCGCTCGCGCGCTCTCCGCGCAGGACAGGTCGGCGAG 474
Qy 244 CTATCCCGCAGGCGATGGACAGGTCGGCAAGGAGGCGCTCATCCGTCGAGGAGTCC 303
Db 475 CTATCCCGCAGGCGATGGACAGGTCGGCAAGGAGGCGCTCATCCGTCGAGGAGTCC 534
Qy 304 CAGACCTTCGGTCTGGAGCTGGAGCTCACCAGGAGTATCGCTTCGACAAAGGGCTACATC 363
Db 535 AACACCTTCGGTCTGGAGCTGGAGCTCACCAGGAGGATGCGCTTCGACAAAGGGCTACCTG 594
Qy 364 TCGCGCTACTTCGCCACCGCAGCATGGAGCGGATGGAGCGCTCGCTCGACGACCCGTAC 420
Db 595 TCCCGGTACATGGTGACCGCAGGAGCGTATGAGGCGCTCTCCGACGAGCCCGTAC 651

RESULT 36
US-08-461-775-9
; Sequence 9, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-461-775-9

Query Match 63.9%; Score 268.2; DB 2; Length 2167;
Best Local Similarity 77.7%; Pred. No. 5.3e-43;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 4 AAGACGACGACGTCGCGGTCGAGTACGACACCGGACCGCTCTCCGCGCAGGCGCTC 63
Db 1083 AAGACCAACGACATCGCGGTCGACGCGACCAACCGGACCGCTGCGCCCGAGCTG 1142
Qy 64 GTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGCGG 123
Db 1143 GTCCGCGAGGCGCTGCGCAACGTCGCGCGCGGCGCTCCCGCGCGCTTCCGCGCGG 1202

124 ATCGAAGGCGCGTCGAGGCGCTCTCCGCGCGCCCTGCTCGAGCAGGCGAAGGATGTCGAG 183
1203 ATCGAGCGCGCGCTCGCGCGCGCTCTCCGCGAGCTGCTCGACACCGCGCGCGCGATCGAC 1262
Qy 184 ACCAAGGAGCAGATCGCTTCCACGGGCTCCATCTCCGCGCGCGGACACCCAGATCGGCGAG 243
Db 1263 GACAAGTCCGACATCGCGCGCGCTCTCCGCGCAGGACAGCAGGTCGCGCGAG 1322
Qy 244 CTATCCCGCAGGCGATGGACAGGTCGGCAAGGAGGCGTCTATCCGTCGAGGAGTCC 303
Db 1323 CTATCCCGCAGGCGATGGACAGGTCGGCAAGGAGGCGTCTATCAACGTCGAGGAGTCC 1382
Qy 304 CAGACCTTCGGTCTGGAGCTGGAGCTCACCAGGAGTATCGCTTCGACAAAGGGCTACATC 363
Db 1383 AACACCTTCGGTCTGGAGCTGGAGCTCACCAGGAGGATGCGCTTCGACAAAGGGCTACCTG 1442
Qy 364 TCGCGCTACTTCGCCACCGCAGCATGGAGCGGATGGAGCGCTCGCTCGACGACCCGTAC 420
Db 1443 TCCCGGTACATGGTGACCGCAGGAGCGTATGAGGCGCTCTCCGACGAGCCCGTAC 1499

RESULT 37
US-09-031-606-9
; Sequence 9, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
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; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
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; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
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; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-031-606-9

Query Match 63.9%; Score 268.2; DB 3; Length 2167;
Best Local Similarity 77.7%; Pred. No. 5.3e-43;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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Qy	4	AAGACGAGCAGCATCTCGCGGTGACGGTTACGACACCGCGACCGGTTCTCGGCCACGAGCGCTC	63
Db	1083	AAGACCAACGACATCTCGCGGTGACGGCACCAACACCGCGACCGGTGCTGGGCCACGAGCGCTG	1142
Qy	64	GTACGCGAGGGCCCTGCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGGC	123
Db	1143	GTCCGCGAGGGCCCTGCGCAACGTCGCGCGCGCGGCGCTCCCGCGCGCCCTGAAAGAGGGC	1202
Qy	124	ATCGAGAAAGCCGTTCGAGGGCGCTCTCGGGCGCCTCTGTGGAGCAGGCGAAGGATGTCGAG	183
Db	1203	ATCGACGCGCGTTCGCGCGCGCTCTCGCGCGAGCTGTCTCGACACCGCGCGCCCGATCGAC	1262
Qy	184	ACCAAGAGCAGATCGCTTCCAGGGCTTCATCTCGCGCGCGGACACCCAGATCGGGCAG	243
Db	1263	GACAAGTCCGACATCGCGCGCGCTGTGCGCGCGCTCTCGCGCAGGACAAGCAGGTTCGGCGAG	1322
Qy	244	CTCATCGCGAGGCGATGGACAAGGTTCGGCAAGGAGGCGTCAATACCGTCGAGGAGTCC	303
Db	1323	CTCATCGCGAGGCGATGGACAAGGTTCGGCAAGGACGGTGTCAATCAACGTCGAGGAGTCC	1382
Qy	304	CAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGCGTACATC	363
Db	1383	AACACCTTCGGTGTGGACCTTGGACCTTACCAGGGGATGCGCTTCGACAAAGGCGTACCTG	1442
Qy	364	TCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGGCGTTCGTCGACGACCCGTTAC	420
Db	1443	TCGCCGTACTGTGTGACCGACCAAGGACGGTATGGAGGCGGTCTCTCGACACCCGTTAC	1499

RESULT 38

US-08-461-775-11
; Sequence 11, Application US/08461775
; Patent No. 5858773

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CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
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 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,775
 FILING DATE:

! MOLECULE TYPE: DNA (genomic)
US-08-461-775-11

Query Match 63.9%; Score 268.2; DB 2; Length 2668;
Best Local Similarity 77.7%; Pred. No. 5.4e-43;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy	4	AAGACGAGCAGCGTTCGCGGTGACGATACGACACCGCGACCGTTCCTCGCCGACGGCGCTC	63
Db	1083	AGAACCAGACATCGCGGTGACGCGACACACCGCGCAGCGTGTGCGCCAGGCGCTG	1142
Qy	64	GTACGCGAGGGCTGCGCAACGTTCGCGCGCGGTGCCAACCCCGATGCTCTCAAGCGCGGC	123
Db	1143	GTCCGAGGGGCTTGGCAACGTTCGCGCGCGCGCTCCCGCGCCCTCTGAAGAAGGCG	1202
Qy	124	ATCGAGAGGCCGTTCGAGGCCGTCTCCGCGGCCCTGCTGGAGCAGCGAAGGATGTTCGAG	183
Db	1203	ATCGACGCGCGTTCGCGCGCGTCTCCGCGGAGCTGCTCGACACCGCGCGCCGATCGAC	1262
Qy	184	ACCAAGGAGGATTCGCTTCACGGGCTCATCTCGCGCGCGACACCCAGATTCGCGCAG	243
Db	1263	GACAAGTCCGACATCGCCGCGCTTCGCGCGCAGCAAGCAGGTTCGCGCAG	1322
Qy	244	CTCATCGCGAGCGATGACAAAGTTCGCGCAGGAGGCGTTCATCACCGTCGAGGAGTCC	303
Db	1323	CTCATCGCGAGCGATGACAAAGTTCGCGCAGGACGSGTTCATCAACGTCGAGGAGTCC	1382
Qy	304	CAGACCTTCGGTCTGAGGCTCGAGCTCACCGAGGGGTATGCGCTTCGACAAAGGCTACATC	363
Db	1383	ARACACCTTCGGTCTGACCTTGACCTTCACCGAGGGCATTGCGCTTCGACAAAGGCTACCTG	1442
Qy	364	TCGGCGTATTTCGCCACCGACATGAGCGGATGGAGGGCGTTCGTCGACGACCCGTTAC	420
Db	1443	TCCCCGTAATGGTATGACCCACGAGCGTATGGAGGCCGCTCTCGACGACCCGTTAC	1499

RESULT 39

US-09-031-606-11
; Sequence 11, Application US/09031606
; Patent No. 6153404

/ GENERAL INFORMATION:
 / APPLICANT: MAZODIER, Philippe
 / APPLICANT: GUGLIEMI, Gerard
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 / TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
 / NUMBER OF SEQUENCES: 15
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Burns, Doane, Swecker & Mathis
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 / CITY: Alexandria
 / STATE: Virginia
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 / ZIP: 22313-1404

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, ZIF# 22313-1104
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, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/031,606
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; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2668 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-09-031-606-11

Query Match      63.9%; Score 268.2; DB 3; Length 2668;
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QY      64 GTACGGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGCGGC 123
DB      1143 GTCGGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGGGC 1202

QY      124 ATCGAAGAGCGCTCGAGGCGCTCTCGCGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAG 183
DB      1203 ATCGAGCGCGCTCGCGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGATCGAC 1262

QY      184 ACCAAGAGCAGATCGTTTCCAGGCTTCATCTCGCGCGCTTCATCTCGCGCGCTTCAG 243
DB      1263 GACAAGTCCGACATCGCGCGCTCTCGCGCGCTCTCGCGCGCTTCAGAGAGTCCGCGAG 1322

QY      244 CTATCGCGCGAGCGATGGAACAGGTGCGCAAGGTGCGCAAGGGCTCATCACCGTCGAGGAGTCC 303
DB      1323 CTATCGCGCGAGCGATGGAACAGGTGCGCAAGGTGCGCAAGGGCTCATCACCGTCGAGGAGTCC 1382

QY      304 CAGACCTTCGGTTCGAGCTGGAGCTCACCAGGGTATGCGCTTCGACCAAGGGCTACATC 363
DB      1383 AACACCTTCGGTTCGAGCTGGAGCTCACCAGGGTATGCGCTTCGACCAAGGGCTACCTG 1442

QY      364 TCGCGTACTTCGCGACCGATGAGCGATGAGCGATGAGCGATGAGCGATGAGCGATGAGCG 420
DB      1443 TCCCGGTACATGTTGACCGACGAGGAGCGTATGAGGCGCTCTCTCGACGACCGCGTAC 1499

RESULT 40
US-09-613-303-32
; Sequence 32, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-09-613-303-32

Query Match      60.7%; Score 254.8; DB 3; Length 888;
Best Local Similarity 81.5%; Pred. No. 1.9e-40;
Matches 295; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY      1 AAGAGACGACGACGTCGCGGTGACGGTACGACACCGCGACCGCTTCTCGCCGAGGGC 60
DB      232 AAGAGACGACGATGACGTCGCGGTGACGGTACGACACCGCGACCGCTTCTCGCCGAGGGC 291

QY      61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
DB      292 TTGGTTTCGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 351

QY      121 GGCATCGAAGGCGCGTCGAGGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGCAGGAGATGTC 180
DB      352 GGCATCGAAGGCGCGTCGAGGAGGTCACCGGAGACCGCTCTCAAGGCGCGCGAGGAGTTC 411

QY      181 GAGACCAAGGAGCAGATCGCTTCCACGGGCTTCATCTCCGCGCGCGACACCGACGATCGGC 240
DB      412 GAGACCAAGGAGCAGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 471

QY      241 GAGCTCATCGCGAGCGATGGAACAGGTGCGCAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
DB      472 GACCTGATCGCGAGGCGATGGAACAGGTGCGCAAGGTGCGCAAGGAGGCGTTCATCACCGTCGAGGAG 531

QY      301 TCCGACACCTTCGGTTCGAGCTGAGCTTCAGGAGGTCATCGGCGGTATGCGCTTCGACGAGGCTAC 360
DB      532 TCCGACACCTTCGGGCTGAGCTTCAGGAGGTCATCGGAGGTCATCGGCTTCGACGAGGCGCAT 591

QY      361 AT 362
DB      592 AT 593

RESULT 41
US-10-267-311-32
; Sequence 32, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match      60.7%; Score 254.8; DB 3; Length 888;
Best Local Similarity 81.5%; Pred. No. 1.9e-40;
Matches 295; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY      1 AAGAGACGACGACGTCGCGGTGACGGTACGACACCGCGACCGCTTCTCGCCGAGGGC 60
DB      232 AAGAGACGACGATGACGTCGCGGTGACGGTACGACACCGCGACCGCTTCTCGCCGAGGGC 291

QY      61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
DB      292 TTGGTTTCGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 351

QY      121 GGCATCGAAGGCGCGTCGAGGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGCAGGAGATGTC 180
DB      352 GGCATCGAAGGCGCGTCGAGGAGGTCACCGGAGACCGCTCTCAAGGCGCGCGAGGAGTTC 411
```

INFORMATION FOR SEQ ID NO: 79:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 S-08-997-362-79

 Query Match 57.4%; Score 241.2; DB 2; Length 360;
 Best Local Similarity 84.9%; Pred. No. 7.7e-38;


```
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
;
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-09-095-855-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTAGCAGTACGACACCGCGACCGTTCGCGCCAGGCG 60
DB 43 AAGAACCCGACGACGTCGCGGGGCGACCGCACACCGCCCGCCCGCTCGCTCAGGCT 102
QY 61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
DB 103 CTGTTTCGCGAAGGCTCGCGCAACGTCGCGAGCGCGGCGCAACCGCTCGGCTCAAGCT 162
QY 121 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 180
DB 163 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 222
QY 181 GAGACCAAGGAGCGATCGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGACCAAGGAGCGATCGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 282
QY 241 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
DB 283 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 342

RESULT 46
US-09-324-542-79
; Sequence 79, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTAGCAGTACGACACCGCGACCGTTCGCGCCAGGCG 60
DB 43 AAGAACCCGACGACGTCGCGGGGCGACCGCACACCGCCCGCCCGCTCGCTCAGGCT 102
QY 61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
DB 103 CTGTTTCGCGAAGGCTCGCGCAACGTCGCGAGCGCGGCGCAACCGCTCGGCTCAAGCT 162
QY 121 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 180
DB 163 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 222
QY 181 GAGACCAAGGAGCGATCGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGACCAAGGAGCGATCGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 282
QY 241 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
DB 283 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 342

RESULT 47
US-09-205-426-79
; Sequence 79, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-205-426-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTAGCAGTACGACACCGCGACCGTTCGCGCCAGGCG 60
DB 43 AAGAAGACCGACGACGTCGCGGGGCGACCGCACACCGCCCGCCCGCTCGCTCAGGCT 102
QY 61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
DB 103 CTGTTTCGCGAAGGCTCGCGCAACGTCGCGAGCGCGGCGCAACCGCTCGGCTCAAGCT 162
QY 121 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 180
DB 163 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 222
QY 181 GAGACCAAGGAGCGATGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGACCAAGGAGCGATGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 282
QY 241 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
DB 283 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 342

RESULT 48
US-09-324-542-79
; Sequence 79, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTAGCAGTACGACACCGCGACCGTTCGCGCCAGGCG 60
DB 43 AAGAACCCGACGACGTCGCGGGGCGACCGCACACCGCCCGCCCGCTCGCTCAGGCT 102
QY 61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
DB 103 CTGTTTCGCGAAGGCTCGCGCAACGTCGCGAGCGCGGCGCAACCGCTCGGCTCAAGCT 162
QY 121 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 180
DB 163 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCGAGAGGATGTC 222
QY 181 GAGACCAAGGAGCGATCGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGACCAAGGAGCGATCGCTTCCACGCGCTCTCATCTCCGCGCGCGACACCCAGATCGGC 282
QY 241 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
DB 283 GAGCTCATCGCGAGCGATGACAAAGGTTCGCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 342
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Db 41 AAGAGAGCGGCGGCTGCGGCTGAGCGGCAACCAACCGGCTGCTCGCCGCG 100
Qy 61 CTGCTAGCGAGGCGCTGCGCAAGCTGCGCGCGGCTGCGCAACCGGCTGCTCAAGCGC 120
Db 101 CTGCTAGCGAGGCTGCGCAAGCTGCGCGCGGCTGCGCAACCGGCTGCTCAAGCGC 160
Qy 121 GGATCGAGAGCGCGCTGCGAGGCGCTGCGCGCGGCTGCGCAACCGGCTGCTCAAGCGC 180
Db 161 GGATCGAGAGCGCGCTGCGAGGCGCTGCGCGCGGCTGCGCAACCGGCTGCTCAAGCGC 220
Qy 181 GAGACCAAGGAGGAGCTGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240
Db 221 GAGACCAAGGAGGAGCTGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 280
Qy 241 GAGCTCATCGCGAGGCGGATGAGCAAGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGG 300
Db 281 GAGCTCATCGCGAGGCGGATGAGCAAGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGG 340

RESULT 52

US-09-902-540-3255
; Sequence 3255, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Wiegand, Roger C.
; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR FILING DATE: 60/217,883

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 3255

; LENGTH: 1651

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-3255

Query Match 50.5%; Score 212.2; DB 3; Length 1651;
Best Local Similarity 71.0%; Pred. No. 2.9e-32;
Matches 296; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

Qy 4 AAGACGAGCAGCTGCGCGGCTGAGCGGCAACCGGCTGCTCGCCGCGGCTC 63
Db 235 AAGACGCTGACGCTGCGCGGCTGAGCGGCAACCGGCTGCTCGCCGCGGCTC 294
Qy 64 GTAGCGAGGCGCTGCGCAAGCTGCGCGCGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 123
Db 295 TTCCGCGAGGCGCGAAGCTGCTGCGCGCGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 354
Qy 124 ATCGAGAGCGCTGCGAGGCGCTGCTCGCGCGGCTGCTCGCGCGGCTGCTCGAG 183
Db 355 ATCGAGAGCGCTGCGAGGCGCTGCTCGCGCGGCTGCTCGCGCGGCTGCTCGAG 414
Qy 184 ACCAAGGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240
Db 415 GACCAAGGAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 474
Qy 241 GAGCTCATCGCGAGGCGGATGAGCAAGCTGCGCAAGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 300
Db 475 ACCATCATCGCGAGGCGGATGAGCAAGCTGCGCAAGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 534
Qy 301 TCCGAGACCTTCCGCTGCGAGCTGAGCTCAGCGGCTGAGCTCAGCGGCTGAGCTCAGCGGCTAC 360
Db 535 GCCAAGGCGCTGAGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTAC 594
Qy 361 ATCTCGCGCTACTTCCGCGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTAC 417
Db 595 CTGTCCCGCTACTTCTGTCGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTAC 651

RESULT 53

US-09-902-540-1150
; Sequence 1150, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Wiegand, Roger C.
; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR FILING DATE: 60/217,883

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1150

; LENGTH: 19954

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-1150

Query Match 50.5%; Score 212.2; DB 3; Length 19954;
Best Local Similarity 71.0%; Pred. No. 3.1e-32;
Matches 296; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

Qy 4 AAGACGAGCAGCTGCGCGGCTGAGCGGCAACCGGCTGCTCGCCGCGGCTC 63
Db 7835 AAGACGCTGACGCTGCGCGGCTGAGCGGCAACCGGCTGCTCGCCGCGGCTC 7894
Qy 64 GTAGCGAGGCGCTGCGCAAGCTGCGCGCGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 123
Db 7895 TTCCGCGAGGCGCGAAGCTGCTGCGCGCGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 7954
Qy 124 ATCGAGAGCGCTGCGAGGCGCTGCTCGCGCGGCTGCTCGCGCGGCTGCTCGAG 183
Db 7955 ATCGAGAGCGCTGCGAGGCGCTGCTCGCGCGGCTGCTCGCGCGGCTGCTCGAG 8014
Qy 184 ACCAAGGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240
Db 8015 GACCAAGGAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 8074
Qy 241 GAGCTCATCGCGAGGCGGATGAGCAAGCTGCGCAAGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 300
Db 8075 ACCATCATCGCGAGGCGGATGAGCAAGCTGCGCAAGGCTGCGCAACCGGCTGCTCGCCGCGGCTC 8134
Qy 301 TCCGAGACCTTCCGCTGCGAGCTGAGCTCAGCGGCTGAGCTCAGCGGCTGAGCTCAGCGGCTAC 360
Db 8135 GCCAAGGCGCTGAGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTAC 8194
Qy 361 ATCTCGCGCTACTTCCGCGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTAC 417
Db 8195 CTGTCCCGCTACTTCTGTCGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTAC 8251

RESULT 54

US-08-105-168B-22
; Sequence 22, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:

; APPLICANT: MABILAT et al.

; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION

; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE

; TITLE OF INVENTION: MYCOBACTERIA

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oliff & Berridge

; STREET: 700 South Washington Street, Suite 300

; CITY: Alexandria,

; STATE: Virginia

; ZIP: 22314

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" DS/HD
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS 3.1
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; FILING DATE: August 12, 1993
;; APPLICATION NUMBER: US/08/105,168B
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR9210094
;; FILING DATE: August 8, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: William P. Berridge
;; REGISTRATION NUMBER: 30,024
;; REFERENCE/DOCKET NUMBER: WPB 28835
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6400
;; TELEFAX: (703) 836-2787
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single-stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 438-787
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
US-08-105-168B-22

Query Match 50.1%; Score 210.6; DB 2; Length 350;
Best Local Similarity 80.7%; Pred. No. 5.7e-32;
Matches 246; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 AAGAGACGACGACGTCGCGGTGACGCTACGACACCGGACCGTCTCGCCCGAGGG 60
|||
DB 46 AAGAGACGACGACGTCGCGGTGACGCTACGACACCGGACCGTCTCGCCCGAGGG 105
|||
QY 61 CTCGTACGCGAGGCGCTCGCGGCTCCATCTCGCGCGGTCGCAACCGGATGGCTCTCAAGGCG 120
|||
DB 106 TTGGTTCGCGAGGCGCTCGCGGCTCCATCTCGCGCGGTCGCAACCGGATGGCTCTCAAGGCG 165
|||
QY 121 GGCATCGAGAGCGCTCGAGGCGCTCTCGCGGCTCTCGGAGCGGCGGATGTC 180
|||
DB 166 GGCATCGAGAGCGCTCGAGGCGCTCTCGCGGCTCTCGGAGCGGCGGATGTC 225
|||
QY 181 GGCATCGAGAGCGCTCGAGGCGCTCTCGCGGCTCTCGGAGCGGCGGATGTC 240
|||
DB 226 GAGACCAAGGAGGATTCGCGGCTCCATCTCGCGCGGTCGCAACCGGATGGCTCTCAAGGCG 285
|||
QY 241 GAGCTCATCGCGAGGCGGATGACCAAGGTCGCGCAAGGAGGCGTCTATACCGTCCAGGAG 300
|||
DB 286 GACCTGATCGCGAGGCGGATGACCAAGGTCGCGCAAGGAGGCGTCTATACCGTCCAGGAG 345
|||
QY 301 TCCCA 305
|||
DB 346 TCCAA 350
|||

RESULT 55
US-08-698-948-22

;; Sequence 22, Application US/08698948
;; Patent No. 5849901
;; GENERAL INFORMATION:
;; APPLICANT: MABILAT et al.
;; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
;; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETECTION
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oliff & Berridge
;; STREET: 700 South Washington Street, Suite 300
;; CITY: Alexandria,
;; STATE: Virginia
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" DS/HD
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS 3.1
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/698,948
;; FILING DATE: August 16, 1996
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/105,168
;; FILING DATE: August 12, 1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR9210094
;; FILING DATE: August 8, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: William P. Berridge
;; REGISTRATION NUMBER: 30,024
;; REFERENCE/DOCKET NUMBER: WPB 28835A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6400
;; TELEFAX: (703) 836-2787
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single-stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 438-787
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
US-08-698-948-22

Query Match 50.1%; Score 210.6; DB 2; Length 350;
Best Local Similarity 80.7%; Pred. No. 5.7e-32;
Matches 246; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 AAGAGACGACGACGTCGCGGTGACGCTACGACACCGGACCGTCTCGCCCGAGGG 60
|||
DB 46 AAGAGACGACGACGTCGCGGTGACGCTACGACACCGGACCGTCTCGCCCGAGGG 105
|||
QY 61 CTCGTACGCGAGGCGCTCGCGGCTCCATCTCGCGCGGTCGCAACCGGATGGCTCTCAAGGCG 120
|||
DB 106 TTGGTTCGCGAGGCGCTCGCGGCTCCATCTCGCGCGGTCGCAACCGGATGGCTCTCAAGGCG 165
|||
QY 121 GGCATCGAGAGCGCTCGAGGCGCTCTCGCGGCTCTCGGAGCGGCGGATGTC 180
|||
|||

166	GGCATCGAAGAGCCGCTGGAGAGGTCACCGAGACCCCTGCTCAAGGGGCCAAGAGGTC	225
Db		
181	GAGACCAAGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCCGACACCCAGATCGGC	240
Qy		
226	GAGACCAAGGAGCAGATTGCGGCCACCGCAGCGNTTTCGCGGGTGACCAAGTCCATCGT	285
Db		
241	GAGCTCATCGCGGCGGATGCAAGGTGCGCAAGGAAGGCGTCTATCCCGTCGAGGAG	300
Qy		
286	GACCTGATCGCGAGGCGATGCAAGGTGGGCAACGAGGGCGTCTATCCCGTCGAGGAG	345
Db		
301	TCCCA	305
Qy		
346	TCCAA	350
Db		

```

RESULT 56
US-08-473-020A-2
; Sequence 2, Application US/08473020A
; Patent No. 5877273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desraux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Giguel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; TITLE OF INVENTION: applications to the synthesis or detection of nucleic
; TITLE OF INVENTION: acids, products of expression of such sequences and
; TITLE OF INVENTION: application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,020A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/523,729
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H
; REGISTRATION NUMBER: 24190
; REFERENCE/DOCKET NUMBER: A54435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-473-020A-2

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Db      101 CTGTTCTGGTGAAGGTCTGCACACGTCGTGCCGGCGCCCAACCCCGTTCGGCCTGAAGCGC 160
QY      121 GGCATCGAGAAGGCCCGCTGAGGCGCGTCTCGGCGCCCTGCTGAGCAGAGCGAAGGATGTC 180
Db      161 GGCATCGAGAAGGCCCGTCAAGAGGTCA CGAGACGCTGCTGAAGAGCGCCAAGGAGTG 220
QY      181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db      221 GAGACCAAGGAGCAGATCGCTGCACCGCGGTATCTCCGCGGTGACCAGTCCATCGGT 280
QY      241 GAGCTCATCGCCGAGCGGATGACAAGGTTCGGAAGAAAGGCGTCA TCACCGTCGAGGAG 300
Db      281 GACCTGATCGCCGAGGCCATGGACAAGGTTCGGAACGAGGGTGTCATCA CCGTCGAGGAG 340

RESULT 57
US-08-473-020A-31
; Sequence 31, Application US/08473020A
; Patent No. 5877273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desraux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Giquel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; TITLE OF INVENTION: applications to the synthesis or detection of nucleic
; TITLE OF INVENTION: acids, products of expression of such sequences and
; TITLE OF INVENTION: application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,020A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/623,729
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H
; REGISTRATION NUMBER: 24190
; REFERENCE/DOCKET NUMBER: A54435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-473-020A-31

```

Query Match 50.0%; Score 210.2; DB 2; Length 342;
Best Local Similarity 80.9%; Pred. No. 6.9e-32;
Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 AAGAAGCGACGACGTCGCGGTGACGGTACACACCGCGACCGTTCGCGCCAGCG 60
|||||
Db 40 AAGAAGACCGATGACGTCGCGGTGACGGCACCACCGCGCCAGCG 99
|||||

QY 61 CTCGTACGAGGCGCTGCGACAGTCCGCGCGCGTGCACCCGATGCTCTCAAGCG 120
Db 100 TTGGTTCCGAGGCGCTGCGCAACGTCGCGCGCGCGCAACCCGCTCGGTCTCAACGC 159
QY 121 GGCATCGAAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGAGCAGCGAAGGATGTC 180
Db 160 GGCATCGAAGGCGCTGCGAGGCTCACCGAGACCTGCTCAAGGCGCGCAAGGATGTC 219
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 220 GAGACCAAGGAGCAGATTCGCGCACCGCAGCGATTTCCGCGCGGTGACCCAGTCCATCGGT 279
QY 241 GAGCTCATCGCGAGGCGATGGACAGGTCCGCAAGGAGGCTCATCAACCGTCGAGGAG 300
Db 280 GACCTGATCGCGAGGCGATGGCAAGGTGGGCAACGAGGCGGTCTATCAACCGTCGAGGAG 339
QY 301 TCC 303
Db 340 TCC 342

RESULT 58

US-08-473-020A-4

; Sequence 4, Application US/08473020A

; Patent No. 5877273

; GENERAL INFORMATION:

; APPLICANT: Hance, Allan J

; APPLICANT: Grandchamp-Desraux, Bernard

; APPLICANT: Levy-Frebault, Veronique

; APPLICANT: Gicquel, Brigitte

; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,

; TITLE OF INVENTION: applications to the synthesis or detection of nucleic

; TITLE OF INVENTION: acids, products of expression of such sequences and

; TITLE OF INVENTION: application as immunogenic compositions.

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Walter H. Dreger

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,020A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/623,729

; FILING DATE: 14-DEC-1990

; NAME: Dreger, Walter H

; ATTORNEY/AGENT INFORMATION:

; REGISTRATION NUMBER: 24190

; REFERENCE/DOCKET NUMBER: A54435

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 343 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

US-08-473-020A-4

Query Match

Best Local Similarity 50.0%; Score 210.2; DB 2; Length 343;

Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCCGCGTACGAGTACGACCAACGCGACCGTTCCTCCCGCAGGCG 60
Db 41 AAGAAGACGATGACGTCCGCGTACGAGTACGACCAACGCGCACCGTTCGTCGCGCAGGCG 100
QY 61 CTCGTACGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCCGATGCTCTCAAGCG 120
Db 101 TTGGTTCCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCCGCTCGGTCTCAACGC 160
QY 121 GGCATCGAAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGAGCAGCGAAGGATGTC 180
Db 161 GGCATCGAAGGCGCTGCGAGGCTCACCGAGACCTGCTCAAGGCGCGCAAGGATGTC 220
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 221 GAGACCAAGGAGCAGATTCGCGCACCGCAGCGATTTCCGCGCGGTGACCCAGTCCATCGGT 280
QY 241 GAGCTCATCGCGAGGCGATGGACAGGTCCGCAAGGAGGCTCATCAACCGTCGAGGAG 300
Db 281 GACCTGATCGCGAGGCGATGGCAAGGTGGGCAACGAGGCGGTCTATCAACCGTCGAGGAG 340
QY 301 TCC 303
Db 341 TCC 343

RESULT 59

US-08-473-020A-5

; Sequence 5, Application US/08473020A

; Patent No. 5877273

; GENERAL INFORMATION:

; APPLICANT: Hance, Allan J

; APPLICANT: Grandchamp-Desraux, Bernard

; APPLICANT: Levy-Frebault, Veronique

; APPLICANT: Gicquel, Brigitte

; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,

; TITLE OF INVENTION: applications to the synthesis or detection of nucleic

; TITLE OF INVENTION: acids, products of expression of such sequences and

; TITLE OF INVENTION: application as immunogenic compositions.

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Walter H. Dreger

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,020A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/623,729

; FILING DATE: 14-DEC-1990

; NAME: Dreger, Walter H

; ATTORNEY/AGENT INFORMATION:

; REGISTRATION NUMBER: 24190

; REFERENCE/DOCKET NUMBER: A54435

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 343 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

US-08-473-020A-5

Query Match 50.0%; Score 210.2; DB 2; Length 343;
Best Local Similarity 80.9%; Pred. No. 6.9e-32;
Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 AAGAAGACCGACGACGTCGCGCGGTACGAGTACGACACCGCGCGTCTCGCCGAGGCG 60
|||
DB 41 AAGAAGACCGACGACGTCGCGCGGTACGAGTACGACACCGCGCGTCTCGCCGAGGCG 100
|||

QY 61 CTGCTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
|||
DB 101 TTGCTCAAGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 160
|||

QY 121 GGCATCAGAGGCGCTCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 180
|||
DB 161 GGCATCAGAGGCGCTCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 220
|||

QY 181 GAGACCAAGGAGGAGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 240
|||
DB 221 GAGACCAAGGAGGAGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 280
|||

QY 241 GAGCTCATCGCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 300
|||
DB 281 GAGCTCATCGCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 340
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QY 301 TCC 303
|||
DB 341 TCC 343
|||

RESULT 60

US-08-473-020A-7
Sequence 7, Application US/08473020A
Patent No. 5877273

GENERAL INFORMATION:

APPLICANT: Hance, Allan J
APPLICANT: Grandchamp-Desaux, Bernard
APPLICANT: Levy-Frebault, Veronique
APPLICANT: Gicquel, Brigitte
TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
TITLE OF INVENTION: applications to the synthesis or detection of nucleic
TITLE OF INVENTION: acids, products of expression of such sequences and
TITLE OF INVENTION: application as immunogenic compositions.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,020A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 343 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-473-020A-7

Query Match 50.0%; Score 210.2; DB 2; Length 343;
Best Local Similarity 80.9%; Pred. No. 6.9e-32;
Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 AAGAAGACCGACGACGTCGCGCGGTGACGTAACGACACCGCGCGTCTCGCCGAGGCG 60
|||
DB 41 AAGAAGACCGACGACGTCGCGCGGTGACGTAACGACACCGCGCGTCTCGCCGAGGCG 100
|||

QY 61 CTGCTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 120
|||
DB 101 TTGCTCAAGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 160
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QY 121 GGCATCAGAGGCGCTCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 180
|||
DB 161 GGCATCAGAGGCGCTCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 220
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QY 181 GAGACCAAGGAGGAGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 240
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DB 221 GAGACCAAGGAGGAGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 280
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QY 241 GAGCTCATCGCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 300
|||
DB 281 GAGCTCATCGCGAGGCGTCTCGCGCGGTGCGCAACCGCGATGCTCTCAAGCGC 340
|||

QY 301 TCC 303
|||
DB 341 TCC 343
|||

Search completed: April 1, 2006, 17:06:27
Job time : 255.586 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:17:36 ; Search time 1130.56 Seconds
(without alignments)
3072.051 Million cell updates/sec

Title: US-10-824-527-43

Perfect score: 420

Sequence: 1 aagaagcggagcagctgcg.....cgctcgagacccgtac 420

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	420	8	US-10-824-527-43 Sequence 43, Appl
2	420	100.0	420	8	US-10-824-527-45 Sequence 45, Appl
3	412	98.1	420	8	US-10-824-527-58 Sequence 58, Appl
4	404	96.2	1623	6	US-10-156-761-3915 Sequence 3915, Ap
5	404	96.2	9025608	6	US-10-156-761-1 Sequence 1, Appl
6	396	94.3	420	8	US-10-824-527-47 Sequence 47, Appl
7	396	94.3	420	8	US-10-824-527-48 Sequence 48, Appl
8	394.4	93.9	420	8	US-10-824-527-3 Sequence 3, Appl
9	394.4	93.9	420	8	US-10-824-527-9 Sequence 9, Appl
10	394.4	93.9	420	8	US-10-824-527-11 Sequence 11, Appl
11	394.4	93.9	420	8	US-10-824-527-20 Sequence 20, Appl
12	392.8	93.5	420	8	US-10-824-527-15 Sequence 15, Appl
13	392.8	93.5	420	8	US-10-824-527-23 Sequence 23, Appl
14	392.8	93.5	420	8	US-10-824-527-55 Sequence 55, Appl
15	391.2	93.1	420	8	US-10-824-527-6 Sequence 6, Appl
16	391.2	93.1	420	8	US-10-824-527-16 Sequence 16, Appl
17	391.2	93.1	420	8	US-10-824-527-22 Sequence 22, Appl
18	388	92.4	420	8	US-10-824-527-24 Sequence 24, Appl
19	388	92.4	420	8	US-10-824-527-36 Sequence 36, Appl
20	388	92.4	420	8	US-10-824-527-61 Sequence 61, Appl
21	386.4	92.0	420	8	US-10-824-527-17 Sequence 17, Appl
22	386.4	92.0	420	8	US-10-824-527-32 Sequence 32, Appl
23	386.4	92.0	420	8	US-10-824-527-34 Sequence 34, Appl

24	386.4	92.0	420	8	US-10-824-527-38	Sequence 38, Appl
25	386.4	92.0	420	8	US-10-824-527-40	Sequence 40, Appl
26	386.4	92.0	420	8	US-10-824-527-46	Sequence 46, Appl
27	386.4	92.0	420	8	US-10-824-527-49	Sequence 49, Appl
28	386.4	92.0	420	8	US-10-824-527-57	Sequence 57, Appl
29	386.4	92.0	422	8	US-10-824-527-18	Sequence 18, Appl
30	384.8	91.6	420	8	US-10-824-527-8	Sequence 8, Appl
31	384.8	91.6	420	8	US-10-824-527-31	Sequence 31, Appl
32	384.8	91.6	420	8	US-10-824-527-35	Sequence 35, Appl
33	383.2	91.2	420	8	US-10-824-527-13	Sequence 13, Appl
34	383.2	91.2	420	8	US-10-824-527-19	Sequence 19, Appl
35	383.2	91.2	420	8	US-10-824-527-26	Sequence 26, Appl
36	383.2	91.2	420	8	US-10-824-527-37	Sequence 37, Appl
37	381.6	90.9	420	8	US-10-824-527-21	Sequence 21, Appl
38	381.6	90.9	420	8	US-10-824-527-25	Sequence 25, Appl
39	381.6	90.9	420	8	US-10-824-527-28	Sequence 28, Appl
40	381.6	90.9	420	8	US-10-824-527-29	Sequence 29, Appl
41	381.6	90.9	420	8	US-10-824-527-60	Sequence 60, Appl
42	380	90.5	420	8	US-10-824-527-14	Sequence 14, Appl
43	378.4	90.1	420	8	US-10-824-527-51	Sequence 51, Appl
44	378.4	90.1	420	8	US-10-824-527-52	Sequence 52, Appl
45	378.4	90.1	420	8	US-10-824-527-53	Sequence 53, Appl
46	378.4	90.1	420	8	US-10-824-527-54	Sequence 54, Appl
47	373.6	89.0	420	8	US-10-824-527-50	Sequence 50, Appl
48	372	88.6	420	8	US-10-824-527-27	Sequence 27, Appl
49	372	88.6	420	8	US-10-824-527-56	Sequence 56, Appl
50	372	88.6	420	8	US-10-824-527-55	Sequence 55, Appl
51	372	88.6	420	8	US-10-824-527-59	Sequence 59, Appl
52	370.4	88.2	420	8	US-10-824-527-5	Sequence 5, Appl
53	370.2	88.1	423	8	US-10-824-527-7	Sequence 7, Appl
54	368.6	87.8	423	8	US-10-824-527-30	Sequence 30, Appl
55	365.6	87.0	420	8	US-10-824-527-4	Sequence 4, Appl
56	362.4	86.3	420	8	US-10-824-527-33	Sequence 33, Appl
57	362.2	86.2	423	8	US-10-824-527-39	Sequence 39, Appl
58	360.8	85.9	420	8	US-10-824-527-10	Sequence 10, Appl
59	359.2	85.5	420	8	US-10-824-527-12	Sequence 12, Appl
60	322.4	76.8	604	8	US-10-500-586-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-10-824-527-43
; Sequence 43, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823 0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 43
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-43

Query Match 100.0%; Score 420; DB 8; Length 420;

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Best Local Similarity 100.0%; Pred. No. 2.3e-98;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAAGCGGACGACGTCGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCAGGCG 60
Db 1 AAGAAGCGGACGACGTCGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGCCAGGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTACGCGAGGCGCTCGCGACGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAGGCGCGTCGAGGCGCTCTCGCGGCGCTCTGAGAGGCGGAAAGGATGTC 180
Db 121 GGCATCGAGAGGCGCGTCGAGGCGCTCTCGCGGCGCTCTGAGAGGCGGAAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGTGCGCAAGGTGCGTCAACCGGCTAC 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGTGCGTCAACCGGCTAC 300
Qy 301 TCCAGACCTTGGTCTGAGGCTGAGCTCACCGAGGATGGCTTTCGACAAAGGGCTAC 360
Db 301 TCCAGACCTTGGTCTGAGGCTGAGCTCACCGAGGATGGCTTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACGACCGCGTAC 420
Db 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACGACCGCGTAC 420

RESULT 2
US-10-824-527-45
; Sequence 45, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 45
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-45

Query Match 100.0%; Score 420; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.3e-98;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAAGCGGACGACGTCGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCAGGCG 60
Db 1 AAGAAGCGGACGACGTCGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGCCAGGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTACGCGAGGCGCTCGCGACGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAGGCGCGTCGAGGCGCTCTCGCGGCGCTCTGAGAGGCGGAAAGGATGTC 180
Db 121 GGCATCGAGAGGCGCGTCGAGGCGCTCTCGCGGCGCTCTGAGAGGCGGAAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGTGCGTCAACCGGCTAC 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGTGCGTCAACCGGCTAC 300
Qy 301 TCCAGACCTTGGTCTGAGGCTGAGCTCACCGAGGATGGCTTTCGACAAAGGGCTAC 360
Db 301 TCCAGACCTTGGTCTGAGGCTGAGCTCACCGAGGATGGCTTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACGACCGCGTAC 420
Db 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACGACCGCGTAC 420

RESULT 3
US-10-824-527-58
; Sequence 58, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 58
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-58

Query Match 98.1%; Score 412; DB 8; Length 420;
Best Local Similarity 98.8%; Pred. No. 2.6e-96;
Matches 415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AAGAAGCGGACGACGTCGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCAGGCG 60
Db 1 AAGAAGCGGACGACGTCGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGCGACGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTACGCGAGGCGCTCGCGACGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAGGCGCGTCGAGGCGCTCTCGCGGCGCTCTGAGAGGCGGAAAGGATGTC 180
Db 121 GGCATCGAGAGGCGCGTCGAGGCGCTCTCGCGGCGCTCTGAGAGGCGGAAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGTGCGTCAACCGGCTAC 300
```

Db 241 GAGCTATCCCGGAGGCGATGGCAAGGTCGGCAAGGAGCGGTCTATCACCCTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACCAAGGCGCTAC 360
Db 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACCAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGCCACCGACATGGAGCGGATGGAGCGGCTGCTCGACGACCCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCGCCACCGACATGGAGCGGATGGAGCGGCTGCTCGACGACCCGCTAC 420

RESULT 4

US-10-156-761-3915
; Sequence 3915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3915
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
US-10-156-761-3915

Query Match 96.2%; Score 404; DB 6; Length 1623;

Best Local Similarity 97.6%; Pred. No. 2.7e-94;

Matches 410; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCGAGCTCCCGGTGACGGTACGACACCGCGCGGTCTTCGCCCGAGGCG 60
Db 232 AAGAGACGAGCGAGCTCCCGGTGACGGTACGACACCGCGCGGTCTTCGCCCGAGGCG 291
QY 61 CTCGTACGCGAGGCGCTCGCGCAACGTCCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
Db 292 CTCGTCCGCGAGGCGCTCGCAACGTAGCGCGCGCGCGCGCAACCGATGGCTCTCAAGGCG 351
QY 121 GCGATCGAGAGCGCGTTCGAGCGCGTTCGCGCGCGCTGCTGGAGCGCGCGAAGGATGTC 180
Db 352 GGTATCGAGAGCGCGTTCGAGCGCGTTCGCGCGCGCTGCTGGAGCGCGCGAAGGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCGACACCGATCGGC 240
Db 412 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCGACACCGATCGGC 471
QY 241 GAGCTCATCGCGAGCGGATGACCAAGGTGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 300
Db 472 GAGCTCATCGCGAGCGGATGACCAAGGTGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACCAAGGCGCTAC 360
Db 532 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACCAAGGCGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGGCGTCTGCTCGACGACCCGCTAC 420
Db 592 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGGCGTCTGCTCGACGACCCGCTAC 651

RESULT 5

US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 96.2%; Score 404; DB 6; Length 9025608;

Best Local Similarity 97.6%; Pred. No. 1.6e-94;

Matches 410; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCGAGCTCCCGGTGACGGTACGACACCGCGCGGTCTTCGCCCGAGGCG 60
Db 4855588 AAGAGACGAGCGAGCTCCCGGTGACGGTACGACACCGCGCGGTCTTCGCCCGAGGCG 4855529
QY 61 CTCGTACGCGAGGCGCTTCGCGCAACGTCCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
Db 4855528 CTCGTCCGCGAGGCGCTTCGCGCAACGTAGCGCGCGCGCGCAACCGATGGCTCTCAAGGCG 4855469
QY 121 GGCATCGAGAGGCGCTCGAGCGCGTCTCCGCGCGCGCTGCTGGAGCGCGAAGGATGTC 180
Db 4855468 GGTATCGAGAGGCGCGTTCGAGCGCGTCTCCGCGCGCGCTGCTGGAGCGCGAAGGATGTC 4855409
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCGACACCGATCGGC 240
Db 4855408 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCGACACCGATCGGC 4855349
QY 241 GAGCTCATCGCGAGGCGATGCGCAAGGTGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 300
Db 4855348 GAGCTCATCGCGAGGCGATGCGCAAGGTGCGCAAGGAGGCGTCTATCACCCTCGAGGAG 4855289
QY 301 TCCGAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACCAAGGCGCTAC 360
Db 4855288 TCCGAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACCAAGGCGCTAC 4855229
QY 361 ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGGCGTCTGCTCGACGACCCGCTAC 420
Db 4855228 ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGGCGTCTGCTCGACGACCCGCTAC 4855169

RESULT 6

US-10-824-527-47
; Sequence 47, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN

APPLICANT: KO, YOUNG HWAN
APPLICANT: KOH, JEONG-SAM
APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BURM
APPLICANT: LEE, HYANG BURM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 47
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces scabiei
US-10-824-527-47

Query Match 94.3%; Score 396; DB 8; Length 420;
Best Local Similarity 96.4%; Pred. No. 3.3e-92;
Matches 405; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCGTGGCGGTGACGATGACGACCGGACCGGCTTCTCGCCAGGCG 60
Db 1 AAGAAGACGAGCGTGGCGGTGACGATGACGACCGGACCGGCTTCTCGCCAGGCG 60
Qy 61 CTCTGACGAGGCGCTGCGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 120
Db 61 CTCTGACGAGGCGCTGCGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 120
Qy 121 GGCAATCGAGAGGCGCTGCGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 180
Db 121 GGCAATCGAGAGGCGCTGCGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 180
Qy 181 GAGACCAAGGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 240
Db 181 GAGACCAAGGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 240
Qy 241 GAGCTCATCGCGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 300
Db 241 GAGCTCATCGCGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 300
Qy 301 TCCGACGACCTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 360
Db 301 TCCGACGACCTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 360
Qy 361 ATCTCGGCGTACTTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 420
Db 361 ATCTCGGCGTACTTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 420

RESULT 7

US-10-824-527-48
Sequence 48, Application US/10824527
Publication No. US20040265873A1
GENERAL INFORMATION:
APPLICANT: KIM, BUM-JOON
APPLICANT: KIM, CHANG-JIN
APPLICANT: KO, YOUNG HWAN
APPLICANT: KOH, JEONG-SAM
APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BURM
APPLICANT: LEE, HYANG BURM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527

CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 48
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces scabiei
US-10-824-527-48

Query Match 94.3%; Score 396; DB 8; Length 420;
Best Local Similarity 96.4%; Pred. No. 3.3e-92;
Matches 405; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCGTGGCGGTGACGATGACGACCGGACCGGCTTCTCGCCAGGCG 60
Db 1 AAGAAGACGAGCGTGGCGGTGACGATGACGACCGGACCGGCTTCTCGCCAGGCG 60
Qy 61 CTCTGACGAGGCGCTTGGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 120
Db 61 CTCTGACGAGGCGCTTGGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 120
Qy 121 GGCAATCGAGAGGCGCTTGGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 180
Db 121 GGCAATCGAGAGGCGCTTGGCAACGTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 180
Qy 181 GAGACCAAGGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 240
Db 181 GAGACCAAGGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 240
Qy 241 GAGCTCATCGCGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 300
Db 241 GAGCTCATCGCGAGGCGTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 300
Qy 301 TCCGACGACCTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 360
Db 301 TCCGACGACCTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 360
Qy 361 ATCTCGGCGTACTTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 420
Db 361 ATCTCGGCGTACTTTCGCGCGCGCTTCCACCGGCTTCCACCGGCTTCCACCGGCTTCTCAAGCGC 420

RESULT 8

US-10-824-527-3
Sequence 3, Application US/10824527
Publication No. US20040265873A1
GENERAL INFORMATION:
APPLICANT: KIM, BUM-JOON
APPLICANT: KIM, CHANG-JIN
APPLICANT: KO, YOUNG HWAN
APPLICANT: KOH, JEONG-SAM
APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BURM
APPLICANT: LEE, HYANG BURM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 3
LENGTH: 420
TYPE: DNA

Db 181 GAGACCAAGGAGCAGATCGCTCCACGGCTCCATCTCCGCCCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCCGAGGCGATGGACAGGTGGCAAGAGGCGTCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCCGAGGCGCATGGACAGGTGGCAAGAGGCGTCATCACCCTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGGTAC 360
Db 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGGTAC 360
Qy 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCGCTCGACGACCCGTAC 420
Db 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGGAGCGGTGCGCTCGACGACCCGTAC 420

RESULT 11

US-10-824-527-20
; Sequence 20, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces chartreusis
US-10-824-527-20

Query Match 93.9%; Score 394.4; DB 8; Length 420;
Best Local Similarity 96.2%; Pred. No. 8.5e-92;
Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 AAGNAGCGGACGACGTCCGCGGTGACGGTACGACACCGGACCGGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGGACGACGTCCGCGGTGACGGTACGACACCGGACCGGACCGTTCGCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTCAAGGAGGCGCTCGGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCAATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCGCTTCGCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
Db 121 GGTATCGAGCGTCCGCTCGAGGCGCTCTCCGCGCGCTTCGCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGCGTCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGCGTCATCACCCTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGGTAC 360
Db 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGGTAC 360

Qy 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCGCTCGACGACCCGTAC 420
Db 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCGCTCGACGACCCGTAC 420

RESULT 12

US-10-824-527-15
; Sequence 15, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces bambergiensis
US-10-824-527-15

Query Match 93.5%; Score 392.8; DB 8; Length 420;
Best Local Similarity 96.0%; Pred. No. 2.2e-91;
Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 1 AAGAAGACGGACGACGTCCGCGGTGACGGTACGACACCGGACCGGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGGACGACGTCCGCGGTGACGGTACGACACCGGACCGGACCGTTCGCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTCAAGGAGGCGCTTCGCGCGGTGCGCAACCGGATGGCTTCGCGCCAGGCG 120
Qy 121 GGCAATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCGCTTCGCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
Db 121 GGTATCGAGAAGGCGCTTCGCGCGGTGCGCAACCGGATGGCTTCGCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGCGTCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGCGTCATCACCCTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGGTAC 360
Db 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGGTAC 360
Qy 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCGCTTCGACGACCCGTAC 420
Db 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGGAGCGGTGCGCTTCGACGACCCGTAC 420

RESULT 13

US-10-824-527-23
; Sequence 23, Application US/10824527
; Publication No. US20040265873A1

GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: KIM, SUN-HUYN
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cinereoruber
US-10-824-527-23

Query Match 93.5%; Score 392.8; DB 8; Length 420;
Best Local Similarity 96.0%; Pred. No. 2.2e-91;
Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGCG 60
DB 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGCG 60
QY 61 CTGCTACGCGAGGGCTCGCAACGTCGCGCGCGTGCACCGACCGTTCGAGCGC 120
DB 61 CTGCTCGCGAGGGCTTCGCAACGTCGCGCGCGTGCACCGACCGTTCGAGCGC 120
QY 121 GGCATCGAGAGGGCGTTCGAGCGCGTTCGCGCGCGTTCGAGCGCGGCGGAGGATGTC 180
DB 121 GGCATCGAGAGGGCGTTCGAGCGCGTTCGCGCGCGTTCGAGCGCGGCGGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGTCATCGCGAGGGCGATCGAAGGTTCGGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
DB 241 GAGTCATCGCGAGGGCGATCGAAGGTTCGGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATCGCTTCGACNAGGGCTAC 360
DB 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATCGCTTCGACNAGGGCTAC 360
QY 361 ATCTCGGGTACTTCGCCACCGACATGAGCGGATGAGGGCGTTCGACGACCCGCTAC 420
DB 361 ATCTCGGGTACTTCGCCACCGACATGAGCGGATGAGGGCGTTCGACGACCCGCTAC 420

RESULT 14
US-10-824-527-55
; Sequence 55, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 55
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces bottropensis
US-10-824-527-55

Query Match 93.5%; Score 392.8; DB 8; Length 420;
Best Local Similarity 96.0%; Pred. No. 2.2e-91;
Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGCG 60
DB 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGCG 60
QY 61 CTGCTACGCGAGGGCTTCGCAACGTCGCGCGCGTGCACCGACCGTTCGAGCGC 120
DB 61 CTGCTCGCGAGGGCTTCGCAACGTCGCGCGCGTGCACCGACCGTTCGAGCGC 120
QY 121 GGCATCGAGAGGGCGTTCGAGCGCGTTCGCGCGCGTTCGAGCGCGGCGGAGGATGTC 180
DB 121 GGCATCGAGAGGGCGTTCGAGCGCGTTCGCGCGCGTTCGAGCGCGGCGGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGTCATCGCGAGGGCGATCGAAGGTTCGGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
DB 241 GAGTCATCGCGAGGGCGATCGAAGGTTCGGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATCGCTTCGACNAGGGCTAC 360
DB 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATCGCTTCGACNAGGGCTAC 360
QY 361 ATCTCGGGTACTTCGCCACCGACATGAGCGGATGAGGGCGTTCGACGACCCGCTAC 420
DB 361 ATCTCGGGTACTTCGCCACCGACATGAGCGGATGAGGGCGTTCGACGACCCGCTAC 420

RESULT 15
US-10-824-527-6
; Sequence 6, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2

```
; SEQ ID NO 6
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces albireticuli
; US-10-824-527-6

Query Match          93.1%; Score 391.2; DB 8; Length 420;
Best Local Similarity 95.7%; Pred. No. 5.7e-91;
Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGTGAAGTACGACCAACCGCAGACCGTCTTCCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGTGAAGTACGACCAACCGCAGACCGTCTTCCGCCAGGCG 60
QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 120
DB 61 CTCGTCAAGGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 180
DB 121 GGCATCGAGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 180
QY 181 GAGACCAAGGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 240
DB 181 GAGACCAAGGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 240
QY 241 GAGCTCATCGCGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 300
DB 241 GAGCTCATCGCGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 300
QY 301 TCCGACGACCTTCGGTCTGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTAC 360
DB 301 TCCGACGACCTTCGGTCTGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGTATGAGGCGGCTCTCGACGACCGGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGTATGAGGCGGCTCTCGACGACCGGCTAC 420

RESULT 17
US-10-824-527-22
; Sequence 22, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cinnamonensis
; US-10-824-527-22

Query Match          93.1%; Score 391.2; DB 8; Length 420;
Best Local Similarity 95.7%; Pred. No. 5.7e-91;
Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGTGAAGTACGACCAACCGCAGACCGTCTTCCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGTGAAGTACGACCAACCGCAGACCGTCTTCCGCCAGGCG 60
QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 120
DB 61 CTCGTCCGAGGCGCTTGGCGAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGT 120
QY 121 GGCATCGAGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 180
DB 121 GGCATCGAGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 180
QY 181 GAGACCAAGGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 240
DB 181 GAGACCAAGGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 240
QY 241 GAGCTCATCGCGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 300
DB 241 GAGCTCATCGCGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTCAAGCGC 300
QY 301 TCCGACGACCTTCGGTCTGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTAC 360
DB 301 TCCGACGACCTTCGGTCTGAGGCGCTGCGCAACGTCGCGCGTGAAGTACGACCAACCGCAGGCGTCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGTATGAGGCGGCTCTCGACGACCGGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGTATGAGGCGGCTCTCGACGACCGGCTAC 420

RESULT 16
US-10-824-527-16
; Sequence 16, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces capilliepiralis
; US-10-824-527-16

Query Match          93.1%; Score 391.2; DB 8; Length 420;
Best Local Similarity 95.7%; Pred. No. 5.7e-91;
Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
```

Db 121 GGTATCGAGAGCCGCTGAGGCGGTCTCGCGCGCCCTGCTGCGCCGAGGCGCAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGGTGACAGAGTGGCGAGGAGGCGTATCAACCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGGTGACAGAGTGGCGAGGAGGCGTATCAACCTCGAGGAG 300
Qy 301 TCCAGACCTTGGCTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTGGCTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
Qy 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCCGTAC 420
Db 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCCGTAC 420

RESULT 18

US-10-824-527-24
; Sequence 24, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-0000
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; TYPE: DNA
; ORGANISM: Streptomyces cirratus
US-10-824-527-24

Query Match 92.4%; Score 388; DB 8; Length 420;
Best Local Similarity 95.2%; Pred. No. 3.8e-90;
Matches 400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 AAGAGACGAGCAGCTGCGCGGTGACCGGTACGAGCAGCGGACCGGTTCTGCGCCAGGCG 60
Db 1 AAGAGACGAGCAGCTGCGCGGCGCAGCGGTACGAGCAGCGGACCGGTTCTGCGCCAGGCG 60
Qy 61 CTCTGCTACGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGGCG 120
Db 61 CTCTGCTACGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGGCG 120
Qy 121 GGCATCGAGAGGCGCTGAGGCGGCTCTCCGCGCGCTTCCAGCGAGCGAGCGGATGTC 180
Db 121 GGCATCGAGAGGCGCTGAGGCGGCTCTCCGCGCGCTTCCAGCGAGCGAGCGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGGTGACAGAGTGGCGAGGAGGCGTATCAACCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGGTGACAGAGTGGCGAGGAGGCGTATCAACCTCGAGGAG 300

Qy 301 TCCAGACCTTGGCTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTGGCTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
Qy 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCCGTAC 420
Db 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCCGTAC 420

RESULT 19

US-10-824-527-36
; Sequence 36, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-0000
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; TYPE: DNA
; ORGANISM: Streptomyces humiferus
US-10-824-527-36

Query Match 92.4%; Score 388; DB 8; Length 420;
Best Local Similarity 95.2%; Pred. No. 3.8e-90;
Matches 400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 AAGAGACGAGCAGCTGCGCGGTGACCGGTACGAGCAGCGGACCGGTTCTGCGCCAGGCG 60
Db 1 AAGAGACGAGCAGCTGCGCGGCGCAGCGGTACGAGCAGCGGACCGGTTCTGCGCCAGGCG 60
Qy 61 CTCTGCTACGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGGCG 120
Db 61 CTCTGCTACGAGGCGCTGCGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGGCG 120
Qy 121 GGCATCGAGAGGCGCTGAGGCGGCTCTCCGCGCGCTTCCAGCGAGCGAGCGGATGTC 180
Db 121 GGCATCGAGAGGCGCTGAGGCGGCTCTCCGCGCGCTTCCAGCGAGCGAGCGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGGTGACAGAGTGGCGAGGAGGCGTATCAACCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGGTGACAGAGTGGCGAGGAGGCGTATCAACCTCGAGGAG 300
Qy 301 TCCAGACCTTGGCTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTGGCTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACCAAGGCTAC 360
Qy 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCCGTAC 420
Db 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTCGACGACCCGTAC 420

RESULT 20

US-10-824-527-61
; Sequence 61, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 61
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces acidiscabies
US-10-824-527-61

Query Match 92.4%; Score 388; DB 8; Length 420;
Best Local Similarity 95.2%; Pred. No. 3.8e-90;
Matches 400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGACGTCGGCGGTGACGGTACGACACCGCGACCGGTCTTCGCCCGAGCG 60
DB 1 AAGAAGACGGACGACGTCGGCGGTGACGGTACGACACCGCGACCGGTCTTCGCCCGAGCG 60
QY 61 CTGCTACGCGAGGCGCTCGCGACGTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTCGCGACGTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 180
DB 121 GGCATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGTGCGACACCGGTGCGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGTGCGACACCGGTGCGC 240
QY 241 GAGCTCATCGCGAGGCGATCGCTTCCACGCGCTCCATCTCCGCGCGGTGCGACACCGGTGCGC 300
DB 241 GAGCTCATCGCGAGGCGATCGCTTCCACGCGCTCCATCTCCGCGCGGTGCGACACCGGTGCGC 300
QY 301 TCCGAGACCTTCGGTCTGAGGTGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGGTGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
QY 361 ATCTCGCGGTACTTCGCGACCGACATGAGCGGTATGAGCGGTCTCCCTGGACGACCGCGTAC 420
DB 361 ATCTCGCGGTACTTCGCGACCGACATGAGCGGTATGAGCGGTCTCCCTGGACGACCGCGTAC 420

RESULT 21
US-10-824-527-17
; Sequence 17, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM

; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces carpinensis
US-10-824-527-17

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGGACGACGTCGGCGGTGACGGTACGACACCGCGACCGGTCTTCGCCCGAGCG 60
DB 1 AAGAAGACGGACGACGTCGGCGGTGACGGTACGACACCGCGACCGGTCTTCGCCCGAGCG 60
QY 61 CTGCTACGCGAGGCGCTTCGCGACGTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTTCGCGACGTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTTCGCGACGTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 180
DB 121 GGCATCGAGAGGCGCTTCGCGACGTCGCGCGCGGTGCGACACCGGTGCGTCTCAAGCGC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGTGCGACACCGGTGCGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGGTGCGACACCGGTGCGC 240
QY 241 GAGCTCATCGCGAGGCGATGAGCAAGGTGCGCAAGGGGTGTCATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGAGCAAGGTGCGCAAGGGGTGTCATCACCCTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGAGGTGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGGTGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
QY 361 ATCTCGCGGTACTTCGCGACCGACATGAGCGGTATGAGCGGTCTCCCTGGACGACCGCGTAC 420
DB 361 ATCTCGCGGTACTTCGCGACCGACATGAGCGGTATGAGCGGTCTCCCTGGACGACCGCGTAC 420

RESULT 22
US-10-824-527-32
; Sequence 32, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580

; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces galilaeus
US-10-824-527-32

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
QY 61 CTCGTACGAGGAGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 61 CTGGTCCGAGGAGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGCGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCGGCGGCGGCGGCT 180
DB 121 GGCATCGAGAGCGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCGGCGGCGGCGGCT 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCGCGCGGACACCGGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCGCGCGGACACCGGATCGGC 240
QY 241 GAGCTCATCGCGAGCGGATGACAGGTCGCGGAGGCGGTCATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGGATGACAGGTCGCGGAGGCGGTCATCACCCTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTCGAGCTGAGCTCACCAGGCTATCGCTTCGACGAGGCTTAC 360
DB 301 TCCAGACCTTCGGTCTCGAGCTGAGCTCACCAGGCTATCGCTTCGACGAGGCTTAC 360
QY 361 ATCTCGGCGTACTTCCGCAACGACATGAGCGGATGAGGCGTCTCGAGCAGCCGTAC 420
DB 361 ATCTCGGCGTACTTCCGCAACGACATGAGCGGATGAGGCGTCTCGAGCAGCCGTAC 420

RESULT 23
US-10-824-527-34
; Sequence 34, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces griseolus
US-10-824-527-34

Query Match 92.0%; Score 386.4; DB 8; Length 420;

Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
QY 61 CTCGTACGAGGAGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 61 CTGGTCCGAGGAGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGCGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCGGCGGCGGCGGCT 180
DB 121 GGCATCGAGAGCGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCGGCGGCGGCGGCT 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCGCGCGGACACCGGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCGCGCGGACACCGGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGGATGACAGGTCGCGGAGGCGGTCATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGGATGACAGGTCGCGGAGGCGGTCATCACCCTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTCGAGCTGAGCTCACCAGGCTATCGCTTCGACGAGGCTTAC 360
DB 301 TCCAGACCTTCGGTCTCGAGCTGAGCTCACCAGGCTATCGCTTCGACGAGGCTTAC 360
QY 361 ATCTCGGCGTACTTCCGCAACGACATGAGCGGATGAGGCGTCTCGAGCAGCCGTAC 420
DB 361 ATCTCGGCGTACTTCCGCAACGACATGAGCGGATGAGGCGTCTCGAGCAGCCGTAC 420

RESULT 24
US-10-824-527-38
; Sequence 38, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces minutiscleroticus
US-10-824-527-38

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
QY 61 CTCGTACGAGGAGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 61 CTGGTCCGAGGAGCGCTCGGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120

QY 121 GGCAATCGAAGGCGCTCGAGGCGCTCTCCGGCGCCCTCTGCTGAGCAGGCGAAGGATGTC 180
DB 121 GGTATCGAAGAGCGCTCGAGGCGCTCTCCGGTCCCTGCTGAGCAGGCGAAGGACGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCAGCACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCAGCAGCTCCAGATCGGC 240
QY 241 GAGCTCATCGCCGAGGCGATGGACAGGTCCGCAAGAGGCGTCATCACCCTCGAGGAG 300
DB 241 GAGCTCATCGCCGAGGCGATGGACAGGTCCGCAAGAGGCGTCATCACCCTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTTCGACAAAGGCGTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTTCGACAAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTTCGACGACCCGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTTCGACGACCCGTAC 420

RESULT 25

US-10-824-527-40
; Sequence 40, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 40
; TYPE: DNA
; ORGANISM: Streptomyces nodosus
US-10-824-527-40

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAGACGAGCAGCGTCCGCGGTGACGCTACGACCAACCGGACCGCTTCTCGCCCGAGCG 60
DB 1 AAGAGACGAGCAGCGTCCGCGGTGACGCTACGACCAACCGGACCGCTTCTCGCCCGAGCG 60
QY 61 CTGCTACGAGGCGCTTCGCAACGCTCGCGCGGTGCAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGCTACGAGGCGCTTCGCAACGCTCGCGCGGTGCAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCAATCGAAGGCGCTTCGAGGCGCTTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 180
DB 121 GGTATCGAAGGCGCTTCGCAACGCTCGCGCGGTGCAACCGGATGGCTCTCAAGCGC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCAGCACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCAGCACCCAGATCGGC 240
QY 241 GAGCTCATCGCCGAGGCGATGGACAGGTCCGCAAGAGGCGTCATCACCCTCGAGGAG 300

DB 241 GAGCTCATCGCCGAGGCGATGGACAGGTTCGCAAGAGGCGTCATCACCCTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTTCGACAAAGGCGTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTTCGACAAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTTCGACGACCCGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTTCGACGACCCGTAC 420

RESULT 26
US-10-824-527-46
; Sequence 46, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 46
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-46

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAGACGAGCAGCGTCCGCGGTGACGCTACGACCAACCGGACCGCTTCTCGCCCGAGCG 60
DB 1 AAGAGACGAGCAGCGTCCGCGGTGACGCTACGACCAACCGGACCGCTTCTCGCCCGAGCG 60
QY 61 CTGCTACGAGGCGCTTCGAGGCGCTTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 120
DB 61 CTGCTACGAGGCGCTTCGAGGCGCTTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 120
QY 121 GGCAATCGAAGGCGCTTCGAGGCGCTTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 180
DB 121 GGTATCGAAGGCGCTTCGCAACGCTCGCGCGGTGCAACCGGATGGCTCTCAAGCGC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCAGCACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCAGCACCCAGATCGGC 240
QY 241 GAGCTCATCGCCGAGGCGATGGACAGGTTCGCAAGAGGCGTCATCACCCTCGAGGAG 300
DB 241 GGTATCGAAGGCGCTTCGCAACGCTCGCGCGGTGCAACCGGATGGCTCTCAAGCGC 300
QY 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTTCGACAAAGGCGTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTTCGACAAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTTCGACGACCCGTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTTCGACGACCCGTAC 420

RESULT 27

US-10-824-527-49
; Sequence 49, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:

; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: PARK, JEONG-SAM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN

; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; FILE REFERENCE: 970612 GENE
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15

; PRIOR APPLICATION NUMBER: KR 2003-24656

; PRIOR FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: KR 2003-80580

; PRIOR FILING DATE: 2003-11-14

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 49

; LENGTH: 420

; TYPE: DNA

; ORGANISM: Streptomyces scabiei

US-10-824-527-49

Query Match

Best Local Similarity 92.0%; Score 386.4; DB 8; Length 420;

Mismatches 0; Conserved 21; Indels 0; Gaps 0;

Qy	1	AAGAAGCGGAGCGAGCGTCCCGGTGACGGTACGACACCGGACCGGTTCTCGCCCGAGCG	60
Db	1	AAGAAGCGGAGCGAGCGTCCCGGTGACGGTACGACACCGGACCGGTTCTCGCCCGAGCG	60
Qy	61	CTCGTACGCGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	120
Db	61	CTCGTACGCGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	120
Qy	121	GGCATCGAGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	180
Db	121	GGCATCGAGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	180
Qy	181	GAGACCAAGGAGGAGATCGCTTCCACGGCTTCATCCCGCGCGGACACCGGACCGGTTCTCGCCCGAGCG	240
Db	181	GAGACCAAGGAGGAGATCGCTTCCACGGCTTCATCCCGCGCGGACACCGGACCGGTTCTCGCCCGAGCG	240
Qy	241	GAGTCTATCGCGGAGGAGATCGCAAGGTCCGCAAGGAGGCGTCCATCCCGTTCGAGGAG	300
Db	241	GAGTCTATCGCGGAGGAGATCGCAAGGTCCGCAAGGAGGCGTCCATCCCGTTCGAGGAG	300
Qy	301	TCCGAGACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAGGAGGCTAC	360
Db	301	TCCGAGACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAGGAGGCTAC	360
Qy	361	ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGGTCGCTTCGACAGGAGGCTAC	420
Db	361	ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGGTCGCTTCGACAGGAGGCTAC	420

RESULT 28

US-10-824-527-57

; Sequence 57, Application US/10824527

; Publication No. US20040265873A1

; GENERAL INFORMATION:

; APPLICANT: KIM, BUM-JOON

; APPLICANT: KIM, CHANG-JIN

; APPLICANT: KO, YOUNG HWAN

; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN

; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; FILE REFERENCE: 970612 GENE

; CURRENT APPLICATION NUMBER: US/10/824,527

; PRIOR FILING DATE: 2004-04-15

; PRIOR APPLICATION NUMBER: KR 2003-24656

; PRIOR FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: KR 2003-80580

; PRIOR FILING DATE: 2003-11-14

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 57

; LENGTH: 420

; TYPE: DNA

; ORGANISM: Streptomyces neyagawaensis

US-10-824-527-57

Query Match

Best Local Similarity 92.0%; Score 386.4; DB 8; Length 420;

Mismatches 0; Conserved 21; Indels 0; Gaps 0;

Qy	1	AAGAAGCGGAGCGAGCGTCCCGGTGACGGTACGACACCGGACCGGTTCTCGCCCGAGCG	60
Db	1	AAGAAGCGGAGCGAGCGTCCCGGTGACGGTACGACACCGGACCGGTTCTCGCCCGAGCG	60
Qy	61	CTCGTACGCGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	120
Db	61	CTCGTACGCGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	120
Qy	121	GGCATCGAGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	180
Db	121	GGCATCGAGAGGCGCTCGGCAACGTCCCGCGGTGACCGGACCGGTTCTCGCCCGAGCG	180
Qy	181	GAGACCAAGGAGGAGATCGCTTCCACGGCTTCATCCCGCGCGGACACCGGACCGGTTCTCGCCCGAGCG	240
Db	181	GAGACCAAGGAGGAGATCGCTTCCACGGCTTCATCCCGCGCGGACACCGGACCGGTTCTCGCCCGAGCG	240
Qy	241	GAGTCTATCGCGGAGGAGATCGCAAGGTCCGCAAGGAGGCGTCCATCCCGTTCGAGGAG	300
Db	241	GAGTCTATCGCGGAGGAGATCGCAAGGTCCGCAAGGAGGCGTCCATCCCGTTCGAGGAG	300
Qy	301	TCCGAGACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAGGAGGCTAC	360
Db	301	TCCGAGACCTTCGCTTCGAGCTGAGCTCACCAGGAGGATGCGCTTCGACAGGAGGCTAC	360
Qy	361	ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGGTCGCTTCGACAGGAGGCTAC	420
Db	361	ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGGTCGCTTCGACAGGAGGCTAC	420

RESULT 29

US-10-824-527-18

; Sequence 18, Application US/10824527

; Publication No. US20040265873A1

; GENERAL INFORMATION:

; APPLICANT: KIM, BUM-JOON

; APPLICANT: KIM, CHANG-JIN

; APPLICANT: KO, YOUNG HWAN

; APPLICANT: KOH, JEONG-SAM

; APPLICANT: PARK, DONG-JIN

; APPLICANT: LEE, HYANG BURM

; APPLICANT: SEUL, HONG KIM

; APPLICANT: KIM, SUN-HYUN

; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; FILE REFERENCE: 970612 GENE

; CURRENT APPLICATION NUMBER: US/10/824,527

; CURRENT FILING DATE: 2004-04-15

QY 61 CTCGTACGAGGCGCTCGCAACGTCGGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTCGTCAAGAAAGGCGCTCGCAACGTCGGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGAGCAGGCGAAGATGTC 180
Db 121 GGCATCGAGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGAGCAGGCGAAGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
Db 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGTATGGAGGGCGTCTCGACGACCCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGTATGGAGGGCGTCTCGACGACCCGCTAC 420
RESULT 32
US-10-824-527-35
; Sequence 35, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 35
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces griseoviridis
US-10-824-527-35

Query Match 91.6%; Score 384.8; DB 8; Length 420;
Best Local Similarity 94.8%; Pred. No. 2.5e-89;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTGCGCGGTGACCGGTACGACACCGGACCGGTCTCGCCCGAGCGG 60
Db 1 AAGAAGACGACGACGTGCGCGGTGACCGGTACGACACCGGACCGGTCTCGCCCGAGGCC 60
QY 61 CTCGTACGAGGCGCTCGCAACCTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTGTCGAAGAGGCGCTCGCAACCTAGCGCGCGGTGCCAACCCGATGGCTCTGAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGAGCAGGCGAAGATGTC 180
Db 121 GGTATCGAGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGAGCAGGCGAAGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
Db 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360

Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
Db 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGTATGGAGGGCGTCTCGACGACCCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGTATGGAGGGCGTCTCGACGACCCGCTAC 420
RESULT 33
US-10-824-527-13
; Sequence 13, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 13
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces anandii
US-10-824-527-13

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTGCGCGGTGACCGGTACGACACCGGACCGGTCTCGCCCGAGCGG 60
Db 1 AAGAAGACGACGACGTGCGCGGTGACCGGTACGACACCGGACCGGTCTCGCCCGAGGCC 60
QY 61 CTCGTACGAGGCGCTCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTGTCGCGAGGCGCTCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTGAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGAGCAGGCGAAGATGTC 180
Db 121 GGTATCGAGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGAGCAGGCGAAGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
Db 241 GAGCTCATCGCAGGCGGATGACAAAGGTTCGCAAGAAAGGCGCTCATCAAGTCGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360

QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGCGTAC 420
|||||
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTCGAGGACCGCGTAC 420

RESULT 34
US-10-824-527-19
; Sequence 19, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cellulosae
US-10-824-527-19

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTCAGCGTACGACACCGCGGATGCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTCAGCGTACGACACCGCGGATGCGTTCGCGCCAGGCG 60
QY 61 CTGTCAGCGAGGCGGCTGCGCAAGCTCGCGCGGCGGTCGCAACCGGATGCGTCTCAAGCGC 120
Db 61 CTGTCAGCGAGGCGGCTGCGCAAGCTCGCGCGGCGGTCGCAACCGGATGCGTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGGCTGCGAGGCGGCTCGCGGCGGCGGTCGCGAGGCGGCGGATGTC 180
Db 121 GGTATCGAGAGGCGGCTGCGAGGCGGCTCGCGGCGGCGGTCGCGAGGCGGCGGATGTC 180
QY 181 GAGACCAAGGACGACATGCTTCCAGCGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGACATGCTTCCAGCGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCG 300
Db 241 GAGCTCATCGCGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCG 300
QY 301 TCCGAGACCTTCGGTCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
Db 301 TCCGAGACCTTCGGTCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGCGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTTCCTTCGACGACCGCGTAC 420

RESULT 35
US-10-824-527-26
; Sequence 26, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cellulosae
US-10-824-527-19

APPLICANT: KIM, BUM-JOON
APPLICANT: KIM, CHANG-JIN
APPLICANT: KO, YOUNG HWAN
APPLICANT: KOH, JEONG-SAM
APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BUM
APPLICANT: SEOUL, HONG KIM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
PRIOR FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 26
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces collinus
US-10-824-527-26

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGGTCAGCGTACGACACCGCGGATGCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTCAGCGTACGACACCGCGGATGCGTTCGCGCCAGGCG 60
QY 61 CTGTCAGCGAGGCGGCTGCGCAAGCTCGCGCGGCGGTCGCAACCGGATGCGTCTCAAGCGC 120
Db 61 CTGTCAGCGAGGCGGCTGCGCAAGCTCGCGCGGCGGTCGCAACCGGATGCGTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGGCTGCGAGGCGGCTCGCGGCGGCGGTCGCGAGGCGGCGGATGTC 180
Db 121 GGTATCGAGAGGCGGCTGCGAGGCGGCTCGCGGCGGCGGTCGCGAGGCGGCGGATGTC 180
QY 181 GAGACCAAGGACGACATGCTTCCAGCGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGACATGCTTCCAGCGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCG 300
Db 241 GAGCTCATCGCGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCGGATGCGAGGCG 300
QY 301 TCCGAGACCTTCGGTCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
Db 301 TCCGAGACCTTCGGTCTGAGGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGCGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTTCCTTCGACGACCGCGTAC 420

RESULT 36
US-10-824-527-37
; Sequence 37, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces collinus
US-10-824-527-26

```
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
US-10-824-527-37

Query Match          91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 60
QY 61 CTCGTACGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 120
Db 61 CTCGTACGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 120
QY 121 GGCATCGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 180
Db 121 GGCATCGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGTCCATCTCGCCCAAGGAG 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGTCCATCTCGCCCAAGGAG 240
QY 241 GAGCTCATCGCGAGGCGATGACCAAGGTGCGCAAGGAGGCGTCCATCTCGCCCAAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGACCAAGGTGCGCAAGGAGGCGTCCATCTCGCCCAAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGCTATCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGCTATCGCTTCGACCAAGGCTAC 360
QY 361 ATCTCGGCGTACTTCCGACCGACGATGAGCGGATGAGGCGTCCGCTCGACCAAGGCTAC 420
Db 361 ATCTCGGCGTACTTCCGACCGACGATGAGCGGATGAGGCGTCCGCTCGACCAAGGCTAC 420
```

RESULT 37

```
US-10-824-527-21
; Sequence 21, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
```

```
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces chattanoogenesis
US-10-824-527-21

Query Match          90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 60
QY 61 CTCGTACGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 120
Db 61 CTCGTACGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 120
QY 121 GGCATCGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGAGTATC 180
Db 121 GGCATCGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGAGTATC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGTCCATCTCGCCCAAGGAG 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCGCGCGCGTCCATCTCGCCCAAGGAG 240
QY 241 GAGCTCATCGCGAGGCGATGACCAAGGTGCGCAAGGAGGCGTCCATCTCGCCCAAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGACCAAGGTGCGCAAGGAGGCGTCCATCTCGCCCAAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGCTATCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGCTATCGCTTCGACCAAGGCTAC 360
QY 361 ATCTCGGCGTACTTCCGACCGACGATGAGCGGATGAGGCGTCCGCTCGACCAAGGCTAC 420
Db 361 ATCTCGGCGTACTTCCGACCGACGATGAGCGGATGAGGCGTCCGCTCGACCAAGGCTAC 420
```

RESULT 38

```
US-10-824-527-25
; Sequence 25, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 25
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces coeruleorubidus
US-10-824-527-25
```

```
Query Match          90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGCGACCGTCTCGCCCAAGGCG 60
```

Db 1 AAGAGAGCGACGAGCTCGCCGGTGACGGTACGACACCGGACCGTTCTCGCCAGGCC 60
Qy 61 CTGCTAGCGAGGCGCTGCGCAACAGTCTCGCCCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTAAGGAAGGCGCTGCGCAACAGTCTCGCCCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAAGGCGCTGCGGAGCGCTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Db 121 GGTATCGAGCGCGCGCTGAGAGCGCTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCCGCCCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCCGCCCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGAGCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGAGCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGAGAGCGTCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 360
Db 301 TCCAGACCTTCGGTCTGAGAGCGTCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 360
Qy 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420

RESULT 39

US-10-824-527-28
; Sequence 28, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces diastaticus
US-10-824-527-28

Query Match 90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 AAGAGACGAGCAGCTCGCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCAGGCC 60
Db 1 AAGAGACGAGCAGCTCGCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCAGGCC 60
Qy 61 CTGCTAGCGAGGCGCTGCGCAACAGTCTCGGCGCCCTGCTGAGCAGGCGTCTCAAGCGC 120
Db 61 CTGCTAGCGAGGCGCTGCGCAACAGTCTCGGCGCCCTGCTGAGCAGGCGTCTCAAGCGC 120
Qy 121 GGCATCGAGAAGGCGCTGCGGAGCGCTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCGAGAAGGCGCTGCGGAGCGCTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180

Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCGCCCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCGCCCGGAGCGTCTCAAGATCGGT 240
Qy 241 GAGCTCATCGCCGAGGCGATGAGCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 300
Db 241 GAGCTCATCGCCGAGGCGATGAGCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGAGAGCGTCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 360
Db 301 TCCAGACCTTCGGTCTGAGAGCGTCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 360
Qy 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420

RESULT 40

US-10-824-527-29
; Sequence 29, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 29
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces djakartensis
US-10-824-527-29

Query Match 90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 AAGAGACGAGCAGCTCGCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCAGGCC 60
Db 1 AAGAGACGAGCAGCTCGCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCAGGCC 60
Qy 61 CTGCTAGCGAGGCGCTGCGCAACAGTCTCGGCGCCCTGCTGAGCAGGCGTCTCAAGCGC 120
Db 61 CTGCTAGCGAGGCGCTGCGCAACAGTCTCGGCGCCCTGCTGAGCAGGCGTCTCAAGCGC 120
Qy 121 GGCATCGAGAAGGCGCTGCGGAGCGCTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Db 121 GGTATCGAGCGCGCGCTGAGAGCGCTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCGCCCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCGCCCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGAGCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGAGCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGAGAGCGTCAAGGTGCGGCAAGGCGTCAATCCCGTTCGAGGAG 360

Db 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGAGGGTATGCGTTCGACCAAGGCTAC 360
Qy 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATCGAGGCGTCTCGACGACCGGCTAC 420
Db 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGGCTCTCGACGACCGGCTAC 420

RESULT 41

US-10-824-527-60
; Sequence 60, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 60
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces acidiscabies
US-10-824-527-60

Query Match 90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCGTCCCGGTGACCGGTACGACACCGCGACCGTTCCTGCCCCAGGCG 60
Db 1 AAGAAGACGAGCGTACGCGCGACGCGACGACCGCGACCGTTCCTGCCCCAGGCG 60
Qy 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGTCTCAAGCGC 120
Db 61 CTGGTCCGCGAGGGCTTCGCAACGTCGCGCGCGGTGCGCAACCGCGTCTCAAGCGC 120
Qy 121 GGCATCGAAGCGCGTTCGAGCGCGTCTCCGCGCGCTTCGAGCAGCGCGAAGGATGTC 180
Db 121 GGCATCGAAGCGCGTTCGAGCGCGTCTCCGCGCGCTTCGAGCAGCGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGATGCTTCCAGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATGCTTCCAGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGCGGATGCAAGGTGCGCAAGGAGGCGTCTATCCCGTTCGAGGAG 300
Db 241 GAGCTCATCGCGAGCGGATGCAAGGTGCGCAAGGAGGCGTCTATCCCGTTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGCTTCGACCAAGGCTAC 360
Qy 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 420
Db 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 420

RESULT 42

US-10-824-527-14

; Sequence 14, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces argenteolus
US-10-824-527-14

Query Match 90.5%; Score 380; DB 8; Length 420;
Best Local Similarity 94.0%; Pred. No. 4.3e-88;
Matches 395; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCGTCCCGGTGACCGGTACGACACCGCGACCGTTCCTGCCCCAGGCG 60
Db 1 AAGAAGACGAGCGTACGCGCGACGCGTCCCGGTGACCGGACGCGACCGTTCCTGCCCCAGGCG 60
Qy 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGTCTCAAGCGC 120
Db 61 CTGGTCCGCGAGGGCTTCGCAACGTCGCGCGCGGTGCGCAACCGCGTCTCAAGCGC 120
Qy 121 GGCATCGAAGCGCGTTCGAGCGCGTCTCCGCGCGCTTCGAGCAGCGCGAAGGATGTC 180
Db 121 GGCATCGAAGCGCGTTCGAGCGCGTCTCCGCGCGCTTCGAGCAGCGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGATGCTTCCAGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATGCTTCCAGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGCGGATGCAAGGTGCGCAAGGAGGCGTCTATCCCGTTCGAGGAG 300
Db 241 GAGCTCATCGCGAGCGGATGCAAGGTGCGCAAGGAGGCGTCTATCCCGTTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGCTTCGACCAAGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGCTTCGACCAAGGCTAC 360
Qy 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 420
Db 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 420

RESULT 43

US-10-824-527-51
; Sequence 51, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM

Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGAGTGGCGGTGACGCTGACGACCGCGACCGTTCGCGCCAGGCG 60
DB 1 AAGAAGACGACGAGTGGCGGTGACGCTGACGACCGCGACCGTTCGCGCCAGGCG 60
QY 61 CTCGTACCGGAGGCGCTGCGACGCTGCGCGCGGTGCGACCGCGTCTCAAGCGC 120
DB 61 CTGGTCCGCGAGGCGCTGCGCAACGCTGGCGCGGTGCGAACCGCGTTCGAGCGC 120
QY 121 GGCATCGAGAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGCGAAGGATGTC 180
DB 121 GGCATCGAGAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGCGAAGGATGTC 180
QY 181 GAGACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACCCGATCGGC 240
DB 181 GAGACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACCCGATCGGC 240
QY 241 GAGCTCATCGCGAGCGATGGAACAAGGTTCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGATGGAACAAGGTTCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
DB 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420

RESULT 46

US-10-824-527-54
; Sequence 54, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 54
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces turgidiscabies

Query Match 90.1%; Score 378.4; DB 8; Length 420;
Best Local Similarity 93.8%; Pred. No. 1.1e-87;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGAGTGGCGGTGACGCTGACGACCGCGACCGTTCGCGCCAGGCG 60
DB 1 AAGAAGACGACGAGTGGCGGTGACGCTGACGACCGCGACCGTTCGCGCCAGGCG 60
QY 61 CTCGTACCGGAGGCGCTGCGAACGCTCGCGCGGTGCGAACCGCGTTCGAGCGC 120
DB 61 CTGGTCCGCGAGGCGCTGCGCAACGCTGGCGCGGTGCGAACCGCGTTCGAGCGC 120

QY 121 GGCATCGAGAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGCGAAGGATGTC 180
DB 121 GGCATCGAGAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGCGAAGGATGTC 180
QY 181 GAGACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACCCGATCGGC 240
DB 181 GAGACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACCCGATCGGC 240
QY 241 GAGCTCATCGCGAGCGATGGAACAAGGTTCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGATGGAACAAGGTTCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
DB 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGTCGACGACCGCTAC 420

RESULT 47
US-10-824-527-50
; Sequence 50, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 50
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces acidiscabies

Query Match 89.0%; Score 373.6; DB 8; Length 420;
Best Local Similarity 93.1%; Pred. No. 1.9e-86;
Matches 391; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGAGTGGCGGTGACGCTGACGACCGCGACCGTTCGCGCCAGGCG 60
DB 1 AAGAAGACGACGAGTGGCGGTGACGCTGACGCGCAGCGCGCGTTCGCGCCAGGCA 60
QY 61 CTCGTACCGGAGGCGCTGCGCAACGCTGCGCGCGGTGCGAACCGCGATGGCTTCGAGCGC 120
DB 61 CTGGTCCGCGAGGCGCTTCGCAACGCTGCGCGCGCGCAACCGCGATGGCTTCGAGCGC 120
QY 121 GGCATCGAGAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGCGAAGGATGTC 180
DB 121 GGCATCGAGAGCGCGTTCGAGGCGCTTCGCGCGCGCTTCGAGCAGCGAAGGATGTC 180
QY 181 GAGACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACCCGATCGGC 240
DB 181 GAGACCAAGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACCCGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGATGGAACAAGGTTCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300

Db 241 GAGCTATCGCCGAGGCGATGACAAAGGTCGCGCAAGGAGGCGTCATCAACGGTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 301 TCGCAGACCTTCGGCTCGGAGCTTGAGCTACCGGAGGCGATGGCTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACAGACCCGCTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACAGACCCGCTAC 420

RESULT 48

US-10-824-527-27
; Sequence 27, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824, 527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces corchorusii
US-10-824-527-27

Query Match 88.6%; Score 372; DB 8; Length 420;
Best Local Similarity 92.9%; Pred. No. 4.8e-86;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGGTTCGCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGCCAGCGTCCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTCAAGGAAGCGCTCGCAACGTCGCGCGCGCGCCAAACCGATGGCTCTGAAGCGC 120
Qy 121 GGATCGAAGAGCGCGTCGAGGCGGTCTCCGCGCCCTGTCGAGCAGGCGAAGGATGTC 180
Db 121 GGATCGAAGAGCGCGTCGAGGCGGTCTCCGCGCCCTGTCGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGATCGCTTCCACGGCTCCATCTCCGCGCCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATCGCTTCCACGGCTCCATCTCCGCGCCCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGCGATGGACAAAGGTTCGGCAAGGAGGCGTATCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGCGATGGACAAAGGTTCGGCAAGGAGGCGTATCATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGGAGGGTATGGCTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACAGACCCGCTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACAGACCCGCTAC 420

RESULT 49

US-10-824-527-44
; Sequence 44, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824, 527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-44

Query Match 88.6%; Score 372; DB 8; Length 420;
Best Local Similarity 92.9%; Pred. No. 4.8e-86;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGGTTCGCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGCGAACGTCGCGCGCGGTTCGAGCAGGCGAAGGATGTC 120
Db 61 CTGCTCGCGAGGCGCTCGCGAACGTCGCGCGCGGTTCGAGCAGGCGAAGGATGTC 120
Qy 121 GGATCGAAGAGCGCGTCGAGGCGGTCTCCGCGCCCTGTCGAGCAGGCGAAGGATGTC 180
Db 121 GGATCGAAGAGCGCGTCGAGGCGGTCTCCGCGCCCTGTCGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGATCGCTTCCACGGCTCCATCTCCGCGCCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATCGCTTCCACGGCTCCATCTCCGCGCCCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGCGATGGACAAAGGTTCGGCAAGGAGGCGTATCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGCGATGGACAAAGGTTCGGCAAGGAGGCGTATCATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGGAGGGTATGGCTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACAGACCCGCTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACAGACCCGCTAC 420

RESULT 50

US-10-824-527-56
; Sequence 56, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM

```
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; TYPE: DNA
; ORGANISM: Streptomyces diastatochromogenes
US-10-824-527-56

Query Match      88.6%; Score 372; DB 8; Length 420;
Best Local Similarity 92.9%; Pred. No. 4.8e-86;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACCAACCGGCGGCTTCTCGCCCGAGGCG 60
Db 1 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACCAACCGGCGGCTTCTCGCCCGAGGCG 60
QY 61 CTCGTACCGGAGGCGCTCGCGCAACGTCGCCCGCGGTGCAACCCCGATGGCTTCTCAAGCGC 120
Db 61 CTGGTCCGGAAGGCGCTCGCGCAACGTCGCCCGCGGTGCAACCCCGATGGCTTCTGAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGCGGCTTCTCGCGCGGCTTCTGGAGCAGCGGAGGATGTC 180
Db 121 GGTATCGAGAAGGCGCTCGAGCGGCTTCTCGCGGTGCGTCTCGACCGGCAAGGAGGTC 180
QY 181 GAGCAACGAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGCGACACCCAGATCGGC 240
Db 181 GAGCAACGAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGGAGGCGATGCAACAGGTGCGGCAAGGAGGCGTTCATCACCGTCCGAGGAG 300
Db 241 GAGCTCATCGCGGAGGCGATGCAACAGGTGCGGCAAGGAGGCGTTCATCACCGTCCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGTTTCGACAAAGGGCTAC 360
Db 301 TCGCAGACCTTCGGGCTCGAGCTTTCGAGCTACCGAGGGCATGCGCTTCGACAAAGGGCTAC 360
QY 361 ATCTCGGCGTACTTCCGCGACGATGAGCGGATGAGGCGTTCGCTCGAGCAGCCCGTAC 420
Db 361 ATCTCGGCGTACTTCCGCGACGATGAGCGGATGAGGCGTTCGCTCGAGCAGCCCGTAC 420

RESULT 52
US-10-824-527-5
; Sequence 5, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces alanosinicus
US-10-824-527-5
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; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; TYPE: DNA
; ORGANISM: Streptomyces diastatochromogenes
US-10-824-527-56

Query Match      88.6%; Score 372; DB 8; Length 420;
Best Local Similarity 92.9%; Pred. No. 4.8e-86;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACCAACCGGCGGCTTCTCGCCCGAGGCG 60
Db 1 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACCAACCGGCGGCTTCTCGCCCGAGGCG 60
QY 61 CTCGTACCGGAGGCGCTCGCGCAACGTCGCCCGCGGTGCAACCCCGATGGCTTCTCAAGCGC 120
Db 61 CTGGTCCGGAAGGCGCTCGCGCAACGTCGCCCGCGGTGCAACCCCGATGGCTTCTGAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGCGGCTTCTCGCGCGGCTTCTGGAGCAGCGGAGGATGTC 180
Db 121 GGTATCGAGAAGGCGCTCGAGCGGCTTCTCGCGGTGCGTCTCGACCGGCAAGGAGGTC 180
QY 181 GAGCAACGAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGCGACACCCAGATCGGC 240
Db 181 GAGCAACGAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGGAGGCGATGCAACAGGTGCGGCAAGGAGGCGTTCATCACCGTCCGAGGAG 300
Db 241 GAGCTCATCGCGGAGGCGATGCAACAGGTGCGGCAAGGAGGCGTTCATCACCGTCCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGTTTCGACAAAGGGCTAC 360
Db 301 TCGCAGACCTTCGGTCTGGAGCTTTCGAGCTACCGAGGGCATGCGCTTCGACAAAGGGCTAC 360
QY 361 ATCTCGGCGTACTTCCGCGACGATGAGCGGATGAGGCGTTCGCTCGAGCAGCCCGTAC 420
Db 361 ATCTCGGCGTACTTCCGCGACGATGAGCGGATGAGGCGTTCGCTCGAGCAGCCCGTAC 420

RESULT 51
US-10-824-527-59
; Sequence 59, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
```

Query Match 88.2%; Score 370.4; DB 8; Length 420;
 Best Local Similarity 92.6%; Pred. No. 1.2e-85;
 Matches 389; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGATGACCAACCGACCGGCTTCTGCGCCAGGGC 60
 DB 1 AAGAAGACGACGACGTCGCGCGGTGACGATGACCAACCGACCGGCTTCTGCGCCAGGGC 60

QY 61 CTGCTACGACGAGGCGCTGCGCAACGTCGCGCGGTGACCAACCGGATGGTCTCAAGCGC 120
 DB 61 CTGCTCAAGGAAGGCGCTGCGCAACGTCGCGCGGTGACCAACCGGATGGTCTCAAGCGC 120

QY 121 GGCATCGAGAAGGCGCGTCGAGGCGCTTCCGCGCGGTGACCAACCGGATGGTCTCAAGCGC 180
 DB 121 GGCATCGAGAAGGCGCGTCGAGGCGCTTCCGCGCGGTGACCAACCGGATGGTCTCAAGCGC 180

QY 181 GAGACCAAGGAGGAGATGCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGG 240
 DB 181 GAGACCAAGGAGGAGATGCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGG 240

QY 241 GAGTCTATCGCGAGGCGGATGAGCAAGGTGCGCAAGGAGGCGGCTTCCAGCGGCTTCCAGCGG 300
 DB 241 GAGTCTATCGCGAGGCGGATGAGCAAGGTGCGCAAGGAGGCGGCTTCCAGCGGCTTCCAGCGG 300

QY 301 TCCGACGACCTTCGCTGAGGCTGAGCTCACCGAGGATGCGCTTCCAGCGGCTTCCAGCGGCTAC 360
 DB 301 AGCAACACCTTCGCTGAGGCTGAGCTCACCGAGGATGCGCTTCCAGCGGCTTCCAGCGGCTAC 360

QY 361 ATCTCGCGCTTACTTCGCGACCGACATGAGCGGATGAGCGGCTGCTCGACGACCGGCTAC 420
 DB 361 ATCTCGCGCTTACTTCGCGACCGACATGAGCGGATGAGCGGCTGCTCGACGACCGGCTAC 420

RESULT 53
 US-10-824-527-7
 ; Sequence 7, Application US/10824527
 ; Publication No. US20040265873A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIM, BUM-JOON
 ; APPLICANT: KIM, CHANG-JIN
 ; APPLICANT: KO, YOUNG HWAN
 ; APPLICANT: KOH, JEONG-SAM
 ; APPLICANT: PARK, DONG-JIN
 ; APPLICANT: LEE, HYANG BUM
 ; APPLICANT: SEOUL, HONG KIM
 ; APPLICANT: KIM, SUN-HUYN
 ; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
 ; FILE REFERENCE: 05823.0260-00000
 ; CURRENT APPLICATION NUMBER: US/10/824,527
 ; PRIOR FILING DATE: 2004-04-15
 ; PRIOR APPLICATION NUMBER: KR 2003-24656
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: KR 2003-80580
 ; PRIOR FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 7
 ; LENGTH: 423
 ; TYPE: DNA
 ; ORGANISM: Streptomyces albobacilli

Query Match 88.1%; Score 370.2; DB 8; Length 423;
 Best Local Similarity 93.9%; Pred. No. 1.4e-85;
 Matches 397; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGATGACCAACCGGATGGTCTTCTGCGCCAGGGC 60
 DB 1 AAGAAGACGACGACGTCGCGCGGTGACGATGACCAACCGGATGGTCTTCTGCGCCAGGGC 60

QY 61 CTGCT---ACGCGAGGCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 117

DB 61 CTGCTCACAGCGAGGCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 120
 QY 118 CGCGGATCGAAGAGGCGGTCGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 177
 DB 121 CGCGGATCGAAGAGGCGGTCGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 180

QY 178 GTCGAGACCAAGGAGCAGATCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 237
 DB 181 GTGAGACCAAGGAGCAGATCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 240

QY 238 GCGAGCTCATCGCGAGGCGGATGAGCAAGGTGCGCAAGGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 297
 DB 241 GCGAGCTCATCGCGAGGCGGATGAGCAAGGTGCGCAAGGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 300

QY 298 GAGTCCGACGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 357
 DB 301 GAGTCCGACGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 360

QY 358 TACATCTCGCGCTTACTTCGCGACCGACATGAGCGGATGAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 417
 DB 361 TACATCTCGCGCTTACTTCGCGACCGACATGAGCGGATGAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 420

QY 418 TAC 420
 DB 421 TAC 423

RESULT 54
 US-10-824-527-30
 ; Sequence 30, Application US/10824527
 ; Publication No. US20040265873A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIM, BUM-JOON
 ; APPLICANT: KIM, CHANG-JIN
 ; APPLICANT: KO, YOUNG HWAN
 ; APPLICANT: KOH, JEONG-SAM
 ; APPLICANT: PARK, DONG-JIN
 ; APPLICANT: LEE, HYANG BUM
 ; APPLICANT: SEOUL, HONG KIM
 ; APPLICANT: KIM, SUN-HUYN
 ; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
 ; FILE REFERENCE: 05823.0260-00000
 ; CURRENT APPLICATION NUMBER: US/10/824,527
 ; PRIOR FILING DATE: 2004-04-15
 ; PRIOR APPLICATION NUMBER: KR 2003-24656
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: KR 2003-80580
 ; PRIOR FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 30
 ; LENGTH: 423
 ; TYPE: DNA
 ; ORGANISM: Streptomyces erumpens

Query Match 87.8%; Score 368.6; DB 8; Length 423;
 Best Local Similarity 93.6%; Pred. No. 3.6e-85;
 Matches 396; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGATGACCAACCGGATGGTCTTCTGCGCCAGGGC 60
 DB 1 AAGAAGACGACGACGTCGCGCGGTGACGATGACCAACCGGATGGTCTTCTGCGCCAGGGC 60

QY 61 CTGCT---ACGCGAGGCGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 117
 DB 61 CTGCTCACAGCGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 120

QY 118 CGCGGATCGAAGAGGCGGTCGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 177
 DB 121 CGCGGATCGAAGAGGCGGTCGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCAAG 180

QY 178 GTCCAGACCAAGGAGCAGATCGTTTCAACGGCTTCCATCTCCGCCCGGACACCCAGATC 237
|||
Db 181 GTCCAGACCAAGGAGCAGATCGTTTCAACGGCTTCCATCTCCGCCCGGACACCCAGATC 240
|||
QY 238 GCGAGCTCATCCCGAGGCGATGGACAAAGTCCGCAAGGAGGCGTTCATCCGTCGAG 297
|||
Db 241 GCGAGCTCATCCCGAGGCGATGGACAAAGTCCGCAAGGAGGCGTTCATCCGTCGAG 300
|||
QY 298 GAGTCCAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCG 357
|||
Db 301 GAGTCCAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCG 360
|||
QY 358 TACATCTCGGCGTACTTTCGCAACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCG 417
|||
Db 361 TACATCTCGGCGTACTTTCGCAACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCG 420
|||
QY 418 TAC 420
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Db 421 TAC 423
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RESULT 55

US-10-824-527-4
; Sequence 4, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces aculeolatus
US-10-824-527-4

Query Match 87.0%; Score 365.6; DB 8; Length 420;
Best Local Similarity 91.9%; Pred. No. 2.1e-84;
Matches 386; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 AAGAGACGGACGACGTCCGCGGTGACGGTACGACACCGCGACCGTTCGCCCGCAGGG 60
|||
Db 1 AAGAGACGGACGACGTCCGCGGTGACGGTACGACACCGCGACCGTTCGCCCGCAGGG 60
|||
QY 61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
|||
Db 61 CTGGTCAAGGAGGGCTCGCGAAGCTGCGCGCGGTGCGCAACCCGATGCTGAGCGC 120
|||
QY 121 GGCATCGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGAGGAGGATGTC 180
|||
Db 121 GGCATCGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGAGGAGGATGTC 180
|||
QY 181 GAGACCAAGGAGCAGATCGTTCACAGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
|||
Db 181 GAGACCAAGGAGCAGATCGTTCACAGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
|||
QY 241 GAGCTCATCGCGCGATGGACAAAGGTCCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
|||

Db 241 GAGCTCATCGCGAGGCCATGGACAAAGGTCCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
|||
QY 301 TCCAGACCTTCGGTCTGAGGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
|||
Db 301 TCCAGACCTTCGGGCTGAGGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
|||
QY 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTCAT 420
|||
Db 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGAGGACCCGTCAT 420
|||

RESULT 56

US-10-824-527-33
; Sequence 33, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces griseochromogenes
US-10-824-527-33

Query Match 86.3%; Score 362.4; DB 8; Length 420;
Best Local Similarity 91.4%; Pred. No. 1.4e-83;
Matches 384; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 AAGAGACGGACGACGTCCGCGGTGACGGTACGACACCGCGACCGTTCGCCCGCAGGG 60
|||
Db 1 AAGAGACGGACGACGTCCGCGGTGACGGTACGACACCGCGACCGTTCGCCCGCAGGG 60
|||
QY 61 CTGCTACGCGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
|||
Db 61 CTGGTCAAGGAGGGCTTCGCAAGCTCGCGCGGTGCGCAACCCGATGCTCTGAAGCGC 120
|||
QY 121 GGCATCGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGAGGAGGATGTC 180
|||
Db 121 GGCATCGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGAGGAGGATGTC 180
|||
QY 181 GAGACCAAGGAGCAGATCGTTCACGCGCTCCATCTCCGCGCGCGCGACACCCAGATCGGC 240
|||
Db 181 GAGACCAAGGAGCAGATCGTTCACGCGCTCCATCTCCGCGCGCGCGACACCCAGATCGGC 240
|||
QY 241 GAGCTCATCGCGAGGCGATGGACAAAGGTCCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
|||
Db 241 GAGCTCATCGCGAGGCGATGGACAAAGGTCCGCAAGGAGGCGTTCATCACCGTCGAGGAG 300
|||
QY 301 TCCAGACCTTCGGTCTGAGGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
|||
Db 301 AGCAACACCTTCGGTCTGAGGCTCACCGAGGCGTTCGCTTCGACAAAGGCGTAC 360
|||
QY 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGTCAT 420
|||
Db 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGAGGACCCGTCAT 420
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; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces aminophilus
US-10-824-527-12

Query Match      85.5%; Score 359.2; DB 8; Length 420;
Best Local Similarity 91.0%; Pred. No. 9.3e-83;
Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCGACGTCGCGGTGACGGTAGCACCGCGACCGTTCCTCGCCCGAGGCG 60
   |||||
Db 1 AAGAAGACGAGCGACGTCGCGGTGACGGTAGCACCGCGACCGCGACCGTTCCTCGCCCGAGGCG 60

QY 61 CTCGTACGCGAGGGCTCGCGCAACGTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 120
   |||||
Db 61 CTGGTCAAGGAGGGCTCGCGCAACGTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 120

QY 121 GGCATCGAGAACGCGTCGAGCGCTCTCCGCGCGCTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 180
   |||||
Db 121 GGCATCGAGAACGCGTCGAGCGCTCTCCGCGCGCTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 180

QY 181 GAGACCAAGGAGCGATGCGTTCACGGCTTCATCTCCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 240
   |||||
Db 181 GAGACCAAGGAGCGATGCGTTCACGGCTTCATCTCCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 240

QY 241 GAGCTCATCGCGAGGGCGATGCAAGGTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 300
   |||||
Db 241 GAGCTCATCGCGAGGGCGATGCAAGGTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 300

QY 301 TCCGAGACCTTCGCGTTCGAGCTCGAGCTCACCGAGGGTATGCGCTTCGACAAAGGGCTAC 360
   |||||
Db 301 TCCGAGACCTTCGCGTTCGAGCTCGAGCTCACCGAGGGTATGCGCTTCGACAAAGGGCTAC 360

QY 361 ATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCTCGACGACCGCTAC 420
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Db 361 ATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCTCGACGACCGCTAC 420
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RESULT 60
US-10-500-586-34
; Sequence 34, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIE
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 34
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Mycobacterium phlei
US-10-500-586-34
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Query Match      76.8%; Score 322.4; DB 8; Length 604;
Best Local Similarity 85.5%; Pred. No. 2.6e-73;
Matches 359; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCGACGTCGCGGTGACGGTAGCACCGCGACCGTTCCTCGCCCGAGGCG 60
   |||||
Db 50 AAGAAGACGAGCGATGTCGCGGTGACGGTAGCACCGCGACCGTTCCTCGCCCGAGGCG 109

QY 61 CTCGTACGCGAGGGCTCGCGCAACGTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 120
   |||||
Db 110 CTGGTCCGCGAGGGTCTCGCGCAACGTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 169

QY 121 GGCATCGAGAACGCGTCGAGCGCTCTCCGCGCGCTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 180
   |||||
Db 170 GGTATCGAGAACGCGTCGAGAGGTTCACCGAGACCGCTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 229

QY 181 GAGACCAAGGAGCGATGCGTTCACGGCTTCATCTCCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 240
   |||||
Db 230 GAGACCAAGGAGCGATGCGTTCACGGCTTCATCTCCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 289

QY 241 GAGCTCATCGCGAGGGCGATGCAAGGTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 300
   |||||
Db 290 GAGCTCATCGCGAGGGCGATGCAAGGTTCGCGCGCGGTGCAACCCCGATGGCTCTCAAGCGC 349

QY 301 TCCGAGACCTTCGCGTTCGAGCTCGAGCTCACCGAGGGTATGCGCTTCGACAAAGGGCTAC 360
   |||||
Db 350 AGCAACACCTTCGCGTTCGAGCTCGAGCTCACCGAGGGTATGCGCTTCGACAAAGGGCTAC 409

QY 361 ATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGGTGCTCGACGACCGCTAC 420
   |||||
Db 410 ATCTCGGCTACTTCGCGCGGTGCAACCCCGATGGCTCTCGAGGATCCGCTAC 469

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 (without alignments)
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Title: US-10-824-527-43
 Perfect score: 420
 Sequence: 1 aagagacgagcagctgcg.....cgctgcgagcaccgtac 420

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : Published Applications NA_New.*

- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1.*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
- 10: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq1.*
- 12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.4	47.7	555	14	US-11-055-637-99
2	157.2	37.4	1632	8	US-10-467-657-1019
3	157.2	37.4	1716	8	US-10-467-657-1021
4	148.2	35.3	2035	11	US-11-077-619-107
5	144.4	34.4	1638	11	US-11-232-406A-27
6	141.8	33.8	2032	11	US-11-077-619-33
7	141	33.6	552	14	US-11-055-637-111
8	132	31.4	552	14	US-11-055-637-108
9	131	31.2	1626	11	US-11-074-176-29
10	129.6	30.9	1620	11	US-11-232-406A-31
11	129	30.7	1654	11	US-11-201-916-3
12	127.2	30.3	1662	11	US-11-201-916-5
13	125	29.8	552	14	US-11-055-637-89
14	125	29.8	552	14	US-11-055-637-101
15	125	29.8	1665	11	US-11-201-916-1
16	122.4	29.1	1838	8	US-10-615-668-7
17	121.8	29.0	552	14	US-11-055-637-98
18	119.2	28.4	552	14	US-11-055-637-99

19	119.2	28.4	552	14	US-11-055-637-104
20	118.6	28.2	552	14	US-11-055-637-90
21	117.6	28.0	2047	11	US-11-077-619-35
22	117	27.9	552	14	US-11-055-637-87
23	115.4	27.5	552	14	US-11-055-637-92
24	114.4	27.2	552	14	US-11-055-637-103
25	107.4	25.6	552	14	US-11-055-637-91
26	106.4	25.3	553	14	US-11-055-637-107
27	106.2	25.3	1661	11	US-11-201-916-7
28	105.8	25.2	552	14	US-11-055-637-95
29	102.6	24.4	552	14	US-11-055-637-110
30	101	24.0	552	14	US-11-055-637-94
31	100.6	24.0	1620	8	US-10-793-626-789
32	100.6	24.0	3885	8	US-10-793-626-3883
33	100	23.8	552	14	US-11-055-637-105
34	97.6	23.2	555	14	US-11-055-637-113
35	95.8	22.8	1647	14	US-11-038-686-9525
36	95.8	22.8	1457619	14	US-11-038-686-8739
37	95.2	22.7	552	14	US-11-055-637-102
38	94.8	22.6	1719	9	US-10-932-182A-77733
39	94.8	22.6	1719	9	US-10-932-182A-77733
40	94.6	22.5	2211	14	US-11-128-061-526
41	94.6	22.5	2211	14	US-11-128-049-526
42	93.8	22.3	2175	14	US-11-136-527-3831
43	93.6	22.3	552	14	US-11-055-637-100
44	93.6	22.3	552	14	US-11-055-637-109
45	93	22.1	552	14	US-11-055-637-96
46	91	21.7	552	14	US-11-055-637-112
47	90.4	21.5	552	14	US-11-055-637-97
48	89.8	21.4	552	14	US-11-055-637-85
49	89.8	21.4	552	14	US-11-055-637-86
50	89.8	21.4	552	14	US-11-055-637-93
51	88.2	21.0	552	14	US-11-055-637-106
52	87.4	20.8	2258	14	US-11-000-688-1372
53	83.2	19.8	552	14	US-11-055-637-114
54	80.8	19.2	684	9	US-10-932-182A-4757
55	80.8	19.2	684	9	US-10-932-182A-4757
56	71.6	17.0	422	14	US-11-000-688-1371
57	59.8	14.2	1876	11	US-11-096-568A-21213
58	56.8	13.5	556	10	US-10-301-480-304422
59	56.8	13.5	556	10	US-10-301-480-304422
60	56.8	13.5	561	6	US-09-925-065A-218359

ALIGNMENTS

RESULT 1
 US-11-055-637-99
 ; Sequence 99, Application US/11055637
 ; Publication No. US20050260619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BROUSSEAU, Roland
 ; APPLICANT: DUBOIS, Jason
 ; APPLICANT: EDGE, Tom
 ; APPLICANT: MASSON, Luc
 ; APPLICANT: TREVORS, Jack T.
 ; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
 ; CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
 ; TITLE OF INVENTION: 2139-33US
 ; FILE REFERENCE: 2139-33US
 ; CURRENT APPLICATION NUMBER: US/11/055,637
 ; PRIOR FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: US 60/543,288
 ; PRIOR FILING DATE: 2004-02-11
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 99
 ; LENGTH: 555
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe for DNA array
 ; US-11-055-637-99

Query Match 47.7%; Score 200.4; DB 14; Length 555;
Best Local Similarity 70.6%; Pred. No. 2.2e-42;
Matches 267; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 40 GCGACCGTCTCGCCAGGCGCTGTCAGCGAGGGCTCGCAACGTCGCGCGCGTGC 99
DB 1 GCGACGCTGCTGGCGCAGGCGATGATCGCGAGGGTCTGAAGAACGTCGCGCTGTTGG 60
QY 100 AACCCGATGGCTCTCAAGCGCGGATCGAGAACGCGTTCGAGCGCGTCTCGCGCGCGCTG 159
DB 61 AACCCGATGGCTCTCGCGCGCGCTGAGAACGCGTTCGAGCGCGTTCGAGCGCGCTG 120
QY 160 CTGGAGCAGCGGAGGATTCGAGAACGAGGAGGATCTCCACGCGCTCATCTCC 219
DB 121 AAGAAGATCGGAAGCGGCTCCAGGGCCGCAAGAACATCGCGAGGTTGCGCGCATCTCG 180
QY 220 GCGCGCGACCCAGATCGCGGAGCTCATCGCGAGGCGATGACAAAGTTCGCGCAAGGAA 279
DB 181 GCTGTTTCGAACGAAATCGCGGAGCTCATCGCGATGCGATGGAAGGTTGCGAACGAC 240
QY 280 GCGGTCTATCAACGTCGAGGAGTCCAGACCTTCGCTGTCGAGCTTGAAGCTTCACCGAGGT 339
DB 241 GCGGTGATCAACGTCGAGGAGTTCGAAGGCTTCACGACCGAGCTTGAAGTTCGTGAGGGT 300
QY 340 ATGCGCTTCGACAAAGGCTACATCTCGCGCTACTTCGCCACCGACATGAGCGGATGAG 399
DB 301 ATGCGATTCGACCGCGCTACATCTCGCGCTACATGCTGAGCGGACCGCGGCAAGATGGAG 360
QY 400 GCGTGGCTCGACGACCGC 417
DB 361 GCTGTGCTGACGAGCGC 378

RESULT 2

US-10-467-657-1019
; Sequence 1019, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1019
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1019

Query Match 37.4%; Score 157.2; DB 8; Length 1632;
Best Local Similarity 62.7%; Pred. No. 2.8e-31;
Matches 262; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGATGACACACCGGACCGTCTCGCGCGAGGCGTC 63
DB 238 AAAACCAACGACGTCGCGGTGACGATGACACACCGGACCGTCTCGCGCGAGGCGTC 297
QY 64 GTACGCGAGGCGTCCGACGCTCGCGCGGTGACACCGGATGCTCTCAAGCGCGGC 123
DB 298 GTTCCGAGGCGATGAATACGTTTACCGCGGCGATGAACCGGATCTGAACCGCGGC 357
QY 124 ATCGAGAGGCGGTCGAGGCGCTCTCGCGCGCGCTGCTGGAGCGAGGCGGATGTCGAG 183
DB 358 ATCGACAAAGCGGTCGCGCTTTGGTTGAAGAGCTGAANAACATCGCCAAACCTTGGAT 417

QY 184 ACCAAGGACGATCGCTTCCACGCGCTCCATCTCGCG---CGCCGACACCCAGATCGGC 240
DB 418 ACTTCAAAGAAATCGCCCAAGTCGCGCTCGATTTTCGCCCACTCCGACGAAACAAGTCGGC 477
QY 241 GAGCTCATCGCGAGCGGATGACAAAGTTCGCGCAAGGAGGCTCATCACCGTCGAGGAG 300
DB 478 GCGATTATCGCGAGCGGATGGAAGAATCGCGCAAGAGGCGGTGATTACCGTTGAAGAC 537
QY 301 TCCAGACCTTCGCTGTCGAGCTGAGCTTCACCGAGGGTATGCGTTCGACAAAGGCGCTAC 360
DB 538 GGCMAATCTTTGMAAAACGAGCTGAGCGTGTGAAGGTATGCACTTCGACCGCGCTAC 597
QY 361 ATCTCGCGCTACTTCGCCACCGACATGAGCGGATGAGGCGGTGCGCTCGACGACCGCT 418
DB 598 CTGTCCCTTACTTTATCAACGACGCGGAAACAAATCGCGCGTCTGGCAATCCGT 655

RESULT 3

US-10-467-657-1021/C
; Sequence 1021, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1021
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1021

Query Match 37.4%; Score 157.2; DB 8; Length 1716;
Best Local Similarity 62.7%; Pred. No. 2.7e-31;
Matches 262; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGATGACACACCGGACCGTCTCGCGCGAGGCGTC 63
DB 1428 AAAACCAACGACGTCGCGGTGACGATGACACACCGGACCGTCTCGCGCGAGGCGTC 1369
QY 64 GTACGCGAGGCGTTCGCGACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGC 123
DB 1368 GTTCCGAGGCGATGAATACGTTTACCGCGCGGATGAACCGGACCGATCTGAACCGCGC 1309
QY 124 ATCGAGAGGCGGTCGCGCGCTCTCGCGCGCTCTGGAGCAGCGGAGGATGTCGAG 183
DB 1308 ATCGACAAAGCGGTTCCGCTTTGGTTGAAGAGCTGAANAACATCGCCAAACCTTGGAT 1249
QY 184 ACCAAGGACGATCGCTTCCACGCGCTCCATCTCGCG---CGCCGACACCCAGATCGGC 240
DB 1248 ACTTCAAAGAAATCGCCCAAGTCGCGCTCGATTTTCGCCCACTCCGACGAAACAAGTCGGC 1189
QY 241 GAGCTCATCGCGAGCGGATGGAAGAATCGCGCAAGGCGTTCATCACCGTCGAGGAG 300
DB 1188 GCGATTATCGCGAGCGGATGGAAGAATCGCGCAAGAGGCGGTGATTACCGTTGAAGAC 1129
QY 301 TCCAGACCTTCGCTCTGAGCTGAGCTTCACCGAGGATGCGTTCGACAAAGGCGCTAC 360
DB 1128 GGCMAATCTTTGMAAAACGAGCTGAGCGTGTGAAGGTATGCACTTCGACCGCGCTAC 1069
QY 361 ATCTCGCGCTACTTCGCCACCGACATGAGCGGATGAGGCGGTGCTCGACGACCGCT 418
DB 1068 CTGTCCCTTACTTTATCAACGACGCGGAAACAAATCGCGCGTCTGGCAATCCGT 1011

Query Match 34.4%; Score 144.4; DB 11; Length 1638;
Best Local Similarity 60.8%; Pred. No. 5.4e-28;
Matches 254; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

Query Match 35.3%; Score 148.2; DB 11; Length 2035;
Best Local Similarity 59.7%; Pred. No. 5.6e-29;
Matches 249; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

417	ACAGCAAGAAAGAAATCGCCCAACGGTAGGTTCTATCTCTGCTAACTCCGACACATCTCTGTTGGC	477
418		
419		
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421	GAGCTCATCGCCGAGCGGATGGACAAGAGTCCGCAAGGAAGCGCTCATCACCGTCGAGGAG	3000
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427	CAAAATTATTGCTGATCGCATGGACAAGTAGGTAGGTTAAAGAGGCGTGATCACTGTTGAAGAC	5378
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RESULT 6
US-11-077-619-33
; Sequence 33, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09

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; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009999
; CURRENT APPLICATION NUMBER: US/11/077,619
; PRIOR FILING DATE: 2003-09-09

```


Db 1 GCTACAGTCTTCTCAAGCGATGATTCGCGAAGGCTTGAAAACGTTAACAGCGGTGCA 60
QY 100 AACCCGATGCTCTCAAGCGCGCATCGAAGCGCGTGGAGCGCGTCTCGCGCGCCCTG 159
Db 61 AACCCGATGGTTATGCGCAAGGTATCGAAGGCGAGTTCGTGCGACAGTAGAAGACTG 120
QY 160 CTGAGGAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCGCTCCATCTCC 219
Db 121 CATGCGATTTCTAAACCAATCGAAGGTAAAGATCTATCGCACAGTAGCAGCTATTTCT 180
QY 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGCGATGACACAGGTTCGCGAAGGA 279
Db 181 GCTGCTGATGAGAAATCGGCCAACTGATGCTGGAAGCTATGGAAGGTAGGAAAGAT 240
QY 280 GCGCTCATCACCGTTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GGGTTATCACAGTAGAAGATCAAGGCTTCACACAGAACTGATGTTGTAGAGGT 300
QY 340 ATGCGCTTCGACAAAGGCTACATCTCGCGGTACTTCGCCACCGACATGAGGCGATGGAG 399
Db 301 ATGCAATTCGACCGCGATACGCTTCTCCATACATGATCACGGATACTGATAAGATGGAA 360
QY 400 GCGTCTCGACACCGCTA 419
Db 361 GCAGTCTTGATAATCCGTA 380

RESULT 9

US-11-074-176-29
; Sequence 29, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1626)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 406; GroEL - 60 kDa chaperonin
US-11-074-176-29

Query Match 31.2%; Score 131; DB 14; Length 1626;
Best Local Similarity 57.0%; Pred. No. 1.5e-24;
Matches 239; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 2 AGAAGCGACGACGTGCGCGGTGACGTTACGACACCGGACCGTTCGCGCCGAGGCGC 61
Db 233 AAAGACTAACGACATGCGCGGTGACGTTACTACTGCAACTGTTTGTACTCAAGCAA 292
QY 62 TGTAGCGGAGGCGCTTGCGCAAGCTGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGCG 121
Db 293 TTGCTGTGAAGGTATGAAGAAGCTTACTGCTGGTGTCTAACCTGTAGGCAATCGTCGCG 352
QY 122 GCATCGAAGAGGCGCTCGAGGCGCGTCTCGCGCGCGCTGTGAGGAGCGGCAAGGATGTG 181

Db 353 GTATTGAAGAGCAACTAAGGCTGCTGTGTGATGAATTAACAAGATTAGCCCAAGGTTG 412
QY 182 AGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCGCGCGCGACACCCAGATCGGCG 241
Db 413 AATCAAGGAACAATTTGCTAACGTAGCTGCTGTTTCTTTCAGATCTAAAGAAAGTTGGT 472
QY 242 AGCTCATCGCGAGCGATGGACAAGGTGGCAAGGAAGGCGTCAACCGTCGAGGAGT 301
Db 473 AATTGATCGCTGACGCTATGGAAAAGTTGGTCAAGTGTGTTTACTATCGAAGATT 532
QY 302 CCCAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGATGCGCTTCGACAAGGGCTACA 361
Db 533 CACGTGGTATCAATATCTGAACCTTTTCAGTAGTTGAAGGTATGCAATTCGATCGTGTACT 592
QY 362 TCTCGGCGTACTTCCGCCACCGACATGGAGCGATGAGCGCTCGCTCGACGACCCGTAC 420
Db 593 TGTCAATATCATGTGTAATCTGACACGACGATGGAAGACGACCTTGTATAACCATAC 651

RESULT 10

US-11-232-406A-31
; Sequence 31, Application US/11232406A
; Publication No. US20060030011A1
; GENERAL INFORMATION:
; APPLICANT: USUDA, Yoshihiro
; APPLICANT: NISHIO, Yosuke
; APPLICANT: YASUEDA, Hiseashi
; APPLICANT: SUGIMOTO, Shinichi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING POLYPEPTIDES INVOLVED IN THE STRESS RES:
; TITLE OF INVENTION: ENVIRONMENTAL CHANGES IN METHYLOPHILUS METHYLOTROPHUS
; FILE REFERENCE: 232744USO
; CURRENT APPLICATION NUMBER: US/11/232,406A
; CURRENT FILING DATE: 2005-09-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent version 3.1
; SEQ ID NO 31
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Methylophilus methylotrophus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1620)
US-11-232-406A-31

Query Match 30.9%; Score 129.6; DB 11; Length 1620;
Best Local Similarity 58.7%; Pred. No. 3.5e-24;
Matches 244; Conservative 0; Mismatches 169; Indels 3; Gaps 1;
QY 4 AAGCGGACGACGTGCGCGGTGACGCTACGACACCGCGACCGTTCGCGCCGAGCGCTC 63
Db 238 AAACAGCTGACGTGGCGCGGTGACGCTACGACTACCGTACCGTCTGCTCGCTCAGGCGATT 297
QY 64 GTACGCGAGGCGCTGCGCAACGTGCGCGCGCGTGCACACCGGATGGCTCTCAAGCGCGCG 123
Db 298 GTACAAAGAGGAGTGAAGTCAGTTCGCGCTCCGCGCATGAAATCCACCGACTAAAACGTGG 357
QY 124 ATCGAAGAGCGCTGAGGCGCTCTCGCGCGCGCTGCGAGCGAGCGGAGGATGTCGAG 183
Db 358 ATTGATAAAGCGGTGACAGCGCTGCTGATGAGCTTAAATCCATGTCGCAAGCTATCACC 417
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTTCATCTCCGC---CGCGACACCCAGATCGGC 240
Db 418 ACCATAAAGAAATTTGCCAAGTCGGTCCGATTTCTGCAACTCTGACCATGCTCCATTGGC 477
QY 241 GAGTCTATCGCGAGCGCATGACAAAGTTCGCGCAAGGAAGGCGTCAATCACCGTTCAGGAG 300
Db 478 CAGATCATCGCGCATGCGTGAAGAAAGTCGTAAGAAAGGCGCTGATTAACGTTGCGTGAAGAA 537
QY 301 TCCAGACCTTCGGTCTGAGCTCACCGAGGATGCGCTTCGACAAGGGCTAC 360
Db 538 GGTAACTCCTGCAAAATGAACTCGAAGTGTGCGAGGCGATGCAAGTTTGAACCGCGCTAT 597

QY 124 ATCGAGAGCGCTCGAGGCGCTCTCGGCGCCCTGCTGAGAGCAGCGAAGGATGCGAG 183
Db 372 ATCGACAAAGCTGTGCGCTCGCTGTTGAAGAAGTGAAGAGCGCTGTCGTTACGCTCT 431
QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCG---CGCCGACACCCAGATCGGC 240
Db 432 GACTCTAAGCCATGCTCAGGTAGGTACCATCTCGCTAACTCCGACGAACCCGTAGGT 491
QY 241 GAGCTCATCGCCGAGGCGATGGAACAAGGTCCGCAAGGAAGGCGTCTATCACCCTGCGAGGAG 300
Db 492 AACTGATCGCGAAGCGATGGAATAAGTCGTTAAAGAGGCGTGATCACCCTGTTGAAGAC 551
QY 301 TCCGAGACCTTCGCTGAGGCTGAGGCTCACCAGGAGTATGCGCTTCGACAAAGGCTAC 360
Db 552 GGTACCGGCTGGAAGACGAACGTAAGTGGAGTGAAGTATGCAAGTTCGACCGCGCTTAC 611
QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGCGATGAGGCGTTCGCTCGACGACCGGTAC 420
Db 612 CTGTCCCATCTTTCATCAACAGCCAGAACTGGCGCTGTTGAGCTGGAAGCCCGTTTC 671

RESULT 13

US-11-055-637-89

; Sequence 89, Application US/11055637

; Publication No. US20050260619A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason

; APPLICANT: EDGE, Tom

; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.

; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND

; FILE REFERENCE: 2139-33US

; CURRENT APPLICATION NUMBER: US/11/055,637

; PRIOR APPLICATION NUMBER: US 60/543,288

; PRIOR FILING DATE: 2005-02-11

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 89

; LENGTH: 552

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-89

Query Match 29.8%; Score 125; DB 14; Length 552;
Best Local Similarity 58.0%; Pred. No. 5.8e-23;
Matches 221; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 40 GCGAGCGTTCGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCCGCGCGTCC 99
Db 1 GCGACAGTTCTAGCTCAGGCGATGATTCGCGAAGGCTTTAAAGACGTAATCTCGCGCGCT 60
QY 100 AACCCGATCGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGGCGCTCTCGCGCGCCCTG 159
Db 61 AACCTGTAGGCGTGGCAAGGATATCGAGCGAGGCTGTGCTGTAGCTGTTGAAGCCCTG 120
QY 160 CTGGAGCAGCGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCC 219
Db 121 AAGAGAAATCTTAACCAATTGAAGGCAAGAAATCAATCGCACAAAGTTGCTTCAATCTCC 180
QY 220 GCGCGGACACCCAGTCCGCGAGCTCATCGCGAGGCGATCGACAGGTTCGGCAAGGAA 279
Db 181 GCTGACAGACGAAGAGTTCGGAAGCCCTGATCGCTGAAGCAATGGAGCGGTTCGGCAACGAC 240
QY 280 GCGCTCATCAGCGTTCGAGAGTCCACAGACCTTCGCTGAGCTGAGCTCACCGAGGT 339
Db 241 GGTGTATCAGCATCGAAGATCCAAAGGATTCACACAGAGCTTGAAGTGTGAGGT 300
QY 340 ATGCGCTTCGACAAAGGCTTACATCTGCGGTACTTGGCCACCGACATGGAGCGGATGGAG 399

Db 301 ATGCAAGTTCGACCGCGATATCGTCTCTTACATGGTACGGAATTCGATAGATGGA 360
QY 400 GCGTCGCTCGACGACCCGCTAC 420
Db 361 GCGGTTCTTGAGATCCGCTAC 381

RESULT 14

US-11-055-637-101

; Sequence 101, Application US/11055637

; Publication No. US20050260619A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason

; APPLICANT: EDGE, Tom

; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.

; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND

; FILE REFERENCE: 2139-33US

; CURRENT APPLICATION NUMBER: US/11/055,637

; PRIOR APPLICATION NUMBER: US 60/543,288

; PRIOR FILING DATE: 2005-02-11

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 101

; LENGTH: 552

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-101

Query Match 29.8%; Score 125; DB 14; Length 552;
Best Local Similarity 58.0%; Pred. No. 5.8e-23;
Matches 221; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 40 GCGAGCGTTCGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCCGCGCGTCC 99
Db 1 GCAACCGTACTAGCGCAAGCGATGATCCGTGAAGGTCTAAAAACGTAACATCCGCTGCG 60
QY 100 AACCCGATCGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGGCGCTCTCCGCGCGCCCTG 159
Db 61 AACCCAGTAGCAATTCGCGCGGAATTGAAAAGCAACCGAAGTCGCTACTCAGGAATTT 120
QY 160 CTGGAGCAGGCGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCC 219
Db 121 CGCAAAATCTCTAAGCCAATCGAAGCGCGAGTCCATTTCTCAGGTAGCTTCCATCTCT 180
QY 220 GCGCGGACACCCAGATCGCGAGCTCATCGCGAGGCGATCGCAAGGTTCGGCAAGGAA 279
Db 181 GCTTCCGATACGAAGTTCGCGAGCTGATGCTGAAGCGATGAGAGCGGTAGGAACCGAT 240
QY 280 GCGCTCATCAGCTCGAGAGTCCACAGACCTTCGCTGAGCTGAGCTCACCGAGGT 339
Db 241 GCGGTATTAACAATTGAAGATCTAAGGTTTCAATACAGAACTAGAGTGTGTAAGGT 300
QY 340 ATGCGCTTCGACAAAGGCTTACATCTCGCGGTACTTTCGCGCAACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAAGTTCGACCGCGCTATGCTTCTCCATACATGTTTACAGACCAAGGATAAATGGA 360
QY 400 GCGTCGCTCGACCGCGTAC 420
Db 361 GCGGTTCTTGAGATCCCTTAC 381

RESULT 15

US-11-201-916-1

; Sequence 1, Application US/11201916

; Publication No. US2006003922A1

; GENERAL INFORMATION:

APPLICANT: Mizzen, Lee
APPLICANT: Wisniewski, Jan
TITLE OF INVENTION: STREETOCCAL HEAT SHOCK PROTEINS OF THE
TITLE OF INVENTION: HSP60 FAMILY
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/201,916
FILING DATE: 11-AUG-2005
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/001,737
FILING DATE: 31-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 870109.408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1649
US-11-201-916-1

Query Match 29.88; Score 125; DB 11; Length 1665;
Best Local Similarity 59.4%; Pred. No. 5.4e-23;
Matches 231; Conservative 0; Mismatches 155; Indels 3; Gaps 1;
QY 4 AAGACGACGACGCTGCGCGGTGACGGTACGACCAACCGGACCGCTTCTCGCCCGGCGCTC 63
DB 252 AAGCGAAGCAGCTGCGAGGTGACGGTACCAACCGGACCGTACTGCTGCTCAGTCCATC 311
QY 64 GTACGAGGCGCTGCGCGAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123
DB 312 ATCACTGAAGCGCTGAAAGCGGTGTGCTGCGGGCATGAACCGGATGGATCTGAAACGTTGT 371
QY 124 ATGAGAGGCGCTGAGGCGCTCTCGCGCGCTGCTGCGAGCGGCGAAGGATGTCGAG 183
DB 372 ATCGACAAAGCTGCTGCTGCTGCTGTTGAAGAACTGAAAGCACTGTCCTGACCGTGTCC 431
QY 184 ACCAAGGACGACGCTGCTTCCAGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 432 GACTCTAAGACTATTGCTCAGGTGGTACCATCTCCGCTAACTCCGACGAAACCGTAGGT 491
QY 241 GAGCTATCGCGAGGCGATGGACAAGGTGCGGCAAGGAAGGCGTCAATCAGCTCGAGGAG 300
DB 492 AAACGTATGCTGAAGCGATGGACAAGGTGCGTAAAGAGGCGGTGATCAGCTGTGAAGAC 551
QY 301 TCCGACACCTTGGCTGAGGCTGAGCTCAGGAGGATGCGCTTCGACAGGCGTAC 360
DB 552 GGTACCGGTCTGACGAGGACGAACCTGACGCTGTTGAAGGTATGACGATTCGACCGGTGCTAC 611
QY 361 ATCTCGCGCTACTTTCGCGCACCGACATGGA 389

DB 612 CTGCTCTCTTACTTCTATCAACAAGCCGGA 640
RESULT 16
US-10-615-668-7
; Sequence 7, Application US/10615668
; Publication No. US20050276819A1
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; APPLICANT: Bugnoli, Massimo
; APPLICANT: Telford, John
; APPLICANT: Macchia, Giovanni
; APPLICANT: Rappuoli, Rino
; TITLE OF INVENTION: Helicobacter Pylori CAI Antigen Polynucleotides
; FILE REFERENCE: CHIR0337
; CURRENT APPLICATION NUMBER: US/10/615,668
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 08/471,491
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/256,848
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: 09/410,835
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1838
; TYPE: DNA
; ORGANISM: Helicobacter pylori
US-10-615-668-7

Query Match 29.1%; Score 122.4; DB 8; Length 1838;
Best Local Similarity 57.4%; Pred. No. 2.5e-22;
Matches 241; Conservative 0; Mismatches 176; Indels 3; Gaps 1;
QY 4 AAGACGACGACGCTGCGCGGTGACGGTACGACCAACCGGACCGCTTCTCGCCCGGCGCTC 63
DB 292 AAAACCGCTGATGCTGCGCGGATGCGACGACCAACCGGACCGCTGCTAGCTTATAGCAT 351
QY 64 GTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGC 123
DB 352 TTTAAAGAAGGTTTGAGGAATATACGCGTGGGGCTAACCCCTATTGAAGTGAACACGAGC 411
QY 124 ATCGAAGAAGCGCTGCGAGCGCTCTCGCGCGCTCTGAGCAGCGGAGGATGTCGAG 183
DB 412 ATGATTAAGCTGCTGAGCGATCATTAATGAGCTTAAAAAGCGAGCAAAAAGTAGGC 471
QY 184 ACCAAGGACGACGCTTTCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
DB 472 GGTAAAGAAGAAATACCCAAAGTGGCGCACATTTCTGCAAACTCCGATCACAATATCGGG 531
QY 241 GAGCTATCGCGAGGCGATGGACAAGGTGCGCAAGGAGGCGTCAATCAGCTCGAGGAG 300
DB 532 AAACCTATCGCTGACGCTATGGAAGGTTGGGTAAGAGCGGCGTGTATCAGCTGTGAGGAA 591
QY 301 TCCGACACCTTGGCTGCGAGCTGAGGCTCACCGAGGTTATGCGCTTCGACAAAGGCGTAC 360
DB 592 GCTAAGGCAATTGAAGATGAATTTGGATGCTGTAGAGGATGCAATTTGATAGAGGCTAC 651
QY 361 ATCTCGCGCTACTTTCGCGCACCGACATGAGCGGATGAGGCGGTGCTGCTCGACGACCGGTAC 420
DB 652 CTCTCCCTTATTTTGAACGACGCTGAGAAATGACCGCTCAATTGGATATGCTTAC 711

RESULT 17
US-11-055-637-88
; Sequence 88, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-88

Query Match 29.0%; Score 121.8; DB 14; Length 552;
Best Local Similarity 57.5%; Pred. No. 3.8e-22;
Matches 219; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGTGC 99
Db 1 GCGACAGTTCTTCCGCAAGCAATGATCCGTGAAGGCTTAAACACGTAACAGAGCGCT 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAGCGCGCTCGAGGCGCTCTCCGCGCGCTG 159
Db 61 AATCCTGTAGGCTTCTGAAGGTATGGAAGCTGTAGCGTTCGATCGAAACTTA 120
QY 160 CTGAGCAGCGGAGAGATGTGAGACCAAGAGAGAGATCGTTCCAGCGCTCCATCTCC 219
Db 121 AAGAAATTTCTAAGCAATCGAAGGCAAGAGTCTATCGCTCAGGTTCTCGATCTCT 180
QY 220 GCGCGGACACCCAGATCGCGAGCTCATCGCGAGGCGCATCGCAAGTGCAGAGGAA 279
Db 181 GCTGCTGATGAGAGTCTGAAGCCTTATCGCTGAAGCAATGAGCGGTAGGCAACGAC 240
QY 280 GCGTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GCGGTTATCAATCGAAGCTTAAAGCTTCAACATGAGCTTGAAGTTGTTGAGGT 300
QY 340 ATGCGGTTGACAGGCTTACATCTCGGCTACTTCGCGCAGCATGAGGCGATGAG 399
Db 301 ATGCAATTCGACCGCGATGCGTCTCTTACATGTAAGTAACTGACTCTGTAAGATGAA 360
QY 400 GCGTCGTCGACCGCTAC 420
Db 361 GCGGTTCTTGACAATCTTAC 381

RESULT 18
US-11-055-637-98
; Sequence 98, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 552
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-98

Query Match 28.4%; Score 119.2; DB 14; Length 552;
Best Local Similarity 57.1%; Pred. No. 1.8e-21;
Matches 217; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTGCGCAACGTCGCGCGGTGC 99
Db 1 GCGACCGTTCTCGCCAGCGCAATGATCCGTGAAGGCTTGAACACGTAACAGAGCGCA 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGGCGCTCTCCGCGCGCTG 159
Db 61 AACCCGTTGGCATCCGCAAGGGATTGAACAGCGTTGCGGCTGCTGTTGAAGATTA 120
QY 160 CTGAGCAGCGGCAAGAGATGTGAGACCAAGAGAGAGATCGTTCCAGCGCTCCATCTCC 219
Db 121 AAGCCATTTTCGAACCAATCGAAGGCAAGCTTCCATCGCCCAAGTTGCTGCAATTTCC 180
QY 220 GCGCGGACACCCAGATCGCGAGCTCATCGCGAGGCGATCGCAAGTTCGCAAGGAA 279
Db 181 TCTGCTGACGAAGAGTTGGCGAATTGATCGCTGAAGCAATGGAACGCGTGGGCAACGAC 240
QY 280 GCGTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GCGGCTATCATTCATTGAAGATCAAAAGCTTCTCAACGGAATTGACGTTGTGAGGG 300
QY 340 ATGCGCTTCGACAGGCTTACATCTCGGCTACTTCGCGCAGCATGAGGCGGATGAG 399
Db 301 ATGCAAGTTGACCGTGGCTTATGCAATCGCTTACATGTTAAACGATTCGACAAATGGA 360
QY 400 GCGTCGTCGACCGCTGTA 419
Db 361 GCTGTTCTGGATAACCCCTTA 380

RESULT 19
US-11-055-637-104
; Sequence 104, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-104

Query Match 28.4%; Score 119.2; DB 14; Length 552;
Best Local Similarity 57.1%; Pred. No. 1.8e-21;
Matches 217; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTGCGCAACGTCGCGCGGTGC 99
Db 1 GCAACAGTTCTTGTCTCAGGCAATGATCCGTGAAGGCTTAAAGACGCTAATGTCAGGTCT 60

QY 100 AACCCGATGCTCTCAAGCGCGGCATCGAGAAGCCGCTCGAGGCGGCTCTCGGCGCCCTG 159
|||||
Db 61 AACCAATGGCATCCGCAAGGATTTGAAGAAGCGTTTCTACTGCTGTTGAAGATT 120
QY 160 CTGGAGCAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGTTCCACGGCTCCATCTCC 219
|||||
Db 121 AAGCTATTTCAAAACCTATCGAAACCAAGAATCTATCGACACAGGTTGCTGCTATTCT 180
QY 220 GCGCGCAGACCCAGATCGGGAGCTCATCGCGAGGCGATGAGCAAGGTCGGCAAGGAA 279
|||||
Db 181 GCTGCTGACAAATGAAGTTGGCCAGCTGATCGCTGAAGCAATGGAGCGCGTTGGCAAGAT 240
QY 280 GCGCTCATACCGTCGAGGAGTCCAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGT 339
|||||
Db 241 GGTGTTATCAATCGAAGATCTAAAGGTTTCACACTGAGCTTGATGTTGTAAGGT 300
QY 340 ATGGCTTCGACAGGCTCATCTCGCGCTACTTCGCCACCGACATCGAGCGGATGGAG 399
|||||
Db 301 ATGCAATTCGACCGGATAGGCTTCACCATACATGTTACAGATTCTGATAAGATGGA 360
QY 400 GCGTCGCTCGAGCACCCGTA 419
|||||
Db 361 GCGGTTCTTGAACCCCTTA 380

RESULT 20

US-11-055-637-90
; Sequence 90, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-90

Query Match 28.2%; Score 118.6; DB 14; Length 552;
Best Local Similarity 57.0%; Pred. No. 2.6e-21;
Matches 217; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGGCGCTCGTAGCGAGGGCTCGGCAACGTCGCGCGCGGTGCC 99
Db 1 GCGACTGACTTGGCAGGCTATGATCGCGAAGGCGCTTAAAAACGTAACCTGCGGGGCT 60
QY 100 AACCCGATGCTCTCAAGCGCGGCATCGAGAGGCGCTCGAGGCGCTCTCGGCGCCCTG 159
Db 61 AACCTGTCGCGGTGCGTAAGGATGTAAGCAAGCCGTGACTGTAGCAATCGAAAACTTA 120
QY 160 CTGGAGCAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGTTCCAGGCGCTCCATCTCC 219
Db 121 AAGAAATTTCTAAGCCGATCGAAGCAAGAGTCTATCGTCAAGTTGCTGCGATCTCT 180
QY 220 GCGCGCAGACCCAGATCGGAGCTCATCGCGAGGCGATGGAAGAAGTTCGGCAAGGAA 279
Db 181 GCTGCTGATGAGGAAGTCGGAAGCTTATCGCTGAAGCAATGGAGCGCGTAGGAACGAC 240
QY 280 GCGGTATCATCCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339

Db 241 GCGGTCATCACATCGAAGTCTAAGGTTTCACAACTGAGCTTGAAGTTGTTGAAGGT 300
QY 340 ATGCGCTTCGACAAGGCTACATCTCGGCGTACTTCGCCACCGACATGAGCGGATGGAG 399
Db 301 ATGCAATTCGACCGCGGATATGCGTCTCCTTACATGCTGACTCTGTATAAGATGGA 360
QY 400 GCGTCGCTCGAGCACCCGTCAC 420
Db 361 GCGGTTCTTGAACAATCCTTAC 381

RESULT 21

US-11-077-619-35
; Sequence 35, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Fesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2047)
; OTHER INFORMATION: grol
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1847)
US-11-077-619-35

Query Match 28.0%; Score 117.6; DB 11; Length 2047;
Best Local Similarity 56.7%; Pred. No. 4.3e-21;
Matches 238; Conservative 0; Mismatches 179; Indels 3; Gaps 1;
QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGCTTCTCGCCAGGCGCTC 63
Db 438 AAGCAAAACGACGTCGCGGCGACGGTACCACACTGCAACCGCTCTGGCTCAGGCTATC 497
QY 64 GTACGCGAGGCTCGCGCGCGGTCGCAACGTCGCGGTCGCAACCGGTCCTCAAGCGCGC 123
Db 498 ATCACTGAAGGTCTGAAGCTGTTGTCGCGGGCATGAACCCGATGACCTGGAACGTTGT 557
QY 124 ATCGAAGGCGCTCGAGGCGGCTCTCGGCGCGCTCTCGGCGAGGCGGAAGGATGTCGAG 183
Db 558 ATCGAAGGCGGTTACCGCTGCGTGTGAAGAACTGAAGCGGCTGTCCGATCATGCTCT 617
QY 184 ACCAAGAGCAGATCGCTTCCACGCGCTCCATCTCGCG-----CGCGGACACCCAGATCGGC 240
Db 618 GACTCTAAAGCGATTGCTCAGGTTGGTACCATCTCGGCTAACTCCGACGAAACCGTAGGT 677
QY 241 GAGCTCATCGCGGCGGATGGAAGGTCGCAAGGCGCAAGGCGTCATCACCGTCGAGGAG 300
Db 678 AACTGATCGCTGAAGCGATGGAAGTCCGTAAGAGGCGGTTATCACCGTTGAAGAC 737
QY 301 TCCAGACCTTCGCTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360

Db 738 GTTACCGTCTCGAGGAGCAACTGGAGCTGGTTGAAGGTATGACAGTTTCGACCGTGGCTAC 797
Qy 361 ATCTCGCGTACTTTCGCCACCGACATGGAGCGGATGAGCGCTCGCTCGACGACCGCTAC 420
Db 798 CTGTCTCTTACTTATCATCAACAGCCGGAACCTGGCGCAGTAGAACTGGAAACCCGCTTC 857

RESULT 22
US-11-055-637-87
; Sequence 87, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-87

Query Match 27.9%; Score 117; DB 14; Length 552;
Best Local Similarity 56.7%; Pred. No. 6.6e-21;
Matches 216; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

Qy 40 GCGACCGTTCGCGCCAGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGTGC 99
Db 1 GCAACAGTTCTTGGCGCAAGCAATGATCCGTGAAGGCTTAAAAACGTAACAGCGCGT 60
Qy 100 AACCGATGCTTCAAGCGCGGATCGAGAGGCGCTCGAGCGCTTCGCGCGCGCTG 159
Db 61 AACCTGTAGGCGTGGTAAAGGATGGAACAGCTGTAGCGTTCGATCGAATACTTA 120
Qy 160 CTGAGCAGCGAGGATCTCGAGCAAGGAGGAGTCTTCACGCGCTCCATCTCC 219
Db 121 AAGCAATTTCTAAGCAATCGAAGGCAAGAGTCTATCGCTCAGGTTGCTCGATCTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTTCGCAAGGAA 279
Db 181 GCTGCTGATGAGGAGTTCGAGGCTTATCGCTGAAGCAATGGAGCGGTAGAAACGAC 240
Qy 280 GCGCTCATCAGCTCGAGGAGTTCAGACCTTCGAGCTTGGAGCTGAGCTCAACGAGGT 339
Db 241 GCGGTTATCACAATCGAAGAGTCTAAAGGCTTCAACAATGAGCTTGAAGTGTGAAGT 300
Qy 340 ATGCGCTTCGACAGGCTTACATCTCGGCTACTTCGCGCAGCAGCATGGAGCGGATGAG 399
Db 301 ATGCAATTCGACCGCGGATATCGCTCTCTTACATGCTGACTGACTCTGATAAGATGAA 360
Qy 400 GCGTCTGCTCGACGACCGCTAC 420
Db 361 GCGGTTCTTGATATCTTAC 381

RESULT 23
US-11-055-637-92
; Sequence 92, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0

; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-92

Query Match 27.5%; Score 115.4; DB 14; Length 552;
Best Local Similarity 56.4%; Pred. No. 1.7e-20;
Matches 215; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

Qy 40 GCGACCGTTCGCGCCAGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGTGC 99
Db 1 GCGACTGTGTTGCACAGGCTATGATCCGCGAAGGCTTAAAAACGTAACGCGGAGCT 60
Qy 100 AACCGATGCTTCAAGCGCGGATCGAGAGGCGCTCGAGCGCTTCGCGCGCGCTG 159
Db 61 AATCTGTGCGCTGCGTAAAGGTATGGAACAAGCGCTAACCGTGCATTCGAAAACTTA 120
Qy 160 CTGAGCAGGCGAAGGATCTCGAGCAAGGAGGAGTCTTCACGCGCTCCATCTCC 219
Db 121 AAGCAATTTCTAAGCAATCGAAGGCAAGAGTCTATCGCTCAGGTTGCTCGAATCTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTTCGCAAGGAA 279
Db 181 GCTGCTGATGAGGAGTTCGAGGCTTATCGCTGAAGCAATGGAGCGGTAGAAACGAC 240
Qy 280 GCGCTCATCAGCTCGAGGAGTTCAGACCTTCGAGCTTGGAGCTGAGCTCAACGAGGT 339
Db 241 GCGGTTATCACAATCGAAGAGTCTAAAGGCTTCAACAATGAGCTTGAAGTGTGAAGT 300
Qy 340 ATGCGCTTCGACAGGCTTACATCTCGGCTACTTCGCGCAGCAGCATGGAGCGGATGAG 399
Db 301 ATGCAATTCGACCGCGGATATCGCTCTCTTACATGCTGACTGACTCTGATAAGATGAA 360
Qy 400 GCGTCTGCTCGACGACCGCTAC 420
Db 361 GCGGTTCTTGATATCTTAC 381

RESULT 24
US-11-055-637-103
; Sequence 103, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 103
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-103

Query Match          27.2%; Score 114.4; DB 14; Length 552;
Best Local Similarity 56.3%; Pred. No. 3.1e-20;
Matches 214; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 40 GCGACCGTTCTCGCCAGGCGCTCGTACGCGAGGGCCCTGCGCAACGTCGCGCGCGGTGCC 99
DB 1 GCAACAGTTCTAGCGCAAGCAATGATCCGTGAAGGACTTAAAGAGTGTAGTGGTCTATTCT 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAGGCGCTGAGGCCGTCTCCGGCGCCCTG 159
DB 61 AACCCGTTGGCGTTTCGTAAGGGATCGAAGAGCAAGTGAAGTAGCAGCTTGAAGGCTTG 120
QY 160 CTGGAGCAGGCGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCC 219
DB 121 CAGGAGATTTCTAACAATCGAAGCAAGAATCAATTCCTCAAGTTGGTCTATTCT 180
QY 220 GCAGCGACACCCAGATCGCGAGCTCATCGCGAGCGCATGGAAGGTTCGCAAGGAA 279
DB 181 GCAGCAGATGAAGAAGTTGGAAGCCTGATCGCTGAAGCAATGAGCGTGTAGGTAAGCA 240
QY 280 GCGCTCATCCCGTCGAGGATCCAGACCTTCGGTCTGAGCTGAGCTCACCAGGGT 339
DB 241 GCGTGTATCACAATCGAAGAACTTAAAGGGTTTCAAACTGAGCTTGAAGGA 300
QY 340 ATGCGCTTCGACAAAGGCTACATCTCGGGTACTTCGCCACGACATGGAGCGGATGGAG 399
DB 301 ATGCGTTTGACCGCGGATATGCTTACCATAATGTCGCGATTCGATAAGATGGAA 360
QY 400 GCGTCTCGACGACCCCGTAC 420
DB 361 GCGGTTCTTGAATAATCCTTAC 381

RESULT 26
US-11-055-637-107
; Sequence 107, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-107

Query Match          25.3%; Score 106.4; DB 14; Length 553;
Best Local Similarity 55.0%; Pred. No. 3.5e-18;
Matches 209; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 40 GCGACCGTTCTCGCCAGGCGCTCGTACGCGAGGGCTTCGCAACGTCGCGCGCGGTGCC 99
DB 1 GCGAGTTCTAGCTCAAGCGATGATTCGTGAAGGTTCTTAAAGAGCAAGTGAAGTTCG 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAGGCGCTGAGGCCGTCTCCGGCGCCCTG 159
DB 61 AACCCAAATGGGTATCGCTAAGGGATTTGAAAAGCAACAGCTGCTGCGGTTCAGAACTT 120
QY 160 CTGGAGCAGGCGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCC 219
DB 121 AAAAATATTCGAAACCAATCGAAGGCAAGATCAATCGCAAGTTGGGCTAACTCA 180
QY 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGCGCATGGAAGGTTCGCAAGGAA 279
DB 40 GCGACCGTTCTCGCCAGGCGCTCGTACGCGAGGGCTTCGCAACGTCGCGCGCGGTGCC 99
```

```
; SEQ ID NO 103
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-103

Query Match          27.2%; Score 114.4; DB 14; Length 552;
Best Local Similarity 56.3%; Pred. No. 3.1e-20;
Matches 214; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 40 GCGACCGTTCTCGCCAGGCGCTCGTACGCGAGGGCCCTGCGCAACGTCGCGCGCGGTGCC 99
DB 1 GCAACAGTTCTAGCGCAAGCAATGATCCGTGAAGGACTTAAAGAGTGTAGTGGTCTATTCT 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAAGCGCTCGAGGCGCTTCGCGCGCGCTG 159
DB 61 AACCCGTTGGCGTTTCGTAAGGGATCGAAGAGCAAGTGAAGTAGCAGCTTGAAGGCTTG 120
QY 160 CTGGAGCAGGCGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCC 219
DB 121 CAAGAAATCTCCATGAATCGAAGGAAAGAGAGATTGCACAAGTCGCAATCTATTCT 180
QY 220 GCAGCGACACCCAGATCGCGAGCTCATCGCGAGGCGATGGAAGGTTCGCAAGGAA 279
DB 181 TCTGGAGCAGGAAGTTGGAAACTTATTGCTGAAGCAATGGAGCGGTTGGCAAGCAT 240
QY 280 GCGTCTCATCCCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAAGTTCACCGAGGT 339
DB 241 GGTGTCTATTACTATCGAAGTCAAAAGGCTTCAGACTGAAGTGTGTTGAAGGA 300
QY 340 ATGCGCTTCGACAAAGGCTACATCTCGGGTACTTCGCCACCGACATGGAGCGGATGGAG 399
DB 301 ATGCAATTTGACCGCGCTTATGCAATCGCATATGATGCAATGCGGATGATGCAAGGAA 360
QY 400 GCGTCTCGACGACCCCGTAC 419
DB 361 GCGTCTTGGACAAATCCGTA 380

RESULT 25
US-11-055-637-91
; Sequence 91, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-91

Query Match          25.6%; Score 107.4; DB 14; Length 552;
Best Local Similarity 55.1%; Pred. No. 2e-18;
Matches 210; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 40 GCGACCGTTCTCGCCAGGCGCTCGTACGCGAGGGCTTCGCAACGTCGCGCGCGGTGCC 99
```

Db 181 GCAGCTGACGAGGAGTTGGACAAATTTATCGCAGAGCAATGGAACGTGTGGAAAGCAC 240
QY 280 GGGGTCTATCCAGCTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGAGCTCAACCGAGGCT 339
Db 241 GGGGTATTACAAATCGAAGAAATCAAAAGGTTTCTCTACTGAAATTAGAAAGTAGTAGAGGT 300
QY 340 ATGGCTTTCGACAGGCTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTCGATCGTGGTTTCGTTTCTCCATACATGGTAACCGATTCTTGCAAAATGGA 360
QY 400 GCGTCGCTCGACGACCCGTA 419
Db 361 GCAGTCTTGAATAATCCATA 380

RESULT 27
US-11-201-916-7
; Sequence 7, Application US/11201916
; Publication No. US2006003992A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: STRPTOCACAL HEAT SHOCK PROTEINS OF THE
; TITLE OF INVENTION: HSP60 FAMILY
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/201,916
; FILING DATE: 11-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,737
; FILING DATE: 31-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 870109.408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1649
; US-11-201-916-7

Query Match 25.3%; Score 106.2; DB 11; Length 1661;
Best Local Similarity 53.5%; Pred. No. 3.7e-18;
Matches 222; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 4 AAGACGAGCAGCTCGCCGGTGAAGTACGACACCGGACCGGTTCTCGCCCGAGGCGTTC 63
Db 249 AAAACCAATGATTTGCTGTGTGATGGACGACTACTGCAACAGTTTGTGACACAAGCCATT 308
QY 64 GTACGGAGGGCTGGGCAACCTCGCCCGGTGCGCAACCCCGATGGCTCTCAAGCGCGC 123

Db 309 GTTCATGAAGGACTAAAAATGTGACAGCAGGTGTCTAAATCCAATTGGTATCCGTGAGGC 368
QY 124 ATCGAAGGCGCTCGAGGCGCTCTCCGGCGCCCTCTCGAGCAGCGAAGGATGTGCGAG 183
Db 369 ATTGAACAGCAACAGCAACAGCTGTGGAAGCTTTGAAAGCCATTGCTCACTGTATCT 428
QY 184 ACCAAGGACGATCGCTTCCAGCGCTTCCATCTCTCGCCCGCGACACCCAGATCGGCGAG 243
Db 429 GGCAGGAAGCTATTGCTCAGGTCTGAGTATCATCAGCTCTGAAAAAGTTGCGAGAG 488
QY 244 CTCATCGCGGCGGATGCAAGGTCCGCAAGGAGGCGTATCACTCGAGGAGTCC 303
Db 489 TATATCTCAGAAGCTATGAGCGGTGTGGCAACGATGGTGTGATTACCATCGAAGAAATCT 548
QY 304 CAGACCTTCGCTCTGGAGCTCGAGCTCACCGAGGCTATCGCTTCGCAACAGGCTACATC 363
Db 549 CGAGGTATGGAACAGAACTTGAAGTGTGGAAGCATGCAATTTGACCGTGGTTACCTG 608
QY 364 TCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCCGT 418
Db 609 TCTCAATACATGCTCAGACAAATGAAAAAATGGTTGCGAGACCTTGAAAAACCCAT 663

RESULT 28
US-11-055-637-95
; Sequence 95, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-3305
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
; US-11-055-637-95

Query Match 25.2%; Score 105.8; DB 14; Length 552;
Best Local Similarity 54.9%; Pred. No. 5.1e-18;
Matches 209; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 40 GCGACCGTTTCGCCCAGGCGCTGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db 1 GCAACAGTTTTAGCGCAAGCAATGATCCGCAAGGATTGAAAAACGTTACAGCTCGCGCT 60
QY 100 AACCGATGGCTCTCAACGCGGCGCATCGAAGGCGCGTTCGAGGCGCGTCTCCGGCGCCCTG 159
Db 61 AACCAATGGGCATCCGTAAGGTTTGAAGGTTTGAAGGCGGTCTGTGGCAGTAGAAGATTA 120
QY 160 CTGGAGCAGGCGAAGGATGTGAGACCAAGAGCAGATCGCTTCCACGCGCTTCACTCC 219
Db 121 AAAGCAATCTCAACCAATTTCAAGGTAAAGATCGATGTCTCAAGTTGCGAGCGATCTCT 180
QY 220 GCCCGCACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTCCGCAAGGAA 279
Db 181 GCGCTGAGGAAGATTGGTCAATTAATCGCAGAGCAATGGAACGCGTTGGCAACGAT 240
QY 280 GCGCTCATCAGCTCGAGGAGTCCAGACCTTTCGTTCTGGAGCTCGAGCTCAACGAGGT 339
Db 241 GGTGTATCATTAGAAGAAATCGAAGGCTTCGCAACGGAATTAGATGTTGTTCGAAGGT 300

340 ATGCGCTTCGACACGGGTACATCTCGCGGTACTTCGCCACCGGACATGGAGCCGATGGAG 399
301 ATGCAATTTGACCGGTGTTATGTCTCTCCATACATGATTCACAGATACAGAAAAATGGAA 360
400 GGTGCGCTCGACGCCCGGTAC 420
361 GCAGTGTGGAATAATCCATAC 381

RESULT 29

```

US-11-055-637-110
; Sequence 110, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-110

```

RESIST 30

RESULT 30
US-11-055-637-94
; Sequence 94, Application US/11055637

```

; Publication No. US20050260619A1
;
; GENERAL INFORMATION:
;
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DOUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
;
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
;
; FILE REFERENCE: 2139-330S
;
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
;
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
;
; NUMBER OF SEQ ID NOS: 114
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 94
;
; LENGTH: 552
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Probe for DNA array
;
; US-11-055-637-94

```

RESULT 31

RESULT 31
 US-10-793-626-789
 ; Sequence 789, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: P03480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 789
 ; LENGTH: 1620

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-789

Query Match      24.0%; Score 100.6; DB 8; Length 1620;
Best Local Similarity 52.5%; Pred. No. 1e-16;
Matches 220; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 1 AAGAGACGACGACGCTCGCGGTGACGCTACGACACCGCGACCGTCTCGCGCCGAGCG 60
   |||||
Db 232 AATAAACAAATGAATCGCTGGGACGCTACAACTACAGCAACAGTTTATAGCACAATCA 291
   |||||

QY 61 CTCGTACGCGAGGCGCTCGCAACGCTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
   |||||
Db 292 ATGATTACGAGGCTCTTAAGATGTTACAAAGTGTGCAATCTGTAGGCTTAAGACAA 351
   |||||

QY 121 GGCATCGAAGCGCTCGAGCGCTCTCGCGCGCGCTGTGAGCAGCGGCAAGGATGTC 180
   |||||
Db 352 GGTATTGACAAACGACGTGCAAGTGGCTATAGAAAGCGCTTCATGAGATTTCTCAAAAGGTT 411
   |||||

QY 181 GAGACCAAGGACGATCGCTTCCACGGCTTCCACGGCTTCCACGGCGCGACACCGAGTCGCG 240
   |||||
Db 412 GAAATAAAGAACGAGATAGCGCAAGTTGAGGCTATTTTCAGCAGCAGATGAAGAAATCGGT 471
   |||||

QY 241 GAGCTCATCGCCGAGCGATGACAGGTCGCGCAAGGAGCGCTCATCCGCTCGAGGAG 300
   |||||
Db 472 CGTACATTTCTGAGCAATGGATAAGTAGGTAAAGTGGCGGTATCACTATTGAAGAA 531
   |||||

QY 301 TCCACAGCTTCGGTCTGGAGCTGGAGCTCACCGAGGTAAGCGTTTCGACAGGCGCTAC 360
   |||||
Db 532 TCAATGGGTTTAAATACAGAAATAGAAAGTAGTTGAAAGGAATGCAATTTGATCGCGTTAT 591
   |||||

QY 361 ATCTCGCGTACTTCCGACCGACATGAGCGGATGAGGCGTGCCTCGACGACCGGTA 419
   |||||
Db 592 CAATCACCATATATGTAATGTAAGTCACTCAGATAAAATGATAGCTGAATTAGAAGCTCCATA 650
   |||||

RESULT 32
US-10-793-626-3883/c
; Sequence 3883, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3883
; LENGTH: 3885
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3883

Query Match      24.0%; Score 100.6; DB 8; Length 3885;
Best Local Similarity 52.5%; Pred. No. 9.8e-17;
Matches 220; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 1 AAGAGACGACGACGCTCGCGGTGACGCTACGACACCGCGACCGTCTCGCGCCGAGCG 60
   |||||
Db 2639 AATAAACAAATGAATCGCTGGGACGCTACAACTACAGCAACAGTTTATAGCACAATCA 2580
   |||||

QY 61 CTCGTACGCGAGGCGCTCGCGCAACGCTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
   |||||
```

```
Db 2579 ATGATTACGAAAGGCTTTAAGAAATGTTACAAGTGTGCAAAATCCTGTAGGCTTAAGACAA 2520
QY 121 GGCATCGAAGCGCGTTCGAGCGCTCTCCGCGCGCTCTCGAGCAGCGAAGGATGTC 180
   |||||
Db 2519 GGTATTGACAAAGCAGTGCAGTGGCTATAGAAGCGCTTCATGAGATTTCTCAAAAGGTT 2460
   |||||

QY 181 GAGACCAAGGACGATCGCTTCCACGGCTTCATCTCCGCGCGACACCGAGATCGGC 240
   |||||
Db 2459 GAAATAAAGAACGAGATAGCGCAAGTTGGAGCTATTTTCAGCAGCAGATGAAGAAATCGGT 2400
   |||||

QY 241 GAGCTCATCGCCGAGCGATGACAGGTCGCGCAAGGAGGCGTCTATCAACCGCTCGAGGAG 300
   |||||
Db 2399 CGGTACATTTCTGAAGCAATGATGAAGTAGGTAAAGTGGCGTTATCTACTATTGAAGAA 2340
   |||||

QY 301 TCCACAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
   |||||
Db 2339 TCAATGGGTTTAATACAGAAATAGAGTAGTTGAAGGAATGCAATTTGATCGCGTTAT 2280
   |||||

QY 361 ATCTCGCGGCTACTTCCGCCACCGACATGAGGCGGATGAGGCGTGCCTCGACGACCGGTA 419
   |||||
Db 2279 CAATCACCATATATGTTAACTGACTCAGATAAAATGATAGCTGAATTTAGAAGCTCCATA 2221
   |||||

RESULT 33
US-11-055-637-105
; Sequence 105, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jaron
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-330S
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-105

Query Match      23.8%; Score 100; DB 14; Length 552;
Best Local Similarity 53.9%; Pred. No. 1.6e-16;
Matches 205; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTCGCGCAACGCTCGCGCCGCGTCC 99
   |||||
Db 1 GCTACTGTCTTGCAACAAGCTATGATTCGTGAAGCGCTGAAAAACGTAACGCGCTCGCGCG 60
   |||||

QY 100 AACCCGATGGTCTCAAGCGCGGATCGAAGAGCGCTCGAGGCGCTCTCGCGCGCGCTG 159
   |||||
Db 61 AATCCTATGGGCAATTCGTAAGGGGATTCGAAAAAGCTGTGAAGCTGCAATTAGTGAGTTA 120
   |||||

QY 160 CTGGAGCAGGCGAAGGATGTCGAGACCAAGAGCAGATCGCTTCCACCGCTTCCATCTCC 219
   |||||
Db 121 CAAGCTATCTTAACCAATCGAAACAAAGAGTCTATTGACAAAGTTGACAGCAATCTCA 180
   |||||

QY 220 GCGCGCAGCACCGCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTCGCGCAAGGAA 279
   |||||
Db 181 GCTTCTGACGAGAGTGGTCAATTAATTCGTGAAGCAATGGAACGCGTTGCGCAACGAC 240
   |||||

QY 280 GCGCTCATCGCTCGAGGAGTCCAGACCTTCGCTCGTGGAGCTGGAGCTCAACGAGGT 339
   |||||
Db 241 GGTGTTATCACAATTTGAAGAGTCTAAAGGATTTCTCAACTGAATTTGAGCGTAGTAGAGGT 300
   |||||
```


; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-112

Query Match 21.7%; Score 91; DB 14; Length 552;

Best Local Similarity 52.5%; Pred. No. 3.3e-14;

Matches 199; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 40 GCGACGGTTCGCGCCAGGCGCTCGTACGCGAGGGCGCTGCGCAAGCTGCGCGCGGTGCC 99

DB 1 GCAACAGTTTGGACACAAGCCATTGTTTCATGAGGACTTAAATAATGTGACAGAGTGCT 60

QY 100 AACCGGATGCTCTCAAGCGCGGATCGAAGAGCGCGTCAAGCGCGTTCGCGCGCGCTG 159

DB 61 AATCCAAATTGGTATCCGTCGAGGCAATTGAAACAGCAACAGCAACAGCGCTTGAAGCCTTG 120

QY 160 CTGGAGCAGCGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCC 219

DB 121 AAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCTATTGCTCAGGTGCGTCGAGTATCA 180

QY 220 GCGCGCGACACCCAGATCGCGGAGCTCATCGCGAGCGGATGCAAGGTTCGCAAGGAA 279

DB 181 TCAGGCTCTGAAAAGTTGAGAGTATATCTGAGAGCTATGAGGCGTGTGGCAACGAT 240

QY 280 GCGGTATCATCCGTCGAGGAGTCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGT 339

DB 241 GGTGTGATTACCATCGAAGAACTTCGAGGATGATGAAAACAGAACTTGAAGTGGTTGAAGGC 300

QY 340 ATGCGGTTGCAAGGCTACATCTCGGCTACTTCGCCACCGACATGAGGCGGATGGAG 399

DB 301 ATGCAATTTGACCGTGTACCTGTCTCAATACATGCTCACAGACAATGAAAAATGGTT 360

QY 400 GCGTCGCTCGACACCGT 418

DB 361 GCAGACCTTGAAACCCAT 379

RESULT 47

US-11-055-637-97

; Sequence 97, Application US/11055637

; Publication No. US20050260619A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason

; APPLICANT: EDGE, Tom

; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.

; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND

; FILE REFERENCE: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES

; CURRENT APPLICATION NUMBER: US/11/055,637

; PRIOR FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: US 60/543,288

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 97

; LENGTH: 552

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-97

Query Match 21.5%; Score 90.4; DB 14; Length 552;

Best Local Similarity 52.4%; Pred. No. 4.7e-14;

Matches 199; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 40 GCGACGGTTCGCGCCAGGCGCTCGTACGCGAGGGCGCTGCGCAAGCTGCGCGCGGTGCC 99

DB 1 GCAACTGTATTAGCGCAAGCTATGATCTCGTGAAGGTCTTTAAANACGATACAGCTGCTGCT 60

Db 241 GCGCTTATTACTTTAGAGAGTCTAAAGGATTCACAAGATTAGACGTAGTAGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCGTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGATCGTGATATGCATCTCCTTACATGATTACTGATCTCTGACAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTTCTTGATAACCCATAC 381

RESULT 49

US-11-055-637-86
; Sequence 86, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-86

Query Match 21.4%; Score 89.8; DB 14; Length 552;
Best Local Similarity 52.2%; Pred. No. 6.7e-14;
Matches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 40 GCGACCGTTCGCGCCGAGGCGCTCGTAGCGGAGGCGCTGCGCAACGCTCGCGCGCGGTGCC 99
Db 1 GCAACTGTATTAGCGCAAGCTATGATTCGTGAAGGTCTTAAACACGTAACAGCTGGTGGC 60
Qy 100 AACCCGATGGTCTCAAGCGCGCATCGAGAAGCGCGTTCGAGGCGGTCTCCGCGCGCGCTG 159
Db 61 AACCAATGGTCTTCGTAAGGTATCGAAAAGCTGTACTGCTGCAATTGAAGATTA 120
Qy 160 CTGGAGCAGCGAAGGATGTGAGACCAAGGCGATCGCTTCCACGGCTCCATCTCC 219
Qy 220 GCCGCCGACACCGAGATCGGAGCTCATCGCGAGCGATCGCAAGGTTCGCGCAAGGAA 279
Db 181 GCTGCTGACGAAGTAGTGTCAATTAATCGTGAAGGTCTTAAACACGTAACAGCTGGTGGC 240
Qy 280 GCGCTCATCCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 121 AAAACGATTTCTAAACCAATCGAAGGTAAATCTTATCGCAAGTAGCTGCTATTCT 180
Qy 220 GCCGCCGACACCGAGATCGGAGCTCATCGCGAGCGATCGCAAGGTTCGCGCAAGGAA 279
Db 181 GCTGCTGACGAAGTAGTGTCAATTAATCGTGAAGGTCTTAAACACGTAACAGCTGGTGGC 240
Qy 280 GCGCTCATCCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GCGCTTATTACTTTAGAGAGTCTAAAGGATTCACAAGATTAGATGTAGTAGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCGTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGATCGTGATATGCATCTCCTTACATGATTACTGATCTCTGACAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTTCTTGATAACCCATAC 381

RESULT 50

US-11-055-637-93
; Sequence 93, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-93

Query Match 21.4%; Score 89.8; DB 14; Length 552;
Best Local Similarity 52.2%; Pred. No. 6.7e-14;
Matches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 40 GCGACCGTTCGCGCCGAGGCGCTCGTAGCGGAGGCGCTGCGCAACGCTCGCGCGCGGTGCC 99
Db 1 GCAACTGTATTAGCGCAAGCTATGATTCGTGAAGGTCTTAAACACGTAACAGCTGGTGGC 60
Qy 100 AACCCGATGGTCTCAAGCGCGCATCGAGAAGCGCGTTCGAGGCGGTCTCCGCGCGCGCTG 159
Db 61 AACCAATGGTCTTCGTAAGGTATCGAAAAGCTGTAGTTGCTGCAGTAGAAGATTA 120
Qy 160 CTGGAGCAGCGAAGGATGTGAGACCAAGGCGATCGCTTCCACGGCTCCATCTCC 219
Db 121 AAAACGATTTCTAAACCAATCGAAGGTAAATCTTCAATCGCAAGTAGCTGCTATTCT 180
Qy 220 GCCGCCGACACCGAGATCGGAGCTCATCGCGAGCGATCGCAAGGTTCGCGCAAGGAA 279
Db 181 GCGCTGACGAAGTAGTGTCAATTAATCGTGAAGCATGGAGCGCGTGGTAGACGAC 240
Qy 280 GCGCTCATCCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GCGCTTATTACTTTAGAGAGTCTAAAGGATTCACAAGATTAGATGTAGTAGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCGTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGATCGTGATATGCATCTCCTTACATGATTACTGATCTCTGACAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTTCTTGATAACCCATAC 381

RESULT 51

US-11-055-637-106
; Sequence 106, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637

```
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-106

Query Match      21.0%; Score 88.2; DB 14; Length 552;
Best Local Similarity 52.0%; Pred. No. 1.7e-13;
Matches 198; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 40 GCGACGGTCTCGCCAGGCGCTCGTAGCGGGGCTGGCAACCTCGCGCGGTC 99
DB 1 GCAACTGTATTACGCGCAAGCTATGATTCGTGAAGGCTTTAAACCGTAACAGCTGGTGA 60

QY 100 AACCCGATGCTCTCAAGCGCGGCATCGAAGCGCGTGGAGCGCTCTCGCGCGCCCTG 159
DB 61 AACCCATGGCTCTCGTAAGGTATCGAAGAGCTGTACTGCTGCAATTGAAGATT 120

QY 160 CTGAGAGCGGGAAGGATGTGAGACCAAGAGCAGATCGCTTCCAGCGCTCCATCTCC 219
DB 121 AAAGCGATTCTTAACCAATCGAAGGTAATCTTATCGCAAGTAGCTGCTATTTCT 180

QY 220 GCGCGGACACCCAGATCGCGAGCTCATCGCGAGGCGATGGAAGTTCGCGAAGAA 279
DB 181 TCGGCTGAGCAAGAGTAGTCAATTAATCGTGAAGCAATGAGCGCTTGGTAACGAC 240

QY 280 GCGCTCATACCGTCTGAGAGTCCAGACCTTCGGTCTCGAGCTGAGCTCACCGAGGT 339
DB 241 GCGCTTATTCTTAGAGAGTCAAGAGATTCAAGAGATTAGACGTAGTAGAGT 300

QY 340 ATGCGCTTCGCAAGGGCTACATCTCGGCTACTTCGCCACCGACATGAGCGGATGGAG 399
DB 301 ATGCAATTTGATCGTGGATGTCATCTCTTACATGATTACTGATTCTGCACAAATGGAA 360

QY 400 GCGTCTGACGACCCGCTAC 420
DB 361 GCAGTTCTTGATAACCCATAC 381
```

RESULT 52

```
US-11-000-688-1372
; Sequence 1372, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUTGATTE, Remi
; APPLICANT: BIRBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1372
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc feature
; LOCATION: (1)..(2258)
; OTHER INFORMATION: heat shock 60kda protein 1
; OTHER INFORMATION: (chaperonin) (HSPd1) gene.
```

```
Query Match      19.8%; Score 83.2; DB 14; Length 552;
Best Local Similarity 51.6%; Pred. No. 3.3e-12;
Matches 190; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 46 GTTCTCGCCCGGCGCTCGTAGCGGAGGCTCGGCAACGTCGCGCGGTCGCCAACCG 105
DB 7 GTTCTTCGCAAGGTTTTATTGCTGAGGCTGCAAGGTGGTGGCTGCTGGTCAACCT 66

QY 106 ATGGCTCTCAAGCGCGGCGATCGAAGCGCTCGAGGCGCTCTCGGCGCCCTGCTGGAG 165
DB 67 GTATTGATCACTAGAGGCAATTGAGAAAGAGGCTTTGGTAGCGGAGCTCAAGAAA 126
```

US-11-000-688-1372

```
Query Match      20.8%; Score 87.4; DB 14; Length 2258;
Best Local Similarity 53.8%; Pred. No. 2.5e-13;
Matches 203; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGTCGCCGCTGACCGGTACGACACCGCGACCGCTTCTCGCCCGGCG 60
DB 363 AATAACACAAATGAAGAAGCTGGGATGGCACTACCACTGCTACTGTACTGGCAGCTCT 422

QY 61 CTCGTACCGGAGGCGCTGGCAACCTCGCGCGCGGTGCGCAACCGCGATGCTCTCAAGCG 120
DB 423 ATAGCCAAAGGAAGGCTTCGAGAAGATTAGCAAAAGGTGCTAAATCCAGTGGAAATCAGGAGA 482

QY 121 GGCATCGAAGAGCGGCTCGAGGCGCTTCCGCGCGCTTCAAGGCTTAACTTAAAGCGATGTC 180
DB 483 GGTGTGATGTAGCTGTTGATGCTGTATTTGCTGAACCTTAAAGAGCGATCTAACTCTGTG 542

QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGC---CGCCGACACCCAGATC 237
DB 543 ACCACCCCTGAAGAAATTCACAGGTTGCTACGATTTCTGCAACCGAGACAAAGAAAT 602

QY 238 GCGGAGCTCATCGCGAGCGGATGCAAGAGTGGCAAGGAGGCTCATCAAGCTCGAG 297
DB 603 GGCATATATCATCTCTGATGCAATGAAGGTTGGAAGAAAGGTTGTCATCAAGTAAAG 662

QY 298 GAGTCCCGAGACCTTCGGTCTGAGGCTGAGCTCACGAGGGTATCGCTTCGACAAAGGC 357
DB 663 GATGGAAGAAACACTGATGATTAAGAAATTTTGAAGCGATGAAGTTGATCGAGGC 722

QY 358 TACATCTCGGCTACTT 374
DB 723 TATATTTCTCCATCTT 739
```

RESULT 53

```
US-11-055-637-114
; Sequence 114, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-114
```

```
Query Match      19.8%; Score 83.2; DB 14; Length 552;
Best Local Similarity 51.6%; Pred. No. 3.3e-12;
Matches 190; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 46 GTTCTCGCCCGGCGCTCGTAGCGGAGGCTCGGCAACGTCGCGCGGTCGCCAACCG 105
DB 7 GTTCTTCGCAAGGTTTTATTGCTGAGGCTGCAAGGTGGTGGCTGCTGGTCAACCT 66

QY 106 ATGGCTCTCAAGCGCGGCGATCGAAGCGCTCGAGGCGCTCTCGGCGCCCTGCTGGAG 165
DB 67 GTATTGATCACTAGAGGCAATTGAGAAAGAGGCTTTGGTAGCGGAGCTCAAGAAA 126
```

166 CAGCGCAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCC 225
127 ATGCTAAGGAGTTGAAGACAGTGTGCGAGTGTGCGCGGTAGTGCCTGCTAAC 186
226 GACACCCAGATCGCGAGCTATCGCGAGCGGATGACCAAGGTGCGCAAGGAGGCTC 285
187 AATGCAAGAAATGGAAGCATGTTGCTGAAGCAATGAGCAGAGTGGCGCAGGAGGTG 246
286 ATCACCGTCGAGGAGTCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGC 345
247 GTGACACTTGAGGAGGTTAAAGTGCAGAGACGCTCTTACGTGTGGAGGAATGCAA 306
346 TTGCAACAAGGCTACATCTCGGCTACTTCGCCACCGACATGAGCGGATGGAGGCGTCG 405
307 TTTGATCGAGTTATGTTCTCCCTTACTTTTGTGACAGACGCGAGAAATGTCAGTTGAG 366
406 CTCGACGA 413
367 TTCGACAA 374

RESULT 54
US-10-932-182A-4757
; Sequence 4757, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4757
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (659)..(659)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-10-932-182A-4757

Query Match 19.2%; Score 80.8; DB 9; Length 684;
Best Local Similarity 52.8%; Pred. No. 1.4e-11;
Matches 197; Conservative 0; Mismatches 173; Indels 3; Gaps 1;

4 AAGACGGACGACGTGCGCGGTGACGCTACGACCAACCGGACCGTCTCGCCGCGCTC 63
301 AAAACCAATGAAGTGTGCGCGGTGATGTTACTTCTGCACTGTCTTGGGTAGAGCCATT 360

64 GTACCGGAGGCGCTGCGCAAGCTGCGCGGTGCGGTCGCGGTCGCGGTCCTCAAGCGCGGC 123
361 TTCACTGAATCTGTAAAGAACGTCGCTGCGAGGCTGTAAACCAATGAGTGTGAGAGGGGT 420

124 ATCGAGAAAGCGCTGCGCAAGCTGCGCGGTGCGGTCGCGGTCGCGGTCGCGGTCGAG 183
361 TTCACTGAATCTGTAAAGAACGTCGCTGCGAGGCTGTAAACCAATGAGTGTGAGAGGGGT 420

124 ATCGAGAAAGCGCTGCGGCGCTCTCGCGGCGCTGCGGTCGCGGTCGCGGTCGAG 183
421 ACCAGGTGCGGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGAG 480

184 ACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
421 ACCAGGTGCGGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGAG 480

184 ACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
481 ACATCCGAGAAATGCTCAAGTAGCAACCATTTCTGTAACGGGATTTCTATGTTGGT 540

241 GAGCTCATTCGCGGAGGATGGAACAAGGTGCGCAAGGAGGCGCTCATCCGTCGAGGAG 300
541 AAATTTGCTAGCTTACGCAATGGAAGGTTGGTAAAGAGGTGTATCACTATCAGAGAA 600

301 TCCGAGACCTTTCGCTGAGGTCGAGCTCACCGAGGTCGCTTTCGACCAAGGGCTAC 360

601 GGTAGAACGTTGGAAGATGAATGAACTAGAACTGACTGACGCTATGAGATTCGACCGGTGTTNT 660

361 ATCTCGCGCTACT 373
661 ATCTCTCCCTATT 673

RESULT 56

US-11-000-688-1371
; Sequence 1371, Application US/11000688
; Publication No. US2005028754A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois

QY 259 ATGGACAGGTCGCGAAGGAGCGTTCATCACCGTCGAGGAGTCCGAGACCTTCGGTCTG 318
Db 297 ATGAAAAAGTTTGGAGAAAGGGCATCATCACAGTAAGGATGGAAAAACACTGACTGAT 356
QY 319 GAGCTGAGGCTCACCGAGGGTATG 342
Db 357 GAATTAGAAATTATTGAAGGCATG 380

RESULT 59

US-10-301-480-917831
; Sequence 917831, Application US/10301480
; Publication No. US2006005756A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917831
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-917831

Query Match 13.5%; Score 56.8; DB 10; Length 556;
Best Local Similarity 50.6%; Pred. No. 2.1e-05;
Matches 164; Conservative 0; Mismatches 157; Indels 3; Gaps 1;
QY 22 GGTGACGGTAGCACCGGACCGTTCGTCGCCAGCGGCTCGTACCGAGGGCGCTGGCG 81
Db 57 GGGATGGCACTATCACTGCTGTGTAATGCTCTATTTCCAAATAAGCCCTCCAG 116
QY 82 AACCTCGCGCGGTGCCAACCCGATGCTCTCAAGCGCGCATCGAGAGGGCGCTCGAG 141
Db 117 AAGTTAGCAAGGTGCTAATCCAGTGGAAATCAAGAGAGGTGTGATGTAGCTGTGAT 176
QY 142 GCCGTCTCCGCGCCCTGCTGGACGCGGAGGATGTCCGACCAAGGAGCGATCGCT 201
Db 177 GCTGTAATTGTAACCTTAAAGACAGTCTAAACCTGTGACCAAACTGAAGAAATTGCA 236
QY 202 TCCACGGCTCCATCTCCGCC---GCCGACACCCAGATCGCGAGCTCATCGCGAGCG 258
Db 237 CAGTTGCTACAAATTTCTGCAATGGAGACAAAGAAATTGGTAACATCATCTCTGATGCA 296
QY 259 ATGGACAAGGTCCGCAAGGAGCGTTCATCACCGTCGAGGAGTCCGAGACCTTCGGTCTG 318
Db 297 ATGAAAAAGTTTGGAGAAAGGGCATCATCACAGTAAGGATGGAAAAACACTGACTGAT 356
QY 319 GAGCTGAGGCTCACCGAGGGTATG 342
Db 357 GAATTAGAAATTATTGAAGGCATG 380

RESULT 60

US-09-925-065A-218359
; Sequence 218359, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218359
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-218359

Query Match 13.5%; Score 56.8; DB 6; Length 561;
Best Local Similarity 50.6%; Pred. No. 2.1e-05;
Matches 164; Conservative 0; Mismatches 157; Indels 3; Gaps 1;
QY 22 GGTGACGGTAGCACCGGACCGTTCGTCGCCAGCGGCTCGTACCGAGGGCGCTGGCG 81
Db 57 GGGATGGCACTATCACTGCTGTGTAATGCTCTATTTCCAAATAAGCCCTCCAG 116
QY 82 AACCTCGCGCGGTGCCAACCCGATGCTCTCAAGCGCGCATCGAGAGGGCGCTCGAG 141
Db 117 AAGTTAGCAAGGTGCTAATCCAGTGGAAATCAAGAGAGGTGTGATGTAGCTGTGAT 176
QY 142 GCCGTCTCCGCGCCCTGCTGGAGCAGCGGAGGATGTCCGACCAAGGAGCGATCGCT 201
Db 177 GCTGTAATTGCTGAACCTTAAAGACAGTCTTAACCTGTGACCAAACTGAAGAAATTGCA 236
QY 202 TCCACGGCTCCATCTCCGCC---GCCGACACCCAGATCGCGAGCTCATCGCGAGCG 258
Db 237 CAGTTGCTACAAATTTCTGCAATGGAGACAAAGAAATTGGTAACATCATCTCTGATGCA 296
QY 259 ATGGACAAGGTCCGCAAGGAGCGTTCATCACCGTCGAGGAGTCCGAGACCTTCGGTCTG 318
Db 297 ATGAAAAAGTTTGGAGAAAGGGCATCATCACAGTAAGGATGGAAAAACACTGACTGAT 356
QY 319 GAGCTGAGGCTCACCGAGGGTATG 342
Db 357 GAATTAGAAATTATTGAAGGCATG 380

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